FOOT AND HINDLIMB MORPHOLOGY, SOFT TISSUES, AND TRACEMAKING BEHAVIORS OF EARLY CRETACEOUS BIRDS FROM CHINA AND THE REPUBLIC OF KOREA WITH A COMPARISON TO MODERN AVIAN MORPHOLOGY AND BEHAVIOR

BY

AMANDA RENEE FALK

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Co-Chair Stephen T. Hasiotis

Co-Chair David A. Burnham

Paul Selden

J. Fredrick Devlin

David E. Alexander

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The Dissertation Committee for AMANDA RENEE FALK
certifies that this is the approved version of the following dissertation:

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Co-Chairperson: Stephen T. Hasiotis

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Co-Chairperson: David A. Burnham

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ABSTRACT

The avifauna of the Early Cretaceous is composed of a unique combination of primitive and derived forms. Primitive birds with long tails are found preserved in the same strata as modern-type ornithurine birds, the primitive, beaked confuciusornithids, a unique side branch of Aves, and the diverse but extinct enantiornithines. There have been few studies on the trace fossils they produce, detailed reconstruction of soft tissues, or the morphology of their feet and hindlimbs. Furthermore, there are few studies of modern bird feet and hindlimbs for comparison. This dissertation examines bird tracks from the Lower Cretaceous Haman Formation of the Republic of Korea, avian body fossils from the Lower Cretaceous Jehol Group in northeastern China, and the feet and hindlimbs of modern birds for comparison with Early Cretaceous avian fossils. Also studied are the effects of sediment grain size and media water content on the production of traces (i.e., track morphology and bird behavior) by the domestic chicken (*Gallus gallus*) and Mourning Doves (*Zenaida macrocura*).

Early Cretaceous ornithurine avian behavior was already strikingly advanced and included multiple types of feeding behaviors identical to those performed by modern birds. The ichnodiversity of ornithurines was much higher than the body fossil record suggests. Retrodicting what types of tracks certain types of fossil birds would have produced is possible due to a nonsignificant difference (p-value > 0.05) between the soft-tissue toe length and the osteological toe length in birds. Toe width is significantly different, however, neoichnological experiments show that toe width is strongly influenced by media consistency and, therefore, is not a reliable measurement in avian ichnology. The hindlimb of birds has clearly shifted through time with function, as the femur contributed less to hindlimb motion. Under laser fluorescence, *Confuciusornis* is shown to have possessed soft tissues identical to modern birds, and the primary and secondary feather morphology is much rounder than previously interpreted. Neoichnological studies further support the early evolution of modern avian behavior and erect quantification criteria for modern and ancient bird behaviors. This dissertation represents important progress in our understanding of how avian foot morphology and behavior has evolved through time.

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INTRODUCTION

The study of avian fossils encompasses a large field, from body fossils—especially those of the Lower Cretaceous Jehol Group in northeastern China—to trace fossils (tracks, trackways, feeding traces, and associated nonfeeding traces). Comprehensive overviews of both of these types of evidence have been performed separately by experts in avian paleontology (e.g., Zhou and Zhang, 2007; Li et al., 2010; Zhou and Wang, 2010; Lockley and Harris, 2010). The areas of study of avian fossil evidence have remained largely disparate from each other. With respect to modern birds, only a handful of studies have examined behavior through trace production (e.g., Cadhee, 1990), and fewer still have compared modern traces directly to fossil traces (e.g., Genise et al., 2009). Furthermore, studies that directly compare modern and ancient avian foot morphology to tracks have not been performed. The purpose of this dissertation is to: 1) perform behavioral analyses on fossil bird tracks from Lower Cretaceous rocks; 2) correlate osteology with soft tissue of modern bird feet to establish criteria for retrodicting soft tissue morphology in avian fossils; 3) examine the hind limb morphologies of fossil and modern birds to record differences through time and reconstruct life habitat; 4) reconstruct soft tissue and life habitat of the fossil bird *Confuciusornis*; and 5) observe and quantify behaviors and trace morphologies produced by domestic chickens (*Gallus gallus*) in various media. These five goals will lay a foundation from which further study into this relatively open area of avian paleontology can occur.

This study covers both modern and fossil birds. Modern ornithological material from the University of Kansas Ornithology Collections and the University of Ornithology Collections were used. Modern birds were observed in controlled and uncontrolled outdoor environments in Lawrence, Kansas, and Milan, Michigan, USA. Avian body fossil material used in this study is from China—specifically the Liaoning and Gansu provinces—and trace fossil material is from

China and the Republic of Korea. The geological formations that yielded fossils are the Lower Cretaceous Jehol Group and the Lower Cretaceous Xiaogou Formation from China, and the Lower Cretaceous Haman Formation of Korea.

The Lower Cretaceous Jehol Group is a series of fluvial and lacustrine volcanic and volcaniclastic deposits, with some lacustrine limestone (Jiang and Sha, 2006). These lacustrine deposits formed in lake basins that formed from drop-down blocks during faulting (Wang et al., 2009). Whether the sediments were deposited in one single large lake basin or several small basins has not been agreed upon. The Jehol Group is comprised of the Yixian, Jiufotang, and the Fuxin formations (Jiang and Sha, 2006). The Jehol Biota—the exceptionally preserved vertebrate and invertebrate fossils found in the Jehol Group—come from the Yixian and Jiufotang Formation (Chang et al., 2009). Originally, the Jehol Group was identified as Late Jurassic in age (Chen, 2003), however, more recent studies using high-precision Ar40/Ar39 radiometric dating suggest an age of 129.7 mya at the base of the Yixian Formation, and 122.1 mya for the base of the Jiufotang Formation, placing these formations in the Barremian–Aptian ages of the Lower Cretaceous (Chang et al, 2009).

The Lower Cretaceous Haman Formation has been interpreted as a series of fluvial deposits consisting of mainly purplish mudstones and beds of fine- to medium-grained sandstone, often with mud drapes (Choi, 1986). The Haman Formation is known for trace fossils—no body fossils are known from the Haman Formation (Lee, 2003). It is part of the Hayang Group within the large Early to Late Cretaceous Gyeongsang basin, a large down-drop transitional (forearc to intra-arc) basin (Lee and Lee, 2000). The Haman Formation has been interpreted as Aptian-Albian ("late-middle" Cretaceous) based on palynology studies (Kimura, 2000). The Hayang Group itself contains numerous volcanic beds, although none have been strictly assigned to the

Haman Formation. The Kusandong Tuff (and, therefore, the near synchronous Haman Andesite) appears to overlie or incise into the Haman Formation and likely represents a large lahar deposit (Chang et al., 2003). The Kusandong Tuff has been dated to ~113.6 mya using U-Pb dating, and paleomagnetic studies support a late Aptian age (Chang, et al., 2003).

The very first named avian ichnogenus is *Ignotornis mcconnellii*, from the Cretaceous Dakota Formation of Colorado (Mehl, 1931). This tracksite had many tracks and well-preserved trackways; recently, even more have been discovered in the same area (Lockley et al. 2009). The second named ichnogenus is from the Lower Cretaceous Haman Formation in South Korea, *Koreanaornis* (Kim, 1969). This paper, however, was largely ignored and is still very obscure today. The third named ichnogenus is *Aquatilavipes* from the Lower Cretaceous Gething Formation of Canada (Currie, 1981). Since that time, the study and classification of fossil bird tracks has intensified (for a summary see Lockley and Harris, 2010).

Within the past twenty years there has been a phenomenal increase in the number of avian tracks discovered—especially those from Mesozoic strata. The majority of these tracks have been found in East Asia (Lockley et al., 1992, 2006a, 2006b; Lim et al., 2000, 2002; Azuma et al., 2002; Li et al., 2002; Li et al. 2005; Kim et al., 2006; Matsukawa et al., 2006; Li et al., 2009; Xing et al., 2011). There have also been significant discoveries within North and South America as well (e.g., Coria et al., 2002; Anfinson et al., 2009; Lockley et al., 2009; Fiorillo et al., 2011).

There has been a significant divide between researchers of Cenozoic and Mesozoic avian tracks. Cenozoic avian track research developed mainly in Europe, whereas research on Mesozoic avin tracks developed mainly in North America (Lockley and Harris, 2010). As such, there is still a significant divide within the discipline of avian ichnology; for example there is little to no overlap between Mesozoic and Cenozoic ichnogenera. There is also a significant divide between those who study modern birds—ornithologists—and ichnologists who study fossil bird tracks, which has resulted in a relative dearth of papers on modern bird tracks. Only a handful of examples have been published on modern bird tracks (Swennen and van der Baan, 1959; Cadhee, 1990; Genise et al., 2009; Melchor et al., 2012), and only one provides data alongside images of the tracks and trackways (Melchor et al., 2012). The majority of information on modern bird tracks is found in track identification field guides (e.g., Elbroch and Marks, 2001; Brown et al., 2003). This leads to the assumption that avian behavior can only be accurately assessed through direct observation and, therefore, fossil avian behavior is more difficult to ascertain. In fact, many modern avian traces are found long after the bird has produced them, and the tracemaker and tracemaking behavior must be retrodicted from no more information than would be found preserved in a fossil tracksite.

The concept of connecting a tracemaker to a trace has not been a core concept in most of ichnology (Bromley, 1996; Ekdale et al., 1984). One organism can leave multiple types of traces, or multiple organisms can leave similar-looking traces, which may prevent accurate identification of a tracemaker (Ekdale, 1984). The process for naming trace fossils also prohibits naming a trace fossil after its supposed producer, and the identity of the producer of the trace fossil should not enter into the erection of a new ichnotaxon (Bertling et al., 2006). Tracemakers have only been firmly established as trace producers in the rare instance when they have been discovered inside or at the end of the trace they have produced, such as in Solnhofen horseshoe crabs (Lomax and Racay, 2012), crayfish inside their burrows (Hasiotis and Mitchell, 1993), and *Palaeocastor* beavers inside of the burrow *Daemonelix* (Martin and Bennet, 1977). Reconstruction of tetrapod feet with the intent of retrodicting traces produced, however, has generally been restricted to extending the line of each bony toe to account for soft tissue (e.g., Falkingham et al., 2011) or overlaying the articulated foot of a supposed tracemaker over the track produced (e.g., Xing et al., 2009). Some criteria for comparing a tracemaker to a trace have been established (e.g., Fortey and Seilacher, 1997). These criteria include: 1) close association in the field; 2) concurrent stratigraphic range; 3) minimal choice of available potential tracemakers; and 4) consistent biogeographic ranges (Fortey and Seilacher, 1997). Others (e.g., Hasiotis, 2004, 2008) compare potential tracemakers to traces regardless of stratigraphic range, and also use modern organisms and their traces as to interpret fossil tracemakers. Only one study attempts to relate the foot of a fossil bird to tracks found in the same formation. Li et al. (2011) compared the feet of *Cathayornis* to *Tatarornipes* (*Aquatilavipes*) and concluded that *Cathayornis* could not be the tracemaker that produced *Tatarornipes* based on foot morphology.

There are many different types of bird feet and trackways (Fig. 1). The most common type of bird track is anisodactyl, where three toes (2, 3, and 4) point anterior and one toe points posterior (1). Incumbent anisodactyl is an anisodactyl track that has an elevated and reduced or absent hallux. Zygodactyl is a type of foot morphology where two toes point anteriorly (2 and 3) and two toes point posteriorly (1 and 4). Heterodactyl is similar to Zygodactyl foot morphology, where toes 3 and 4 point anteriorly and toes 1 and 2 point posteriorly. Palmate feet have webbing between toes 2, 3, and 4. Totipalmate feet have all four toes bound by webbing. Pamprodactyl feet have all four toes facing anterior. The number of track morphotypes found in the Mesozoic is not as high as the number of foot morphologies in modern birds, however, there are several different morphologies. The majority of Mesozoic bird tracks represent tracks made by aquatic birds or birds that lived in water-margin environments (i.e., *Koreanaornis*, *Hwangsangornipes*), however, *Shandongornipes* represents a unique and important nonwater-margin bird that had a zygodactyl foot morphotype (Li et al., 2005). Palmate tracks are known from the Early Cretaceous (Lim et al., 2000, Kim et al., 2006, Kim et al., 2012). Semipalmate tracks are present in the Cretaceous (Lockley et al., 2004). Anisodactyl and incumbent anisodactyl tracks are relatively common in the Cretaceous (Kim, 1969; Currie, 1981; Lockley et al., 1992, 2001, 2006; Anfinson et al., 2009). Lower Jurassic tracks from Africa, *Trisauropodiscus*, are strikingly birdlike and may represent Early Jurassic birds (Ellenberger, 1972; Lockley, 1992 and references therein).

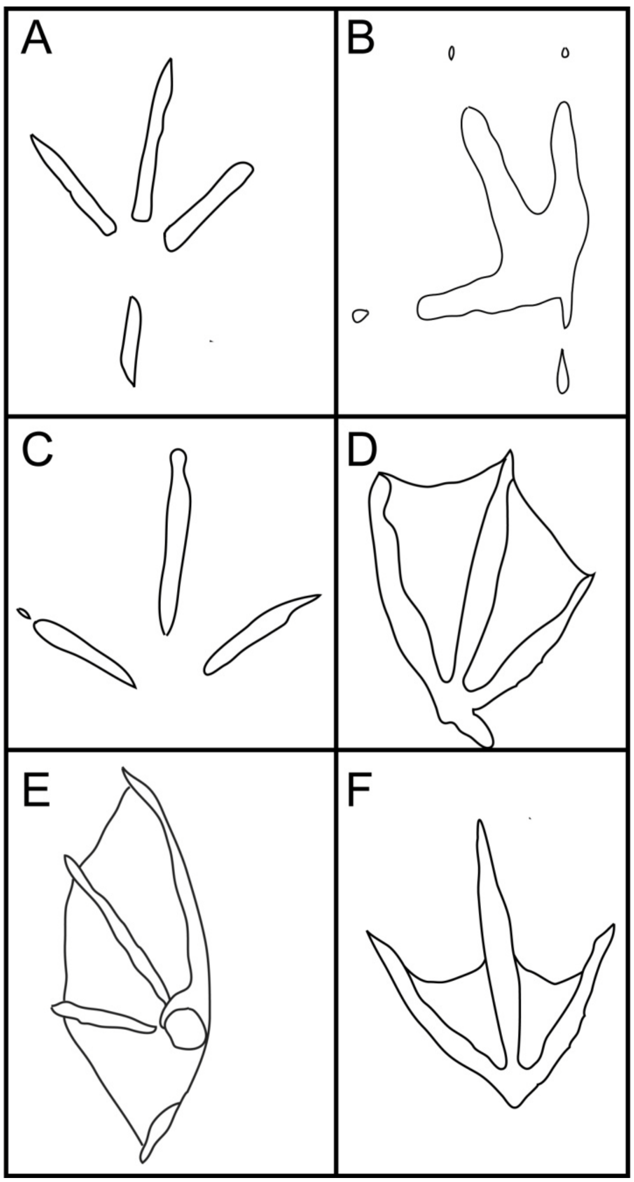

Fig. 1: (Opposite page) Different morphotypes of modern and ancient bird tracks. A.) Anisodactyl. B.) Zygodactyl. C.) Incumbent anisodactyl. D.) Palmate (or webbed). E.) Totipalmate. F.) Semipalmate.

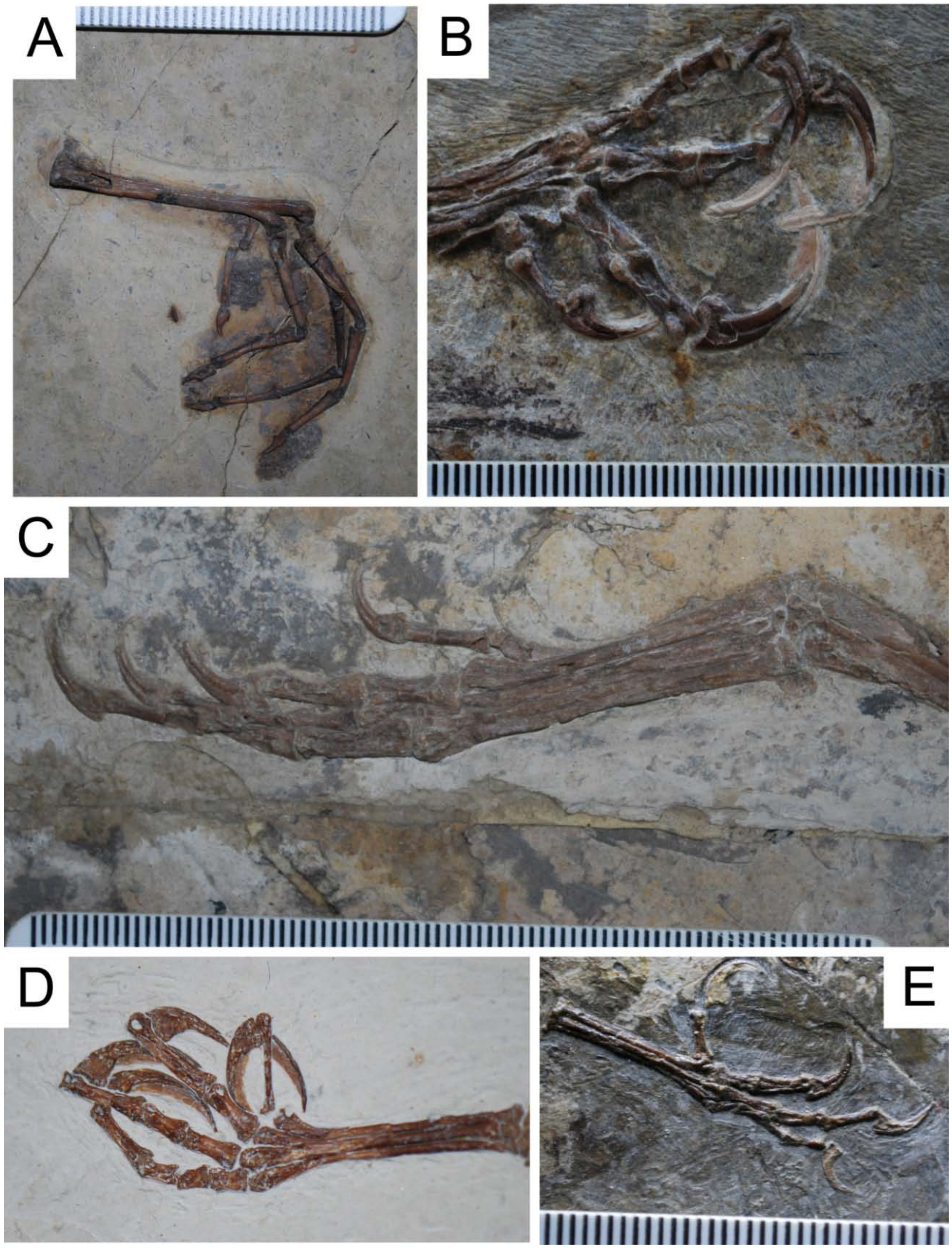

Fig. 2: Photographs of various foot morphologies from the Early Cretaceous birds of China. A.) *Ganus yumenensis* IVPP V 6862 B.) *Confuciusornis sanctus* IVPP V 13156 C.) *Jeholornis prima* IVPP V 13350 D.) *Rapanaxavis* DMNH D 2522 E.) *Daipingfangornis* PMOL-AB00027.

In modern birds, there are no studies relating the morphology of the osteological foot to the morphology of the whole foot covered in soft tissue. Several studies have performed dissections on the foot in order to understand the gross anatomy of the avian hindlimb (e.g., Hudson, 1937; Fisher, 1946; Wilcox, 1952), however, there was no direct comparison to the osteology. There are studies that examine how the soft tissue morphology of the foot changes through time and preservation type in museum specimens, specifically dealing with taxidermied skin specimens (e.g., Greenwood, 1979; Kuczynski et al., 2003; Wilson and McCracken, 2008). There have also been studies examining the difference between specimens preserved in ethanol and formaldehyde, but these have been performed mainly on fish and never on birds (e.g., Kristoffersen and Salvanes, 1998). There have been no studies directly comparing the effect of preservation in ethanol on birds.

Fig. 3: Hindlimb of *Hongshanornis* (IVPP V 14533 B), showing slender hind limb elements and gracile toes.

Establishing a series of criteria and morphological characteristics that link soft tissue morphology to osteology for avian morphotypes is a critical aspect of retrodicting fossil bird soft tissue anatomy, mainly because the known types of fossil birds are highly variable in osteological morphology. The Jehol Group contains 33 genera and 39 species of fossil birds (Zhou and Wang, 2010), and these species show foot morphologies ranging from arboreal to ground-dwelling to aquatic (Fig. 2). *Yanornis* and *Gansus* (the only non-Jehol Lower Cretaceous bird used in this study) both have foot morphologies suggestive of webbed feet, and specimens of *Gansus* have soft tissue preserved between the toes suggestive of webbing (Li et al., 2011). Enantiornithines, including *Dapingfengornis* and *Rapaxavis* have foot morphologies similar to those of modern arboreal birds (Li et al., 2006; Morschhauser et al., 2010). *Jeholornis*, a primitive long-tailed bird, also has arboreal characteristics, but the more advanced characteristics (e.g., proximal phalanx shortening) are not present (Zhou et al., 2003). Ornithurine birds, including *Yanornis* and *Gansus*, have characteristics common to water-margin birds. *Zhongjiangornis* (Zhou et al., 2010) and especially *Hongshangornis* (Zhou and Zhang, 2005) have longer hind limbs. *Hongshangornis* also has very slender hind limbs with very long, gracile toes (Fig. 3). Very primitive birds, including *Sapeornis* and *Confuciusornis* have foot morphologies that do not seem to compare closely to modern morphologies (Fig. 4).

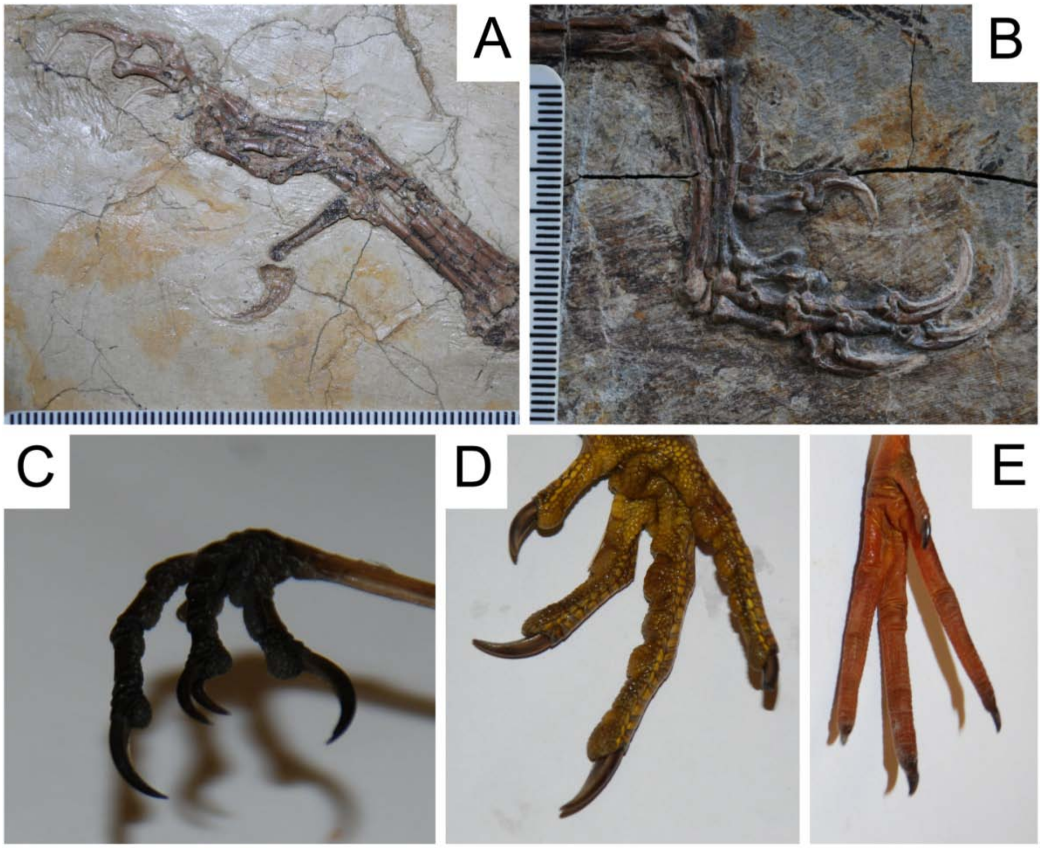

Fig 4: Photograph comparing the foot of A.) *Sapeornis* (IVPP V 13396) and B.) *Confuciusornis* (IVPP V 13156) to C.) a modern perching bird, D.) a modern ground bird, and E.) a modern shorebird.

Confuciusornis is a unique side branch of avian evolution that independently evolved an edentulous beak and endothermy, and has a unique pygostyle (Martin et al., 1998; Zhang et al., 1998; Zhou and Hou, 1998; De Ricqls et al., 2003). Confuciusornithids are characterized by a very large deltopectoral crest on the humerus that usually possesses a large foramen (Fig. 5). The function of this foramen is unknown. *Confuciusornis* has a slightly upturned beak, which is unique amongst Mesozoic birds (Hou et al., 1999). The foot of *Confuciusornis* is also interesting, with a robust toe II and more slender toes III and IV—usually toe III is the most robust. Toe III is the longest toe, however, the claw of toe II is larger than the claw of toe III. Some specimens of *Confuciusornis* also have enigmatic, paired tailfeathers. These paired tailfeathers have been suggested as an indicator of sexual dimorphism (Martin et al., 1998). Originally described as proximally ribbonlike (Chiappe et al., 1999), the morphology of these tailfeathers has been difficult to determine. More recent studies have described them as rachis dominated (e.g., Chuong et al., 2003), or more similar to sheets of broad, undifferentiated barbs (O'Connor et al., 2012).

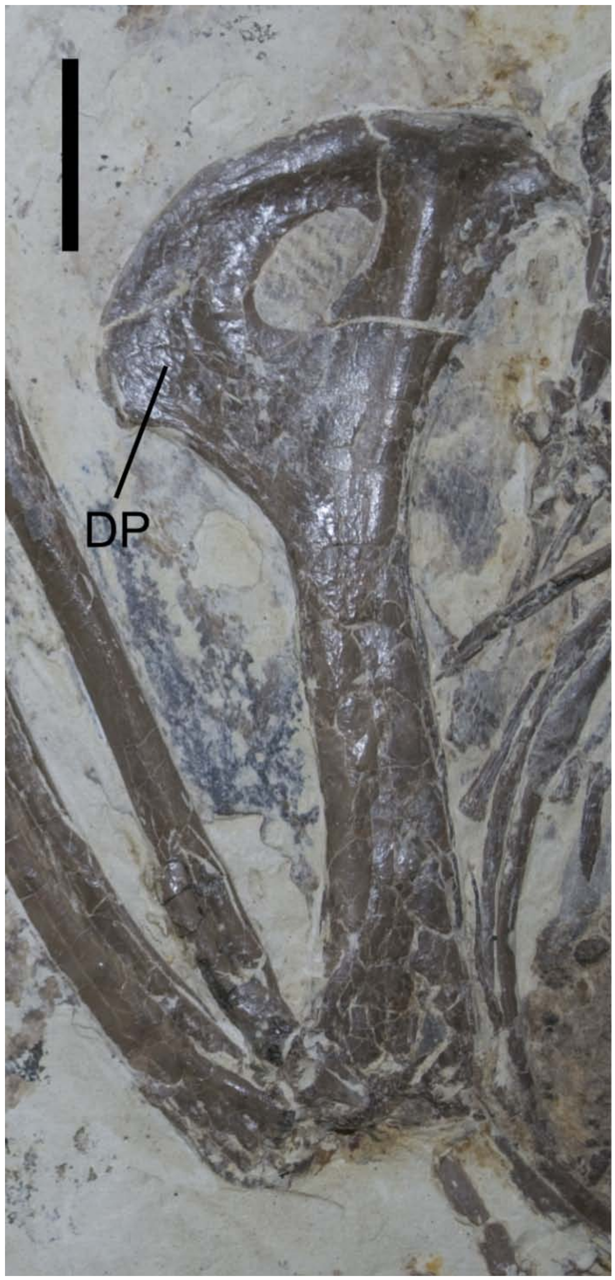

Fig 5: Humerus of *Confuciusornis* (STM13-39) showing the large deltopectoral crest (DP). Scale bar=1 cm.

The flight ability of *Confuciusornis* has been the subject of some debate. *Confuciusornis* was clearly not a soaring bird or particularly a strong flier based on the anatomy. The sternals are fused, and *Confuciusornis* has been reconstructed with a small keel restricted to the posterior area of the sternum (Zhou and Farlow, 2001). *Confuciusornis* does have extremely long primary feathers, and the comparison of the primary feather length to the ulna of *Confuciusornis* compares favorably with such modern fast-flying birds as swallows (Wang et al., 2011). Although previous studies have suggested that the primary feathers rachises of *Confuciusornis* are thin and weak (Nudds and Dyke, 2010), data provided elsewhere (Zheng et al., 2010) and within this dissertation suggest that they are actually strong and robust, easily comparable with modern birds (Fig. 6).

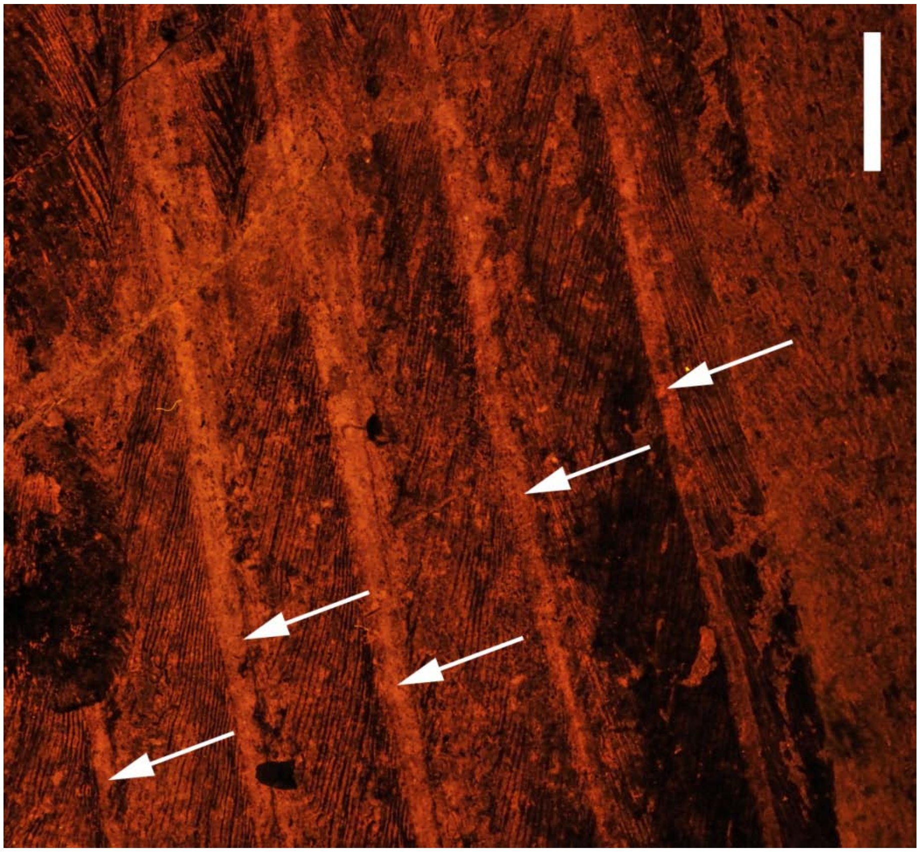

Fig. 6: Photograph of a *Confuciusornis* (IVPP V 13156) wing, with arrows pointing to primary feather rachises. Scale bar=5 mm.

The birds of the Jehol Group are primarily biased towards arboreal birds, with 12 genera of primitive (i.e., nonornithurine, nonenantiornithine) birds, 15 genera of enantiornithines, and 9 genera of ornithurine birds as of 2010 (Zhou and Wang, 2010). The number of enantiornithine birds has increased since then. The avian track record, however, is largely biased towards water-margin, ground-dwelling birds, which are primarily, if not entirely, ornithurine birds. This dichotomy, combined with the tendency to discover tracksites where there are no body fossils, and body fossils where there are no trace fossils, illustrates the use of trace fossils as hidden biodiversity (Hasiotis, 2004, 2007, 2008). The diversity of ornithurine birds was high, perhaps as high as the diversity of enantiornithines, based on such tracksites as the Geyongsamnado Institute of Science Education in Jinju, Republic of Korea. When discussing the diversity of Early Cretaceous birds, a complete picture of both tracksites and body-fossil localities should be used, thereby requiring a collaboration between avian paleontologists and avian ichnologists.

Creating a fundamental synthesis between avian paleontology and avian ichnology, and the study of fossil birds and the study of modern birds is a critical step in the study of ornithology. The number of studies cataloguing and quantifying modern bird tracks and traces has, thus far, been minimal. In order to fully understand the production of traces—i.e., behavior and media consistency—we must observe and record modern birds producing traces. After quantifying modern behaviors, these measurements can then be applied to fossil tracks and trackways.

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A BEHAVIORAL ANALYSIS OF FOSSIL BIRD TRACKS FROM THE HAMAN FORMATION (REPUBLIC OF KOREA) SHOWS A NEARLY MODERN AVIAN ECOSYSTEM

ABSTRACT

The Lower Cretaceous Haman Formation of the Republic of Korea has yielded several localities with thousands of dinosaur, bird, and pterosaur tracks. One such tracksite is found at the Gyeongsangnamdo Institute of Science Education (GISE) in Jinju, South Korea. More than 1,000 bird tracks are exposed on a single bedding plane, and thousands more are found in smaller float blocks on exhibit around the museum or in storage. The morphologic and behavioral diversity is extremely high; there are more than seven different morphologies described herein, and the behaviors range from feeding—including pecking, probing, predator-prey interactions, and scything traces—to landing and running. Arcuate traces and associated webbed-footed trackways are identical to scything feeding traces produced by the extant Black-Faced Spoonbill (*Palatea minor*). Individual peck and probe marks have also been reported, and clustered probing has been observed. The behaviors at this site are strikingly modern with respect to morphology and diversity, indicating that ornithurine birds had a very modern set of behaviors and anatomy, based on the spoonbill-like trackways. The high morphologic diversity of track morphotypes (at least seven) indicates that Early Cretaceous ornithurine birds were very diverse, in contrast to previous assumptions based on the body fossil record that is dominated by their enantiornithine cousins. There is an urgent need for understanding modern avian behaviors and the traces that they produce to close the growing gap between the methodologies used by avian ichnologists and ornithologists.

INTRODUCTION

The bird tracks of the Lower Cretaceous Haman Formation of the Republic of Korea have been well-studied ichnotaxonomically (Lockley and Harris, 2010; Kim et al., 2012). Recently, Lockley and Harris (2010) noted semicircular or arcuate traces associated with web-footed tracks that look extremely similar to traces left by the modern Black-Faced Spoonbill (*Palatea minor*) (Swennen and Yu, 2005). Falk et al. (2010) reported the first description of feeding traces associated with shorebird-like tracks of *Koreanornis hamanensis*. The purpose of this paper is to describe in detail the morphology, feeding traces, and other behaviors recorded from a single locality of the Haman Formation, near Jinju, Republic of Korea.

Modern birds produce a wide variety of feeding traces. These traces are not limited to environments of sediment deposition (e.g., woodpecker holes in trees); however, a large number can be found in water-margin environments. These behaviors include, but are not limited to: probing, pecking, scything, dabbling, and gaping (Swennen and van der Baan, 1959; Cadhee, 1990; Elbroch and Marks, 2001; Swennen and Yu, 2005; Falk et al., 2010). Each of these behaviors is distinctly different and will leave recognizable traces in the sedimentary record. Scything, for example, involves the back and forth movements of the head perpendicular to the direction of the body, with the bill held open a slight distance (Swennen and Yu, 2004). Roseate Spoonbills (*Ajaja ajaja*) and other spoonbill species have a highly pocketed area at the front of their mandible, which likely represents an electromagnetic or other type of sensory system that allows them to tactile feed in this manner (Swennen and Yu, 2004; ARF personal observation, 2010). When the bill encounters a fish or other prey species, it closes sharply around the prey which is then swallowed whole (Swennen and Yu, 2005). Some birds that scythe without a spoon-shaped bill, such as the American Avocet (*Recurvirostra americana*), can also use pecking behavior in sandier media (Quammen, 1982).

Dabbling occurs in birds with broad, ducklike bills (Swennen and van der Baan, 1959; Erickson, 1967). While no descriptions of modern dabble traces exists, traces interpreted as such behaviors have been reported from the Eocene Green River Formation in Utah (Erickson, 1967; Yang et al., 1995). These traces have been attributed to *Presbyornis* (Erickson, 1967). Dabble marks were also observed in the Upper Cretaceous Uhangri Formation, at the Uhangri Dinosaur Museum, near Haenam, South Korea.

Pecking and probing behaviors are performed in specific manners and will leave significantly different traces from each other, as well as other feeding behaviors. Probing is performed by inserting the beak into the sediment and withdrawing it without opening the bill (Burton, 1974). The bill may be closed or partially opened. This behavior is not to be confused with gaping in which the closed bill is inserted into the sediment and is opened before it is withdrawn from the sediment (Elbroch and Marks, 2001). Probing behaviors are found across the order Charadriiformes. Pecking is found across many different avian orders, from the Charadriiformes to the Passeriformes (Elbroch and Marks, 2001; Brown et al., 2003). Probing can leave a number of different patterns, including clustered probing, linear probing, and sinusoidal probing (Elbroch and Marks, 2001). Isolated fossil probe marks associated with *Koreanaornis hamanensis* have been described from the Haman Formation (Falk et al., 2010). Purported probe marks have also been described from the upper Eocene Santo Domingo Formation, associated with *Gruipeda dominguensis* in Argentina (Genise et al., 2009; Melchor et al., 2013). No description or data was provided to support the probe mark interpretation, however, and these trace fossils may represent the invertebrate trace fossil *Arenicolites*.

Pecking occurs when the beak is pressed into the sediment and then drawn back towards the body. Pecking is often extremely shallow, unlike probing, which can be a deep trace depending on the length and morphology of the bill (Lane, 1987). Pecking traces have been reported from the Haman Formation (Falk et al., 2010) and have been suggested as part of the "shorebird ichnofacies," as well as a way to identify bird tracks (Doyle et al., 2000; deValais and Melchor, 2008). These subtle traces have rarely been reported from the fossil record, however, due to their small size and likelihood of being interpreted incorrectly as invertebrate trace fossils.

Few papers deal specifically with the behavioral aspect of avian traces, aside from the *Presbyornis* dabble marks (Erikson, 1967). Lim et al. (2000) mentioned feeding behaviors from the Haman Formation in Jinju, Republic of Korea. Lockley et al. (2009) reinterpreted the morphology and behavior of *Ignotornis mcconnelli* from the Upper Cretaceous Dakota Formation of Colorado, USA (originally described by Mehl, 1931), and described and interpreted new *Ignotornis* material excavated from that same formation and location. Genise et al. (2009) began to identify and classify some behaviors of modern birds and compare them to their specimens of *Gruipeda dominguensis*. Lockley and Harris (2010) and Kim et al. (2012) briefly discussed some of the behaviors interpreted from the Lower Cretaceous Haman Formation tracksites. Falk et al. (2010) described probe and peck marks in detail from the Haman Formation.

Kim (1969) first described bird tracks from the Haman Formation, and later papers discussed the amount of available material (i.e., Baek and Yang, 1997, in Korean). The current named ichnogenera from the Haman Formation are as follows: *Koreanaornis hamanensis* Kim 1967, *Ignotornis yangi* Kim et al. 2006, *I. gajinensis* Kim et al., 2012, and *Goseongornipes markjonesi* Lockley et al., 2006. *Koreanaornis* is a small, incumbent anisodactyl track that may or may not have a hallux impression. *Ignotornis yangi* is a large semipalmate track first described from the Haman Formation of Changseong and Sinsu Islands. *Goseongornipes markjonesi* is a track that is smaller than *Ignotornis* and *Hwangsangornipes* (from the Upper Cretaceous Jindong Formation) (Kim et al., 2012) and is assigned to the Ignotornidae. The original description of *G. markjonesi*, however, is from only two relatively poorly preserved tracks from the Jindong Formation (Lockley et al., 2006). A recent paper by Kim et al. (2012) described tracks attributed to *Goseongoripes*, and erected a new ichnospecies *Ignotornis gajinensis*. The Haman Formation presents a unique opportunity to study a whole-ecosystem behavioral pattern of bird tracks, and to draw evolutionary conclusions based on trackway evidence. Though this study discusses several new morphologies and behaviors, there are still many undescribed specimens from the Haman Formation, indicating a very diverse and advanced avian component of a water-margin ecosystem.

MATERIAL AND METHODS

The materials used in this study originate from a single locality over which the Gyeongsangnamdo Institute of Science Education (GISE) is built, in Jinju, Republic of Korea (Fig 1). The majority of specimens are on large rock slabs that were found during excavation of the building's foundation. There are two separate large floor slabs that contain a large number of well-preserved bird and dinosaur (i.e., theropod and sauropod) tracks and trackways. The Exhibit Hall 1 site alone has between 1,500 and 2,000 bird tracks on the floor slab—this does not count the isolated float blocks that are placed around the museum (Kim et al., 2012). Lim et al. (2000) was the first international publication to discuss the GISE tracksite, and mentioned traces of feeding. The majority of tracks studied are housed at this museum; however, a small sample

(KS064, NHC-IC-002a, NHC-IC-003a, NHC-IC-004) is currently housed at the Natural Heritage Center in Daejeon, Republic of Korea.

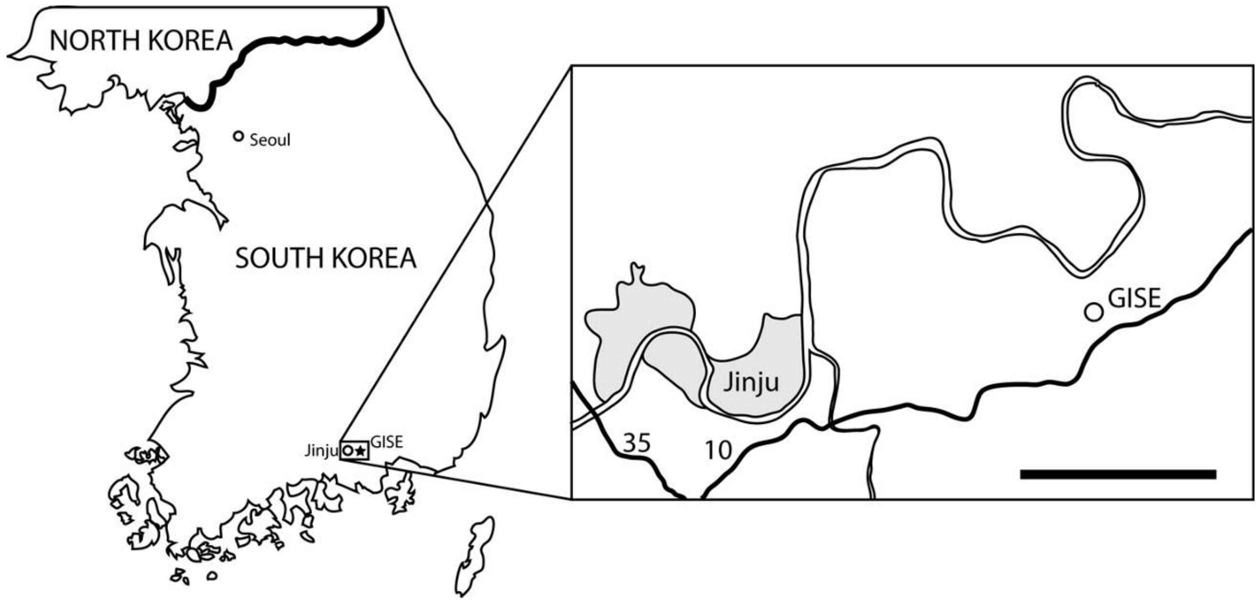


Figure 1: Locality map of the Gyeongsangnamdo Institute of Science Education (GISE) near Jinju, South Korea. Star represents the locality. Scale bar ~7 km.

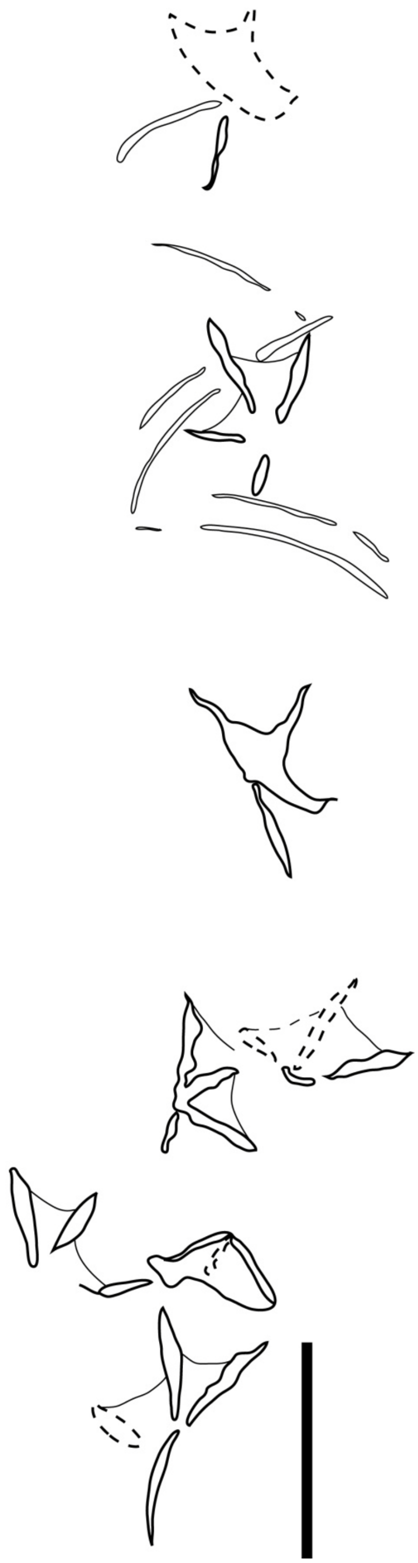
These tracks are assigned to *Koreanornis hamanensis*, *Koreanornis sp.*, and *Ignotornis gajinensis*. Tracks belonging to *Goseongornipes* and several unnamed morphotypes are also present. Specimens used in this study are in the Exhibition Hall 1 floor exhibit (EH1), which includes six separate trackways (Fig. 2); Exhibition Hall 2, which includes 3 separate trackways (Fig. 3), KS 049, GS021, GS012, GS018, GS 007, IB41-1, KS064, NHC-IC-002A, NHC-IC-003a, and KS019 (Fig. 4). The EH1, KS049, GS012, GS021, GS018, GS007, and IB41-1 specimens have been assigned to *Ignotornis gajinensis* (Kim et al., 2012). KS064 is assigned to *Koreanornis sp.* (Falk et al., 2010).

A

B

C

D



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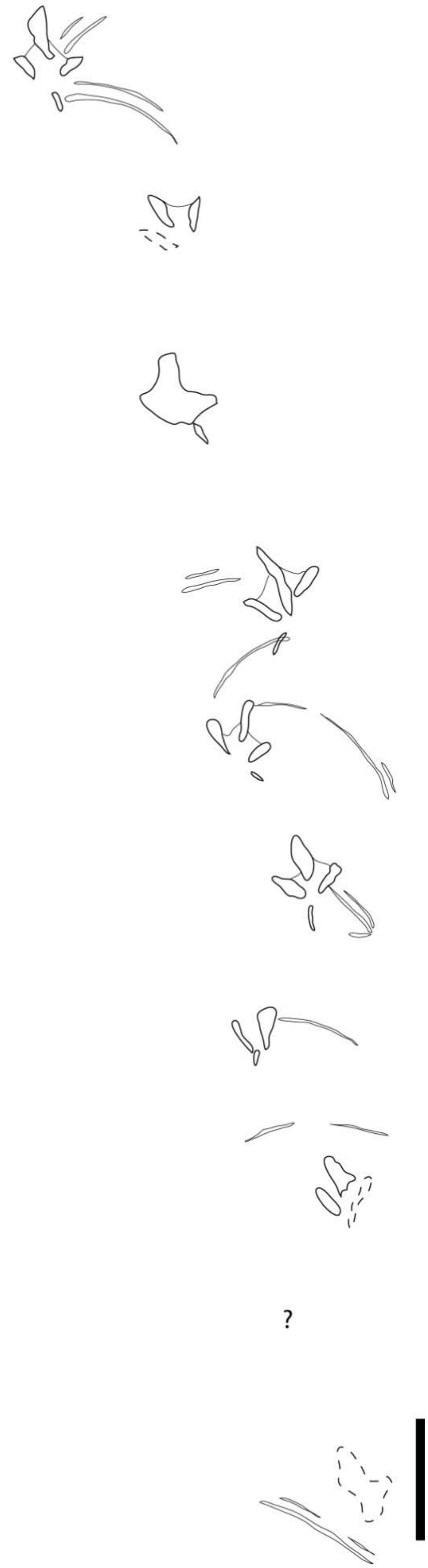

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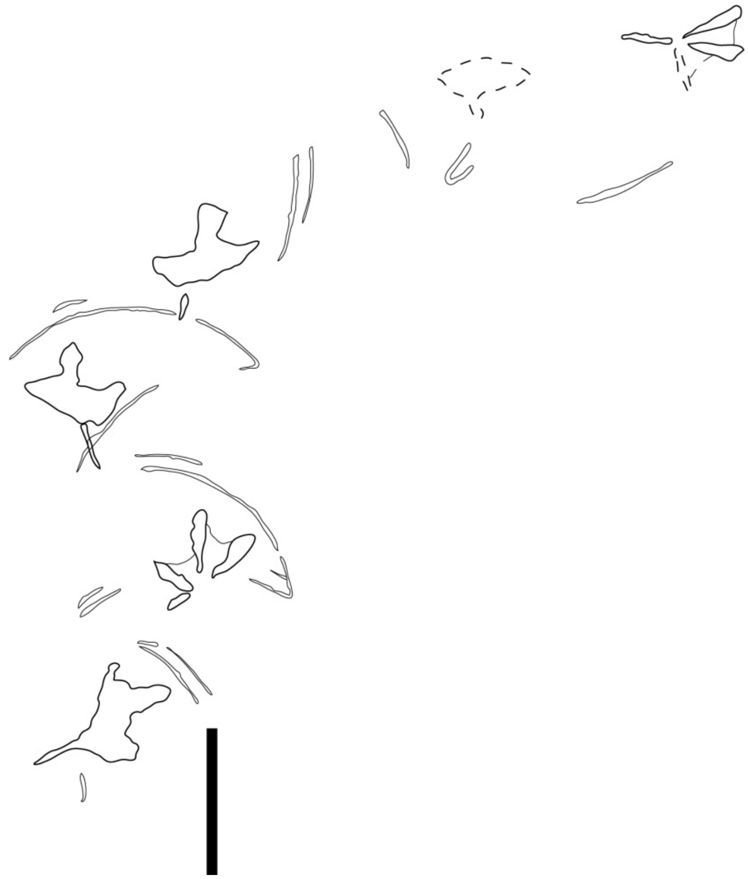

Previous pages: Figure 2: Line drawings of the webbed-footed trackways and associated arcuate bill traces. Scale bars 8 cm. A-F are from Exhibit Hall 1 (EH1), G is from a storage room in the lower level of the building (IB4-1). A.) EH1 trackway 1. B.) EH1 trackway 2. C.) EH1 trackway 3. D.) EH1 trackway 4. E.) EH1 trackway 5. Black lines indicate cracks in the rock. F.) EH1 trackway 6. This page: G.) Specimen no. IB4-1.

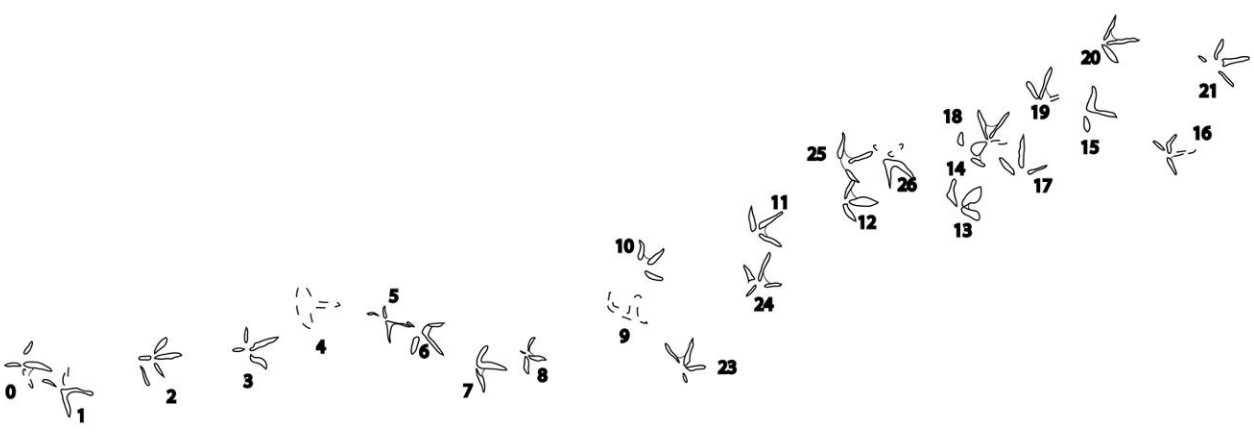

Figure 3: (Opposite page) Numbered line drawing showing *Geoseongornipes* tracks on the floor slab of Exhibit Hall 2. Tracks 0–16, 26 represent trackway 1, 17–22 (track 22 not shown) trackway 2, and 23-25 trackway 3. Scale bar 8cm.

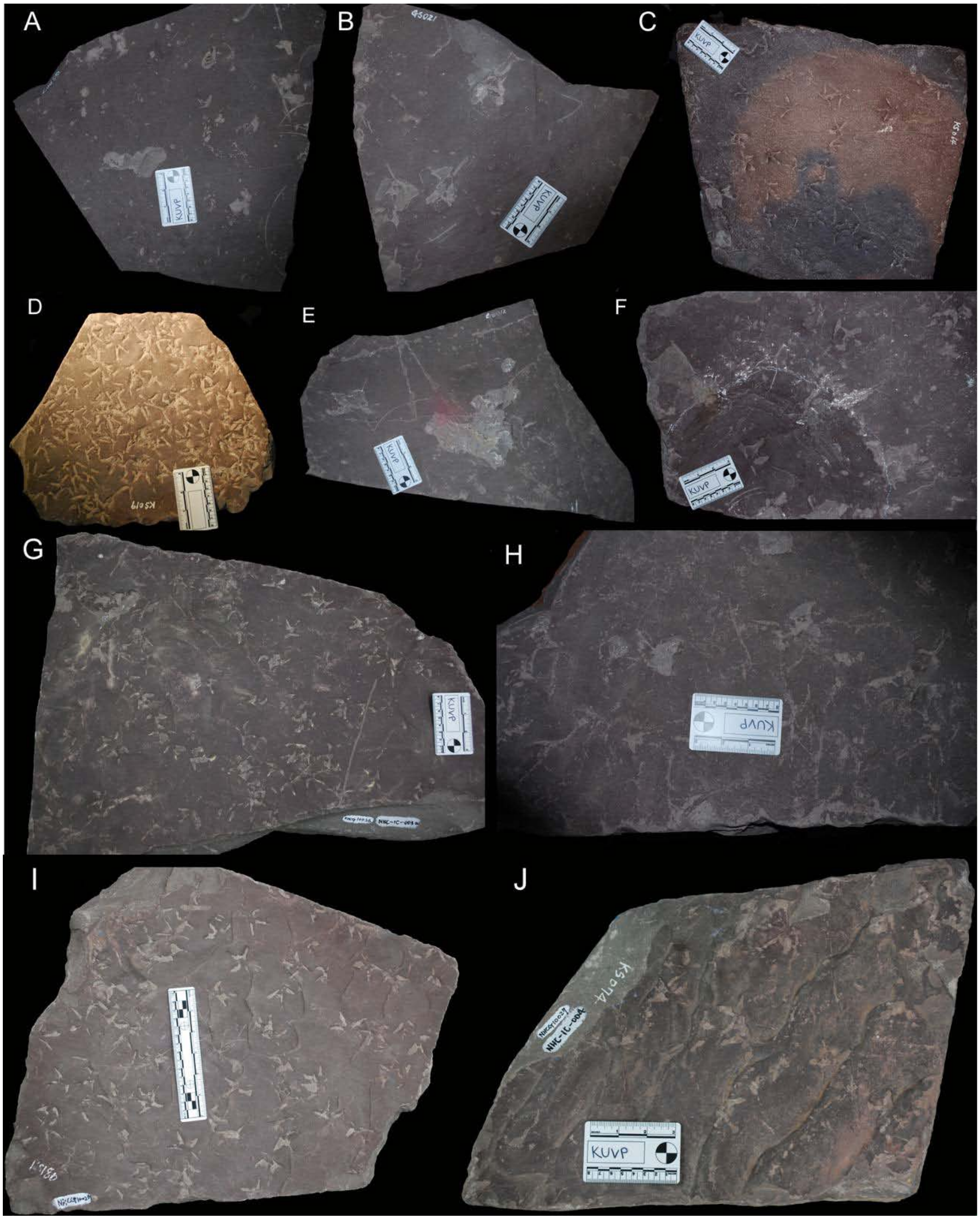

Figure 4: (Opposite page) Plate showing isolated specimens used in this study. A.) GS007. B.) GS021. C.) KS064. D.) KS019. E.) GS0012. F.) KS049. G.) NHC-IC-003a. H.) GS018. I.) NHC-IC-002A (KS0180). J.) NHC-IC-0004 (KS074).

All specimens had the following single-track and multitrack measurements performed: (1) angle of divarication between toes II and III, III and IV and II and IV, (2) length of toes II, III, and IV, (3) width of toes II, III, and IV, (4) foot length, (5) foot width, (6) pace length, (7) stride length, (8) pace width, and (9) angle of divarication from the midline (Fig 5). These measurements were used to both classify the track and to help identify behaviors using quantifiable data.

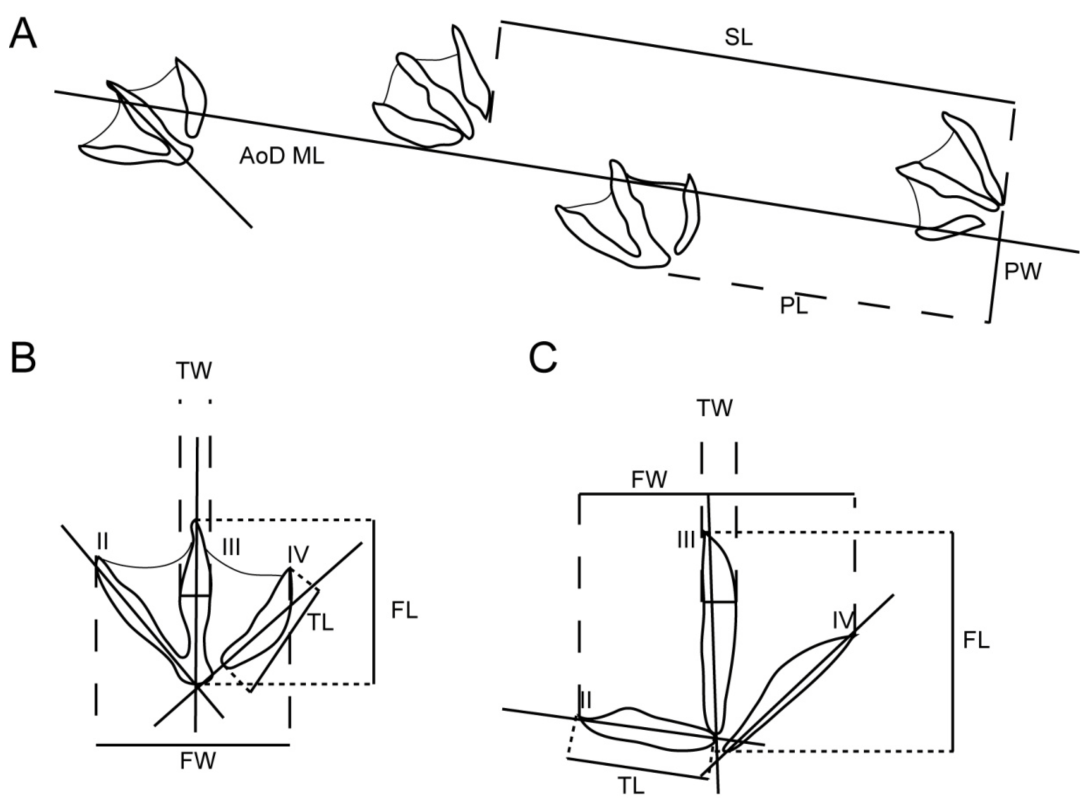

Figure 5: Line drawings representing measurements taken on the tracks. A.) Multi-track measurements performed. B.) Single-track measurements performed on webbed-footed tracks. Note how the AoD measurement must be modified to adjust for the curvature of the toes. C.) Single-track measurements performed on nonwebbed feet.

AoDML=Angle of Divarication from Midline. SL=Stride length. PL=Pace length. PW=Pace width. FW=Foot width. FL=Foot length. TL=Toe length. TW=Toe width. II=Toe 2. III=Toe 3. IV=Toe 4.

A total of 324 footprints were measured (See Appendix I and tables therein); 118 of these are currently assigned to *Ignotornis* and are hitherto referred as spoonbill-like traces (Appendix Table 1), 132 are assigned to *Koreanaornis* (Appendix Table 2), 31 are assigned to *Goseongornipes* (Appendix Table 3), and 13 have not been assigned to an ichnogenus due to the small sample size (Appendix Table 4). Several trace fossils associated with these tracks were also measured and are represented in tables alongside the tracks with which they are associated. Overlapping footprints were carefully examined for crosscutting relationships, and overlapping trackways were carefully assessed using track directionality and whether the tracks were left or right foot to assign the correct tracks to the correct trackway.

GEOLOGIC SETTING

The Lower Cretaceous Haman Formation in the Gyeongsang basin has been interpreted as a fluvial system dominated by sheetflood and floodplain deposits, with no perennial channel deposits present (Choi, 1986). Mudcracks are common, indicating subaerial exposure, although no pedogenic features have been described; none were observed at GISE.

The Haman Formation consists primarily of purple mudstone, siltstone, and fine-grained sandstone, commonly interbedded with mud drapes (Choi, 1986). One rock sample with planar beds and rip-up clasts was observed at GISE (Fig 6). The paleoclimate during deposition of the Haman Formation is thought to have been semiarid or arid (Choi, 1986).

Figure 6: Specimen KS051 illustrating rip-up clasts found in the layer beneath the bird tracks. Arrows point to clasts.

The main slab of tracks and trackways discussed herein contains current ripples (Fig 7A) and such invertebrate traces as *Treptichnus*, *Steinichnus*, and cf. *Naktodemasis* (Fig. 7B–F), which are indicative of very shallow-water environments that experience subaerial exposure. Many float blocks associated with the locality also contained current ripples. The main slab is primarily fine-grained, yellow-grey sandstone with thin, dark purple-red silty drapes. Other track-bearing float blocks exhibit similar lithology and coloring.

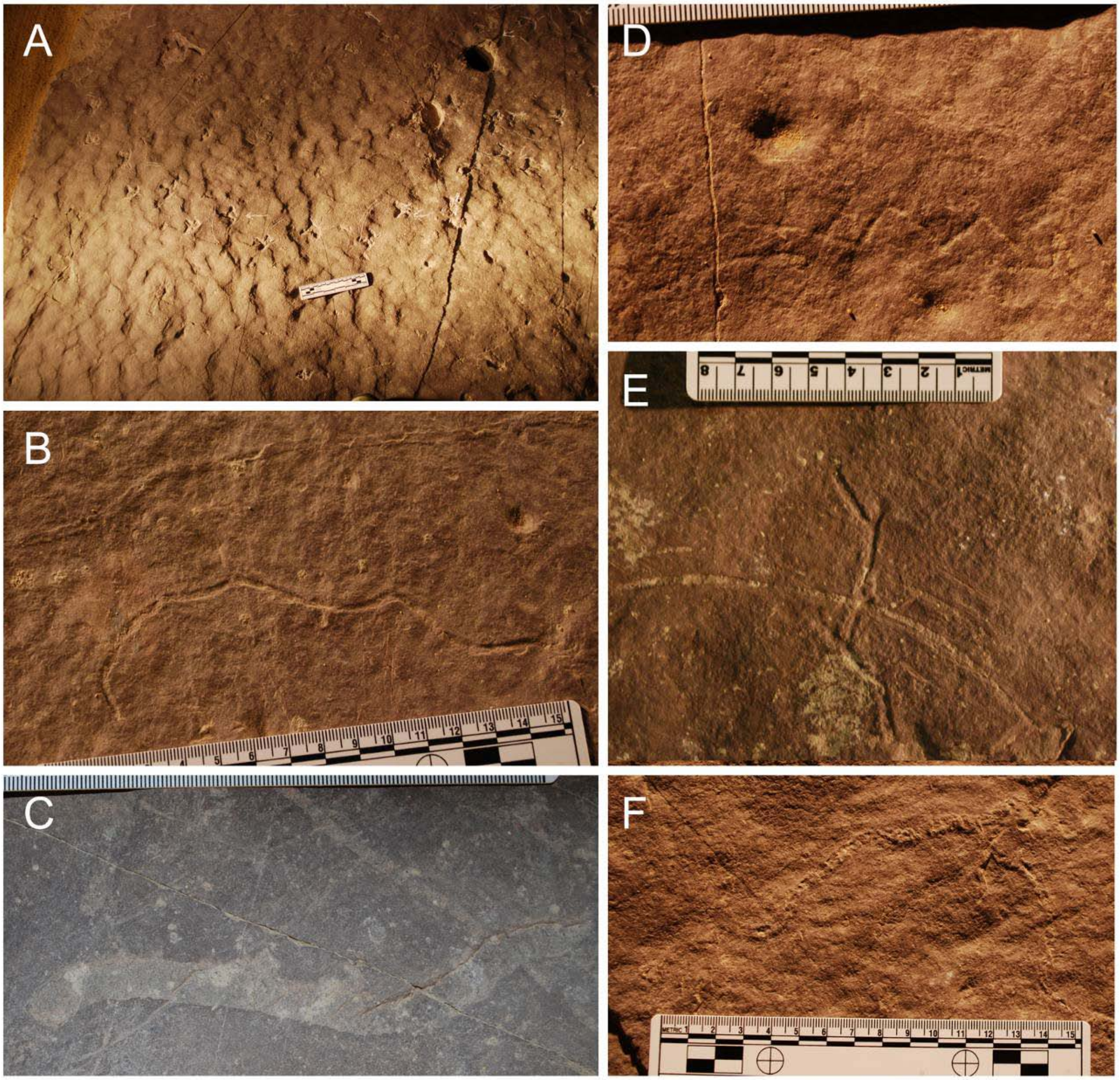

Figure 7: Ripple marks and invertebrate traces found on EH1. A.) Ripple marks; note bird tracks (chalk arrow). B-F.) Invertebrate traces.

RESULTS

Spoonbill-like traces

Sixty-three often paired arcuate traces were found associated with 118 incumbent anisodactyl, webbed-footed (palmate) tracks, and both were measured (see Appendix I Table 1,

Table 5). The footprints themselves had an average foot length of 43.9 mm, an average foot width of 55.55 mm, and an average FL:FW ratio of 0.796. Toe III was the longest on average, with a length of 30.9 mm. Toe III was also the widest on average, at 8.4 mm. The angle of divarication between toes II and IV was 109.92°. Toes II and IV often exhibit inward curvature typical of webbed-footed birds (Fig. 8).

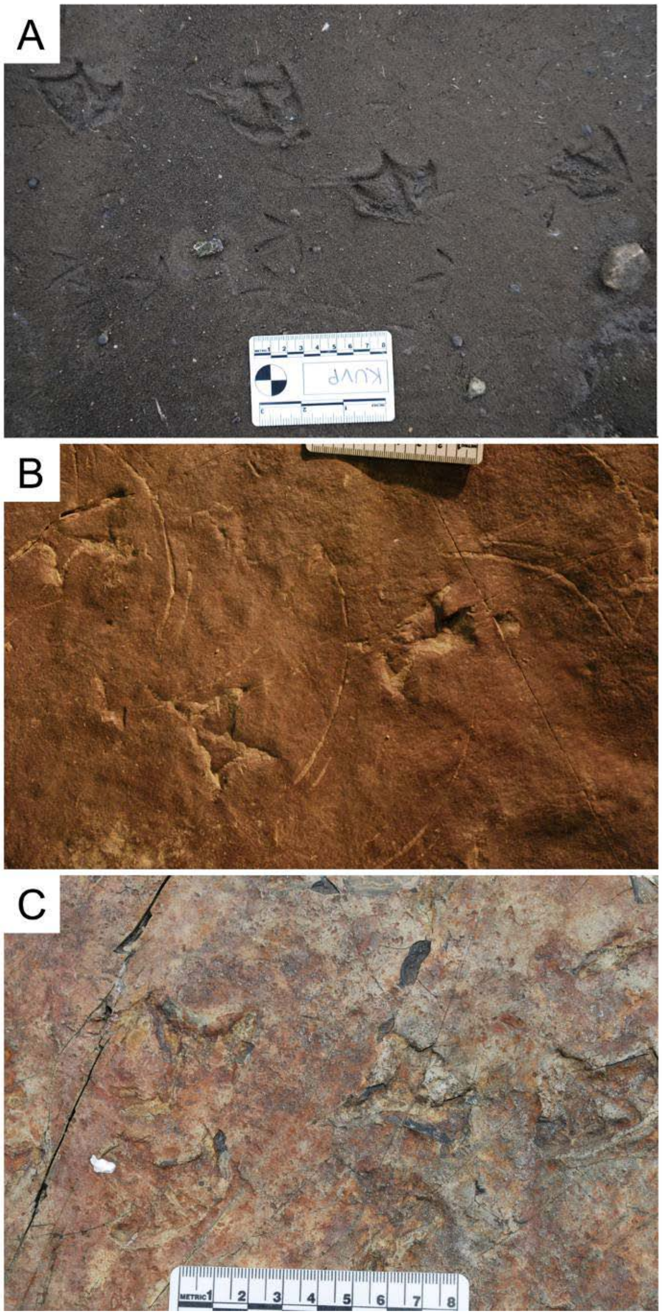

Figure 8: (Opposite page) Modern web-footed bird tracks compared to fossil bird tracks from the Cretaceous of Korea. A.) Franklin's Gull (*Lecucophaeus pipixcan*). Note how the outer toes curve inward towards toe III due to webbing. B.) Spoonbill-like *Ignotornis gajinensis*; note that the outer toes are also curved towards toe III, although not as strongly as in A. C.) *Hwangsanipes* from Haenam, Korea. Note the strongly curved toes II and IV.

Multiple track measurements on the six individual EH1 trackways (Fig. 2A–F) are as follows: Trackway 1 contains 22 individual footprints. The average pace length of trackway 2 is 106 mm, average pace width is 52 mm, and the average stride length is 221.1 mm. Trackway 2 is the longest, consisting of 23 individual footprints, with an average pace length of 96.7 mm, an average pace width of 49.1 mm, and an average stride length of 199.7 mm. Trackway 3 has 16 individual tracks, with an average page length of 135.5 mm, an average pace width of 23.3 mm and an average stride length of 271.4 mm. Trackway 4 is the shortest, with 9 individual trackways, and an average pace length of 79.1 mm, an average pace with of 37 mm, and an average stride length of 151.1 mm. Trackway 5 contains 20 tracks, although only 16 were measured. The average pace length is 120 mm, the average pace width is 28.8 mm, and the average stride length is 255.2 mm. Trackway 6 contains 11 tracks, with an average pace length of 101.6 mm, an average pace width of 41.8 mm, and an average stride length of 212.1 mm (see Appendix I for complete table of multitrack measurements).

Spoonbill-like trackway IB41-1 contains 6 tracks, with an average pace length of 88.6 mm, an average pace width of 68.7 mm, and an average stride length of 172 mm. The Exhibition Hall block specimens (KS049, GS012, GS021, GS018, and GS007, see Fig. 4) were largely isolated tracks and arcuate traces, except for GS018, which contains 6 individual tracks. The average pace length was 123.1 mm, the average pace width was 22.9 mm, and the average stride length was 250.5 mm.

The average length of the upper arcuate trace was 49.2 mm, and the average width was 2.04 mm. The average length of the lower arcuate trace was 86.9 mm, and the average width was 2.7 mm. The average distance between the upper and lower traces was 6.6 mm.

Koreanaornis and associated traces

Specimens KS006, NHC-IC-002A, NHC-IC-003a and NHC-IC-004 are assigned to *Koreanaornis*. Associated with these trackways are invertebrate traces and, in the case of NHC-IC-002A, groups of two-to-three parallel to subparallel traces of enigmatic origin (Fig. 9, Table 1).

#	Component #	Length	Thickness	(in mm)
1				
	1	5.2	1	
	2	10.2	2.5	
	3	9	2.70	
2				
	1	8.5	2.50	
	2	8.2	2.2	
3				
	1	11.5	1.7	
	2	>8.5	2.2	
	3	>3.5	2	
4				
	1	10	2.2	
	2	10.5	2.2	
	3	8.5	3.5	
5				
	1	7	1	
	2	6	1	
	3	4.5	1	
6				
	1	7.7	2	
	2	10	1.2	
	3	9	2	

Table 1: Measurements of enigmatic traces found on NHC-IC-002A.

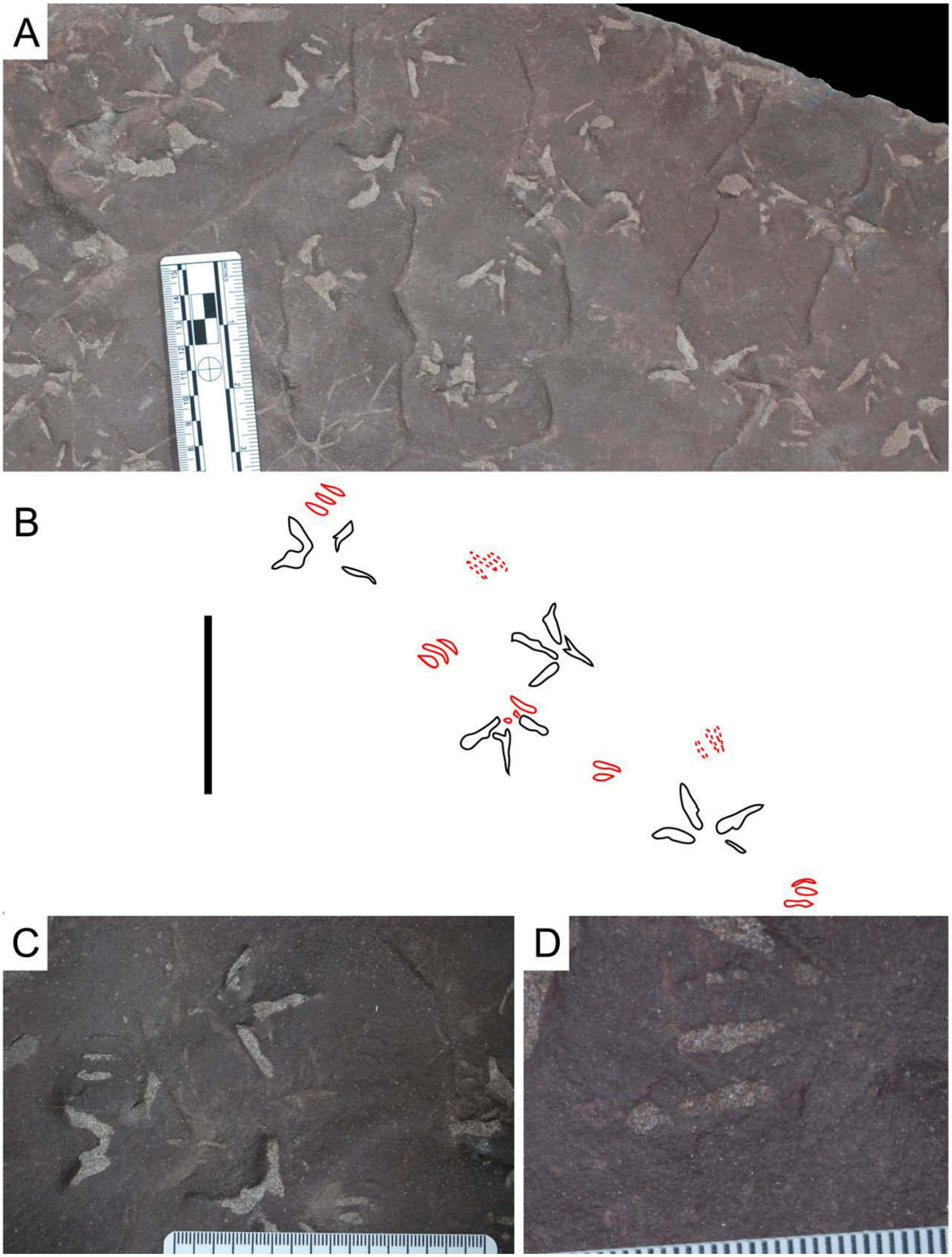

Figure 9: Parallel enigmatic traces from NHC-IC-002A. A.) Note paired traces associated with a shorebird-like

trackway. B.) Closer view of enigmatic traces. C.) Close-up of the enigmatic traces showing a variation in morphology from teardrop shaped to elongated oval shaped.

KS006 contains many incumbent anisodactyl tracks, however, only 7 were measured to get an average sample of this specimen, as a large number of typical *Koreanaornis* specimens were already measured. The average length of toe III is 20 mm, with an average angle of divarication between toes II and IV of 116.3°. The average FL:FW ratio is 0.763.

NHC-IC-003a contains 60 incumbent anisodactyl tracks, separated into 5 recognizable trackways and several isolated tracks (Fig. 10, Appendix I). The average length of toe III is 17.5 mm, the average angle of divarication between toes II and IV is 114.9°, and the average FL:FW ratio is 0.769. Trackway 1 had an average pace length of 63.9 mm and an average stride length of 105 mm. The average pace width is 13.2 mm, and the average angle of divarication from the midline is 16°. Trackway 2 has an average pace length of 66.5 mm and an average stride length of 113.6 mm. The average pace length is 15.9 mm and the average angle of divarication from the midline is 23.6°. Trackway 3 has an average pace length of 81.1 mm and an average stride length of 150.8 mm. The average pace width is 8 mm and the average angle of divarication from the midline is 31°. Trackway 4 has an average pace length of 90.6 mm, and an average stride length of 107 mm. The average pace width is 26.3 mm and the average angle of divarication from the midline is 22.8°. Trackway 5 has an average pace length of 41.9 mm and an average stride length of 68 mm. The average pace width is 28.2 mm and the average angle of divarication from the midline is 40.3°.

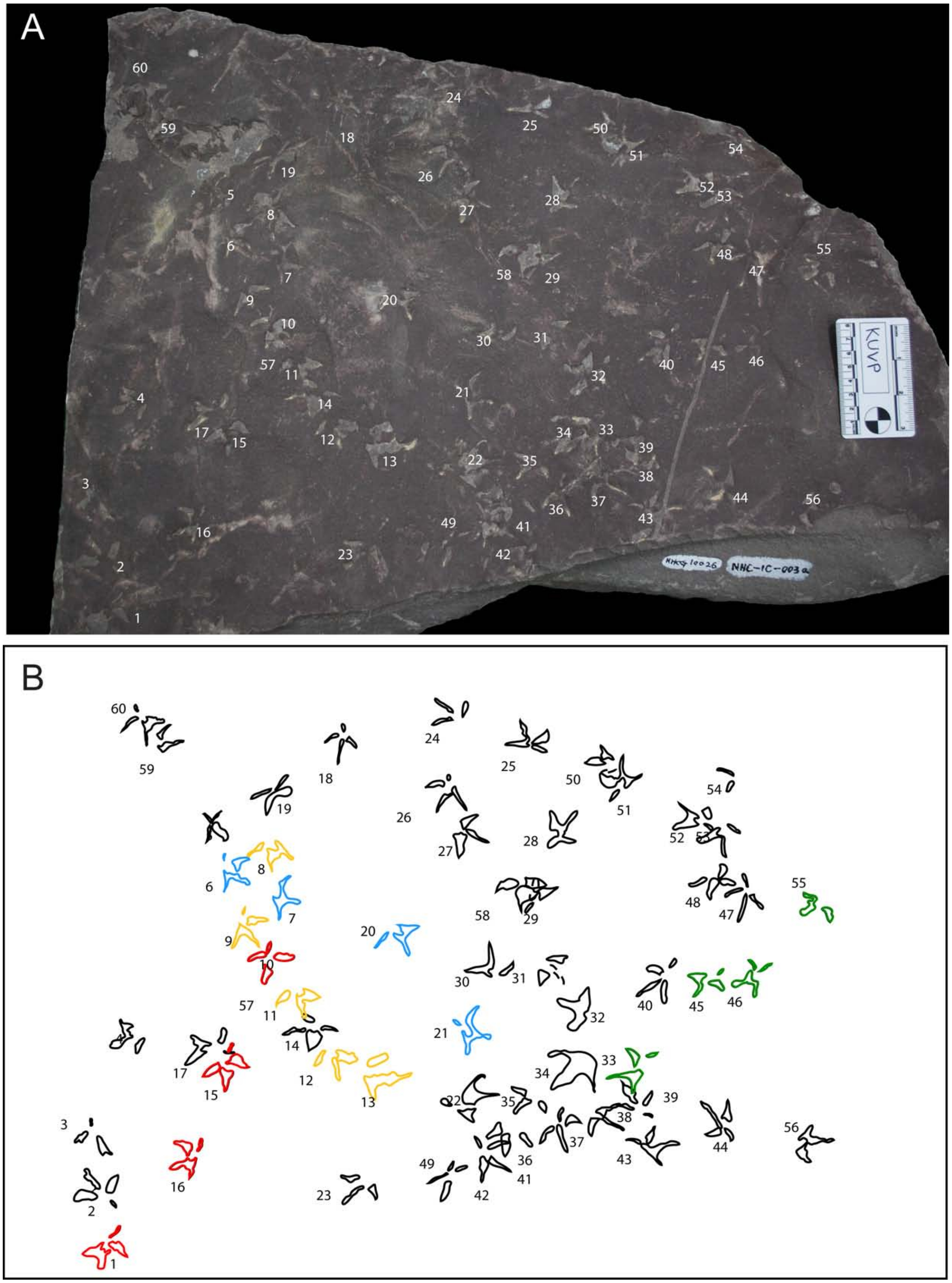

Figure 10: Photograph and line drawing of NHC-IC-0003A. A.) Photograph of specimen. B.) Line drawing of

specimen. Different colors represent different trackways measured on the slab. Some tracks that belong to the colored trackways were not included in the initial measurements and analysis and are, therefore, not colored in.

NHC-IC-004 contains 12 incumbent anisodactyl tracks with no discernable trackways. The average length of toe III is 20.3 mm. The average angle of divarication between toes II and IV is 125.5^{o}, and the average FL:FW ratio is 0.713. Distinct ripple marks are present on this specimen.

NHC-IC-002A contains 53 individual tracks, two short trackways designated as typical and atypical (Fig. 11), and several two-to-three parallel to subparallel linear traces (Fig. 9). The average length of toe III is 19.1 mm, the average angle of divarication between toes II and IV is 125.5^{o}, and the average FL:FW ratio is 0.711. The average pace length of the normal trackway is 56.8 mm, the average stride length is 106 mm, and the average angle of divarication from the midline is 15.7^{o}. The average pace length of the abnormal trackway is 60 mm, the average stride length is 116.7, and the average angle of divarication from the midline is 21^{o}.

The enigmatic traces associated with NHC-IC-002A are either paired or triad. There are a total of six measured clusters (Table 1), although more may be present that were not identified at the time of study. These traces are teardrop shaped or elongated ovals, and appear to occur alongside a trackway (Fig. 9A). The average length of these enigmatic traces is 8.4 mm, although in some cases slightly oblique curvature makes exact length impossible to measure. The average thickness of these traces at their greatest width is 1.9 mm, and the average distance between these traces is 2.6 mm.

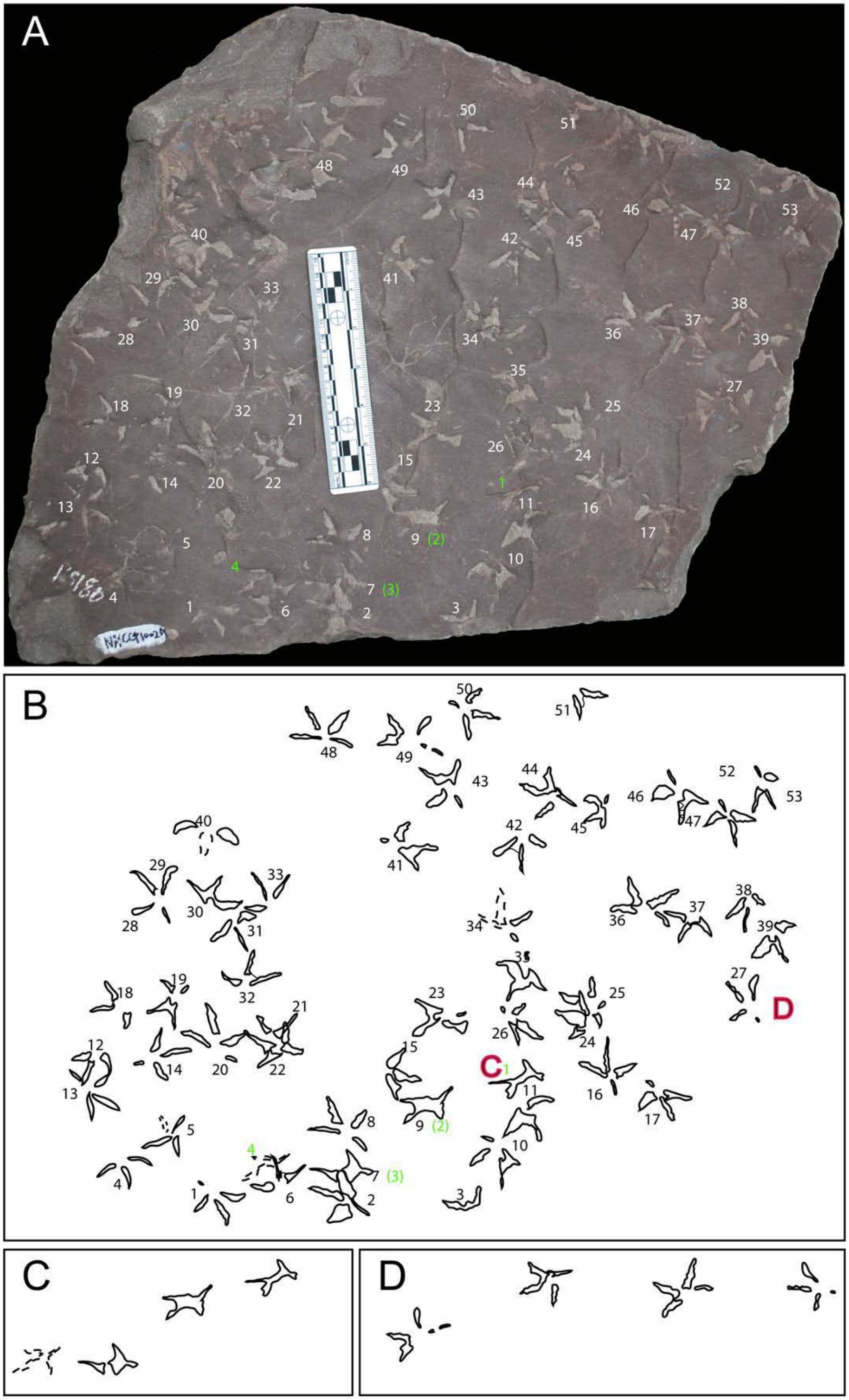
A
B
C
D

Figure 11: (Opposite page) Photograph and line drawing of NHC-IC-0002A. A.) Photograph of specimen. B.) Line drawing of specimen. C.) Trackway with abnormal morphology. D.) Representative trackway with normal track morphology.

KS064: Koreanaornis sp. and associated traces

The specimen KS064, which was previously described as *Koreanaornis sp.* (Falk et al., 2010) may actually be attributable to *Goseongornipes* due to the presence of a small amount of webbing between toes III and IV (Fig 12); their size range, however, is well within the *Koreanaornis* range: average foot length of 24.8 mm, which is skewed slightly by the presence of one very small track with a foot length of 16 mm (see Fig. 13). The average FL:FW ratio of the tracks of KS064 is 0.77, which is also within the range of the tracks attributable to *Koreanaornis*. The average angle of divarication is 108.8^{o}. Unlike *Koreanaornis hamanensis,* there is prominent webbing between toes III and IV in *Goseongornipes*, a strong metatarsal pad impression—which can be also be found in *Koreanaornis*, but is not described as a defining feature—and a longer hallux. *Koreanaornis* often lacks a hallux. Approximately half of the tracks on KS064 posses such a feature, however, and the average hallux length is 9.07 mm, which is approximately the length of the hallux in *Goseongornipes* based upon the line drawing in Lockley et al. (2006).

Figure 12: (Opposite page) A shorebird-like track on KS064 with semipalmate webbing. Arrow points to webbing. Note clear pad impressions on toe II.

These tracks are divided into four trackways (Fig. 13C). Trackway one contains 8–10 tracks—although the last two tracks in the trackway questionably belong with the others—and has an average pace length of 35.6 mm, an average stride length of 74.15, and an average pace width of 31.4 mm. The average angle of divarication from the midline is 9. Trackway two contains 4 tracks. The average pace length is 31.4 mm, the stride length is 45.5 mm. The average pace width is 34.4 mm and the average angle of divarication from the midline is 22^{o}. Trackway 3 contains 6-8 tracks. The affinity of the first two tracks is difficult to determine, as they are somewhat unusual. The average pace length is 34.5 mm, the average stride length is 80.2 mm, and the average pace width is 20.3 mm. Trackway 4 includes 6 tracks. The average pace length is 80.6 mm, the average stride length is 158.2 mm, and the average pace width is 29.8 mm. The average angle of divarication from the midline is 11^{o}.

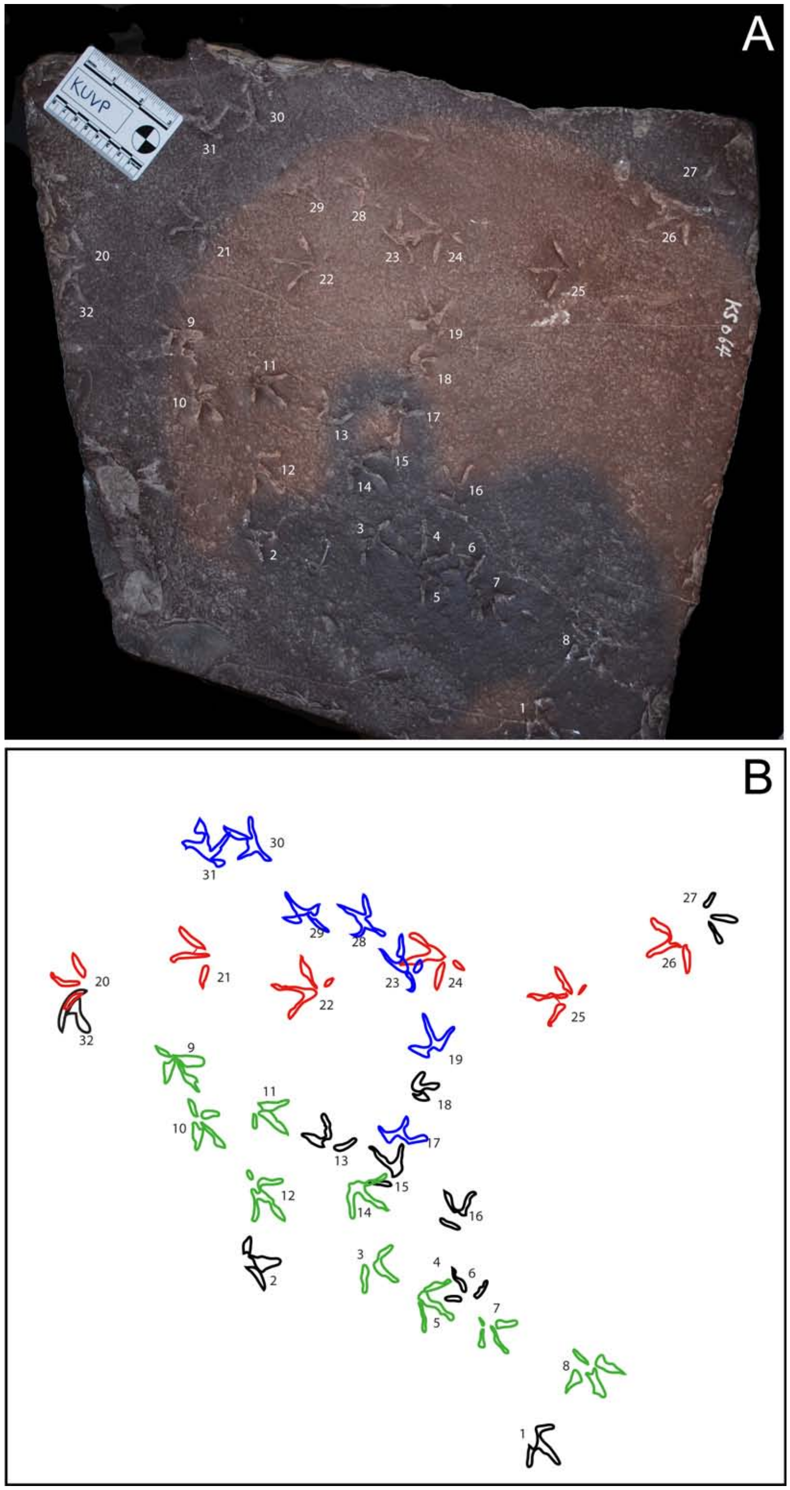

Figure 13: Photograph and line drawing of KS064. A.) Photograph of specimen. B.) Line drawing of the tracks and trackways of KS064. Colors represent different trackways present on the slab.

Geoseongornipes (EH2)

Thirty-one incumbent anisodactyl tracks attributed to *Goeseongornipes* by Kim et al. (2012) are found on the Exhibition Hall 2 (EH2) floor slab (Fig. 3). These tracks are divided into 3 separate trackways. The average toe III length of the EH2 tracks is 25.2 mm. The average angle of divarication between toes II and IV is 126.9^{o}, and the average FL:FW ratio is 0.738. Trackway 1 contains 16 tracks, with an average pace length of 66.9 mm, an average pace width of 28.8 mm, and an average stride length of 141.2 mm. Trackway 2 contains 6 tracks, with an average pace length of 63.2 mm, an average pace width of 27.9 mm and an average stride length of 121.9 mm. Trackway 3 contains 3 tracks, with an average pace length of 114.2 mm, an average pace width of 13.8 mm, and a stride length of 236 mm.

Unassigned ichnogenera

KS005, GS073, and GS068 are all separate blocks of tracks from Exhibit Hall 2 (Fig. 14, Appendix I, Table 4). They are currently unassigned to an ichnogenus due to a relatively small sample size in comparison to such currently well-represented ichnogenera as *Ignotornis* or *Goeseongornipes*. The tracks of KS005 have an average toe III length of 24 mm, an average angle of divarication between toes II and IV of 117.7^{o}, and an average FL:FW ratio of 0.72. There is no webbing present, and many tracks possess a hallux, which has an average length of 8.9 mm.

The tracks of GS073 have an average toe III length of 24.97 mm. The average angle of divaricating between toes II and IV is 117.8^{o}, and the average FL:FW ratio is 0.784. All tracks of

GS073 appear to lack a hallux. Some tracks on GS073 have faint impressions of short semipalmate webbing between toes III and IV.

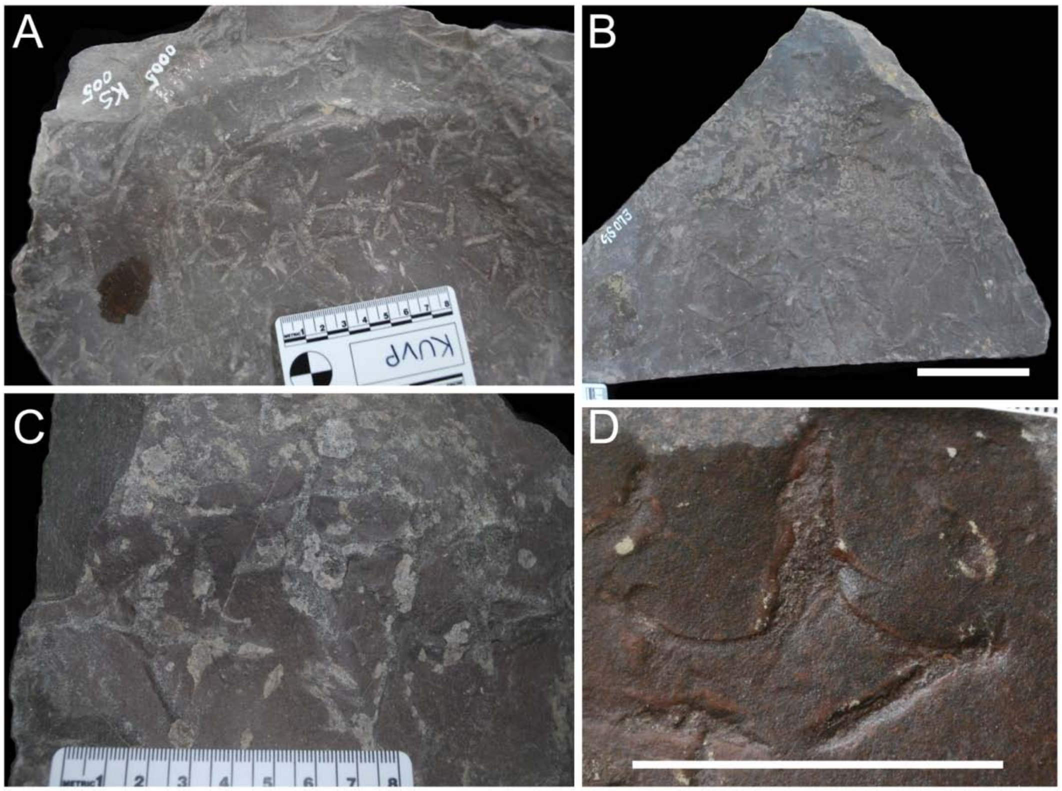

Fig. 14: A.) KS005. Scale bar=8 cm. B.) GS073. Scale bar=8 cm. C.) GS068. Scale bar=8 cm. D.) KS104. Scale bar=4 cm.

The tracks of GS068 have an average toe III length of 27.5 mm. The average angle of divarication between toes II and IV is 133.3^{o}, and the average FL:FW ratio is 0.787. Some tracks of GS068 posses a hallux, which has an average length of 14.8 mm. These tracks lack any impression of webbing.

DISCUSSION

The GISE site is unique not only due to its large number of bird tracks, but also due to the sheer variety of morphologies and behaviors present. There are several types of avian morphologies present at the GSIE site, along with many new types of feeding behaviors that have previously been undescribed from the fossil record. Many of these morphologies belong to established ichnogenera (see Kim et al., 2012), whereas others will require new ichnotaxa to be established.

Types of avian morphologies present

The presence six different morphotypes—*Koreanaornis*, *Goseongornipes*, *Ignotornis*, KS005, GS068, and GS073—indicate a high avian diversity. *Koreanaornis* and *Geoseongornipes* are similar overall, representing smaller, shorebird-like birds similar to sandpipers and plovers. These particular ichnogenera are present in very large quantities, especially *Koreanaornis*.

Ignotornis gajinensis represents an entirely unknown avian morphotype from the Mesozoic. No bird with a spoonbill-like skull has been reported from the Cretaceous (Lockley and Harris, 2010). There are no known fossil spoonbills, although subfossil remains have been recovered from Australia (Baird, 1990); however, the evidence at the GISE locality indicates a much earlier evolution of a spoonbill-like ecomorph. The tracks associated with the arcuate traces are strongly webbed, whereas spoonbills have semipalmate feet with webbing that is not exceptionally extensive (Swennen and Yu, 2004). Tracks that do not have webbing can appear webbed, depending on the sediment consistency (Elbroch and Marks, 2001; Falkingham et al., 2009); semipalmate tracks of modern spoonbills appear alongside arcuate bill traces left by their feeding activities (Swennen and Yu, 2005). The Cretaceous spoonbill-like ecomorph may have possessed webbed or semipalmate (partially webbed) feet, as webbing does appear in many well-preserved specimens (Fig. 15).

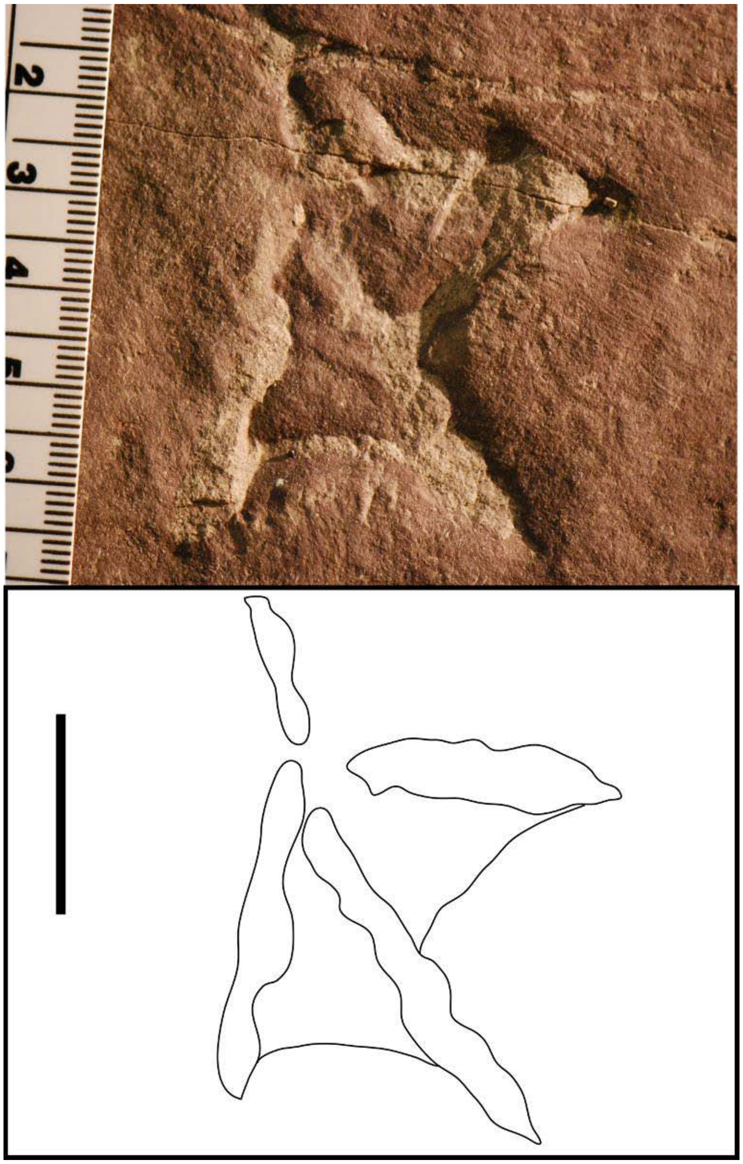

Figure 15: Well-preserved spoonbill-like *Ignotornis gajinensis* showing webbing and line drawing.

Kim et al. (2012) assigned EH2 to *Goseongornipes markjonesi* based on morphology. Some of the EH2 tracks—specifically those that lack a hallux impression and have the semipalmate webbing poorly preserved—superficially resemble *Aquatilavipes*, except that their size is much smaller. Their angle of divarication is smaller than that recorded for the holotype of *Goseongornipes* (126.8^{o} vs. 140–150^{o}). The webbing on the tracks of EH2 is often less distinct than that indicated on the holotype specimens of *Goseongornipes*. These specimens may belong to a new ichnospecies of *Goseongornipes* based on the characters present.

KS005 is similar to *Koreanaornis* except that it is larger—toe IV is 24 mm long instead of the average ~20 mm long—and there is a more pronounced and caudally directed hallux present (Fig. 16). The tracks of KS005 lack the distinctive semipalmate webbing that defines *Goseongornipes*. These tracks represent another type of shorebirdlike bird that was present at this locality.

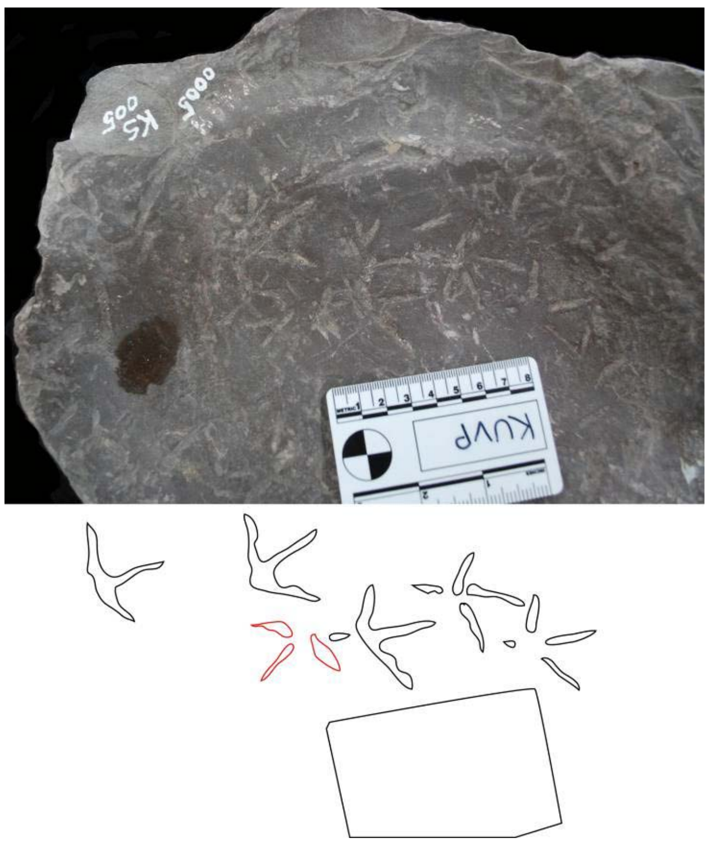

Figure 16: Photograph and line drawing of KS005. Note *Koreanaornis* in red.

The tracks of GS068 are similar in appearance to *Koreanaornis*, but posses a longer hallux—*Koreanaornis* often lacks a hallux—and are larger, with an average toe III length of 27.5 mm as compared to ~20 mm in *Koreanaornis*. These tracks possibly represent a different ichnospecies of *Koreanaornis*. These tracks represent a fourth type of sandpiper- or plover-like bird that was present at this locality.

The tracks of GS073 are approximately the same size as those found on KS005, but are morphologically different. All tracks lack a hallux; where the tracks of KS005 lack a metatarsal pad impression and posses a small hallux, the tracks of GS073 all posses a very clear metatarsal pad impression, and many have claw impressions preserved. There are also faint traces of semipalmate webbing present on some of the tracks, which is not as common or readily pronounced in *Koreanaornis*. These tracks represent a type of shorebird more similar to a plover or other medium-sized shorebird with an elevated or absent hallux. These tracks are highly unlikely to be referred to *Aquatilavipes* based only on the presence of semipalmate webbing.

Types of behaviors interpreted from the trackways

Several types of avian behaviors are present at the GSIE site. The most numerous and most important are the arcuate traces interpreted as scything behavior alongside the tracks of *Ignotornis gajinensis* (Lockley and Harris, 2010). These Cretaceous trackways are very similar in morphology, proportion, and stride length to those of modern Black-Faced Spoonbills (*Palatea minor*) studied by Swennen and Yu (2005, fig. 2a); however, they are smaller than those belonging to *P. minor* (toe III length of 26–43 mm vs 60–70 mm for *I. gajinensis* and *P. minor*, respectively). The *Ignotornis* trackways in our study have an average stride length of 216.6 mm and a standard deviation of 41.8, whereas modern *Palatea minor* trackways have an average stride length of 263 mm with a standard deviation of 32 (Swennen and Yu, 2005). Scything behavior is an important behavioral addition to the track record of Cretaceous birds, indicating that the range of avian-foraging behaviors (i.e., probing, pecking, foot shuffling;

Lockley et al., 2009; Falk et al., 2010) in water-margin environments is potentially far more extensive than has previously been thought.

Among the arcuate traces of EH1 Trackway 1 is a small, elliptical indentation between tracks 7 and 8 (Fig. 17). Spoonbills have been reported to make sharp, jabbing motions when prey is detected beyond the tip of the bill (Swennen and Yu, 2005, p. 23). The elliptical indentation may be a peck or jabbing form of prey-capture movement, given the broad, flattened morphology of the spoonbill's beak and a comparison of the indentation with Swennen and Yu's (2004, fig 1d) frontal view of the spoonbill's beak. This is evidence that the *Ignotornis gajinensis* tracemaker did possess a distally flattened, broad bill. No trace fossil of this jabbing method has been reported previously. The presence of this jabbing behavior indicates that the feeding methodologies of spoonbill-like birds were likely identical to modern spoonbills, and that they used both a scything and a jabbing method of prey capture.

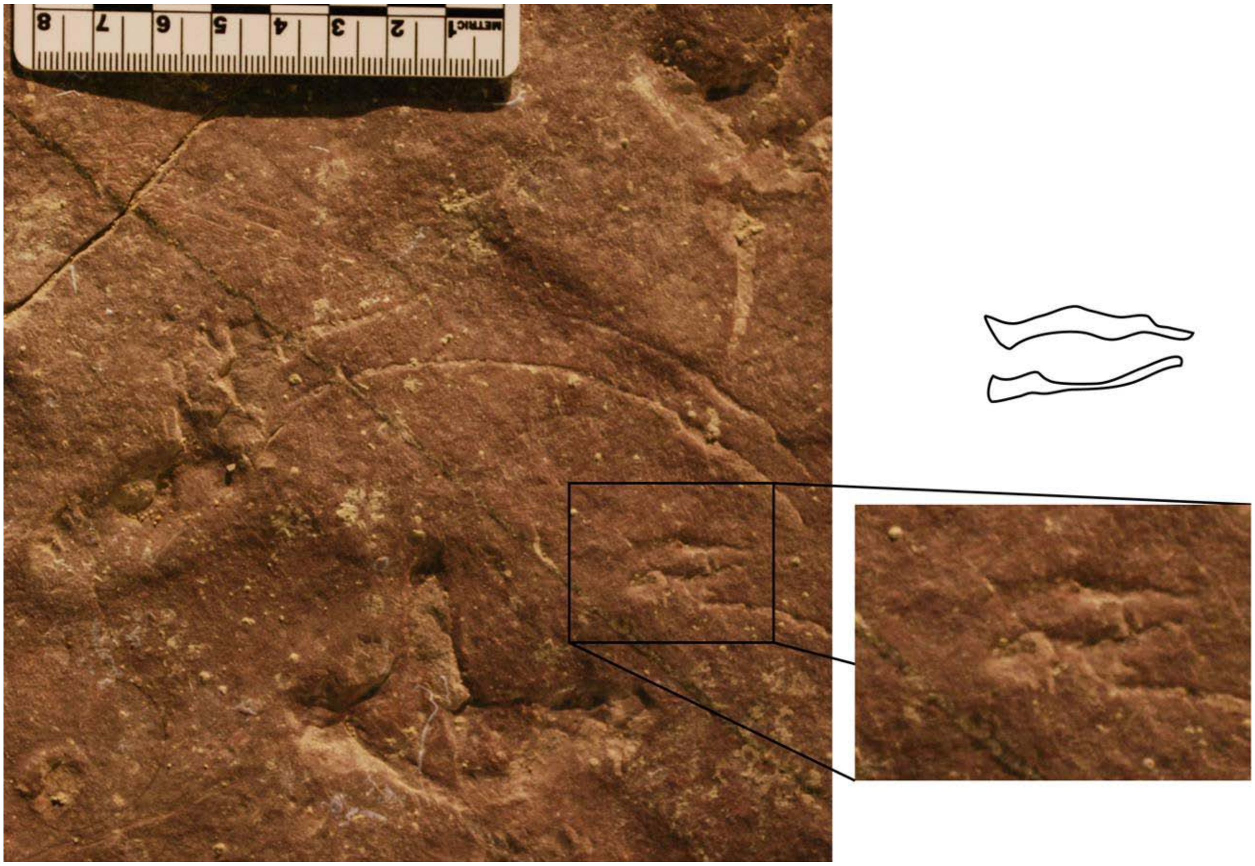

Figure 17: Elliptical beak impression next to EH1 trackway 1.

Another behavior reflected in the spoonbill-like traces can be seen in EH1 trackway 4, which consists of 9 tracks (Fig. 2D). This trackway has an abrupt beginning that is interpreted as a landing. The first three tracks of this trackway suggest that the bird landed and made a stutter-step (third track, which is a partial track) before beginning to forage. The third track perhaps represents the bird producing a trace with a partially clenched foot. The foraging behavior is represented by the paired arcuate traces recorded later in the trackway.

Trackway 5 of EH1(Fig. 2E) indicates that the large sauropod tracks found alongside trackway 5 were produced prior to the bird trackways. High concentrations of *Koreanaornis* and other bird tracks found within the sauropod tracks support this interpretation (Fig. 18). Trackway

5 contains a series of tracks exhibiting the spoonbill-like scything behavior. The bird then clearly steps down into the sauropod track (Fig. 18C). There are no arcuate traces associated with this trackway within the sauropod track; the lack of the feeding traces may reflect relatively deeper water within the sauropod track. This interpretation is supported by the observations of modern spoonbill feeding behaviors, which are only recorded as arcuate traces in very shallow water (Swennen and Yu, 2005).

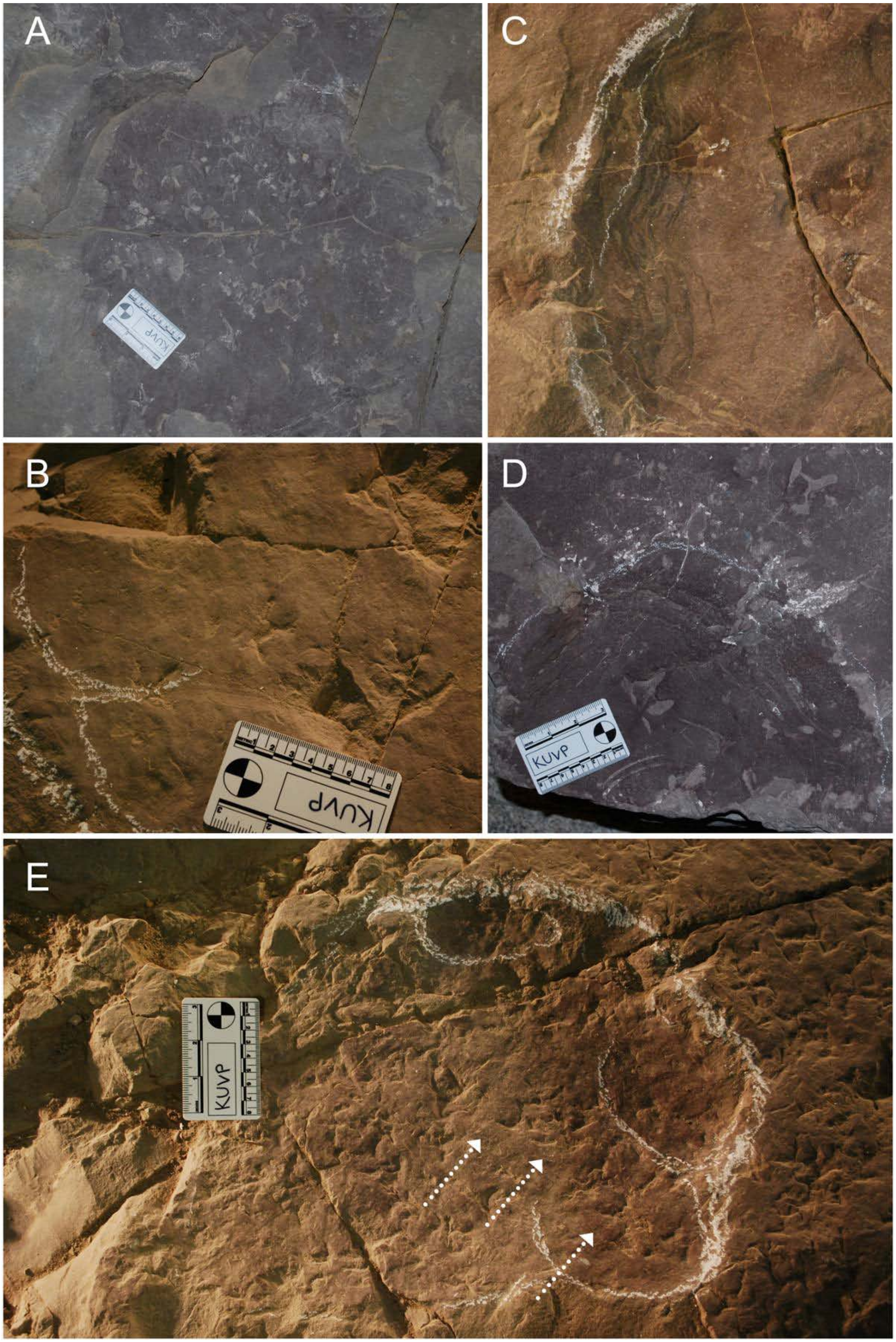
A
C
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Figure 18: (Opposite page) Bird tracks found inside sauropod tracks on EH1 floor slab. A-B.) Shorebird-like tracks found inside sauropod tracks. C-D.) *Ignotornis gajinensis* tracks found inside sauropod tracks. Note that in C the bird is stepping down into the track, while in D the bird is stepping up out of it. E.) Large sauropod track with many shorebird-like tracks found inside (arrows).

Perhaps the association of avian tracks, trackways, and feeding traces with sauropod tracks and trackways may suggest that birds were trailing megaherbivores. This type of trailing behavior is seen in birds today in Africa that follow large herbivores (Dean and MacDonald, 1981), on the ocean following feeding cetaceans (Evans, 1982) and the wakes of boats (Hudson and Furness, 1989; Tasker et al., 2000), and in rural areas where farming equipment disturbs the soil by plowing (Welham and Ydenberg, 1988; Tasker et al., 2000). Thus, the trace-fossil associations in the Haman Formation can be interpreted as follows: as sauropods moved through the water, they stirred up the sediment and benthic invertebrates that were foraged upon by the birds that followed in the wake, snapping up the disturbed prey.

The tracks of EH2 show mostly straight-line to slightly meandering walking. One long trackway is intersected by two other shorter trackways and, therefore, behavioral interpretations of the other two trackways are difficult to determine (see Fig. 3). The EH2 tracemaker exhibited typical heronlike foraging behaviors based on variations in pace length and stride length (Table 2). Herons and other wading birds rarely take regular steps when feeding, and often stop and stand before starting again. Although no traces are present on the EH2 slab to suggest stopping and standing behavior, the intersection of multiple trackways of the same type of tracemaker (if not the same tracemaker) makes such an interpretation more difficult than if all three trackways were isolated.

Trackway 1				Trackway 2	
Pace length				Pace Length	
0-1:	42.42	8-9:	89.54	17-18:	22.25
1-2:	57.04	9-10:	45.42	18-19:	53.52
2-3:	93.29	10-11:	103.23	19-20:	77.63
3-4:	58.44	11-12:	87.56	20-21:	99.35
4-5:	76.48	12-13:	93.76		
5-6:	44.42	13-14:	32.46	Stride Length	
6-7:	54.57	15-16:	79.49	17-19:	70.29
7-8:	45.79			18-20:	132.87*
				19-21:	153.7
Stride Length				21-22:	141.79
0-2:	135	7-9:	141		
1-3:	180	8-10:	129	Pace Width	
2-4:	141	9-11:	153	17-18:	35.07
3-5:	135	10-12:	213	18-19:	34.81
4-6:	121	11-13:	196	19-20:	51.41*
5-7:	102	12-14:	128	20-21:	13.71
6-8:	105	14-15:	98.47		
				AoDfM	
Pace Width				17:	45.76
0-1:	27.39	8-9:	26.52	18:	8.22
1-2:	32.92	9-10:	19.14	19:	26.37
2-3:	16.08	10-11:	40.9	20:	39.75
3-4:	31.94†	11-12:	11.14	21:	N/A
4-5:	40.23	12-13:	77.94	22:	N/A
5-6:	0	13-14:	32.92		
6-7:	32.11	15-16:	56.7*	Trackway 3	
7-8:	16.9			Pace Length	
				23-24:	97.24
AoDfM	(degrees)			24-25:	131.24
0:	25.82				
1:	17.17			Stride Length	
2:	7.57			23-25:	236
3:	9.96				
4:	14.42			Pace Width	
5:	7.69			23-24:	6.24
6:	65.66			24-25:	21.3
7:	20.01				
8:	22.7			AoDfM	
9:	61.68			23:	23.88
10:	22.54			24:	16.09
11:	18.44			25:	32.2
12:	13.16				
13:	31.64				
14:	29.25				
15:	23.24				
16:	<5				

Table 2: (Opposite page) Multiple-track measurements of the floor slab of Exhibit Hall 2.

There are a few interesting behaviors noted on the EH2 slab (Fig. 3). Track 2, originally thought to have a long hallux, is actually a double step; the left foot came down then came back up and was placed a few centimeters forward of its previous position, causing an overlapped track. Toe IV of this first step did not register, and the two toe IIIs appear almost continuous. Only toe II indicates that it is a double step. This bird was likely foraging for food and, therefore, being careful where it placed its feet. Track 9 has toes that are much thicker than other tracks from this floor slab (Appendix I), and between the toes there are small raised areas of sediment (Fig. 19). The particularly long pace length between tracks 8 and 9 (89.5 mm) and tracks 10 and 11 (103.2 mm, see Appendix I), and the twisted morphology of track 9 may be analogous to a specific type of feeding behavior commonly seen in the Reddish Egret (*Egretta rufescens*) of North America. This heron will leap, hover, and rake its feet—stirring up the sediment to either frighten or confuse prey species—before landing to capture prey species that have been disturbed (Meyerriecks, 1959; Kushlan, 1976).

Figure 19: *Goeseongornipes* track showing abnormal morphology—likely due to twisting. Water was used to highlight the track and increase contrast.

Falk et al. (2010) provided a preliminary description of the behaviors of KS064. The peel described in that study, however, was partial, and did not allow for a complete interpretation of the behaviors of the tracemakers. Several behaviors ranging from simple running to feeding traces are present on the slab (Fig. 13) from which the partial peel was made.

The trackway that has tracks labeled as having an atypical morphology (tracks 9 and 10) may represent a landing trace (Fig. 13; green trackway). They are approximately 8 cm from the broken edge of the slab, however, there are no other tracks posterior to them that appear to be associated with this trackway. They have relatively narrow angles of divarication—88^o and 96^o, respectively—and have long halluxes (12 mm and 13.5 mm, respectively). The next track in this series, track 11, lacks a hallux but appears to be impressed somewhat deeper into the sediment than the other tracks (Fig. 13), and tracks 10–11 have an extremely short pace length and narrow pace width (Table 3). Track 11 could be the evidence of the animal slowing quickly as it took the next step after landing. Track 12, the next track in this sequence, is entirely typical, indicating the landing process was complete and the bird was walking normally.

Trackway 1: 9, 10, 11, 12, 14, 3, 5, 7, 1?, 8?

Pace Length	
9-10:	31
10-11:	24
11-12:	34.5
12-14:	42.2
14-3:	42.2
5-7:	39.5
7-1:	65.2
1-8:	6

Stride length	
9-11:	62
10-12:	58
11-14:	78
12-3:	82.5
14-7:	104
3-5:	40.5
5-1:	110
7-8:	58.2

Pace Width:	
9-10:	16
10-11:	34.2
11-12:	38.2
12-14:	46.2
14-3:	30.5
5-7:	15.2
7-1:	20.5
1-8:	50.3

AoDfM		
9:	16	
10:	3	away
11:	3	
12:	14	away
14:	3	away
3:	6	
5:	6	
7:	10	
1:	6	away
8:	23	

Trackway 2: (17) 19, 23, 28, 29, 30, 31

Pace Length	
19-23:	42
23-28:	32
28-29:	31.5
29-30:	58
30-31:	13.5

Stride length		
19-28:	95	(curve)
23-29:	69.2	
28-30:	90	
29-31:	74	

Pace Width:	
19-23:	27.5
23-28:	4.2
28-29:	23.5
29-30:	18
30-31:	28.5

AoDfM	
19:	36
23:	55
28:	3
29:	17
30:	5
31:	48

Trackway 2: 26, 25, 24, 22, 21, 20

Pace Length	
26-25:	80
25-24:	85.5
24-22:	81
22-21:	76.2
21-20:	80.5

Stride length	
26-24:	163
25-22:	167
24-21:	150
22-21:	152.7

Pace Width:	
27-25:	32.2
25-24:	28.2
24-22:	34.2
22-21:	30.7
21-20:	26

AoDfM	
26:	25
25:	4
24:	16
22:	11
21:	5
20:	5

Table 3: (Opposite page) Multiple-track measurements of KS064. Track numbers marked with a "?" indicate there is some question about their affinity with that trackway. "Away" indicates that the foot was turned outward from the midline of the trackway, rather than inward. "Curve" indicates that the trackway was sinuous at this point.

At the end of the landing trackway, track 8 intersects with an invertebrate trace (cf. *Steinichnus*; Fig. 20). Toe III of track 8 has a greater width than that of any other track except for track 31 (Appendix I). The track itself seems smeared, as if the animal pivoted in place (Fig. 20, see also Fig. 13). After this point, the invertebrate trace is not present. There is an elliptical impression on the surface between toes III and IV that is not webbing, and appears morphologically similar to the peck marks previously reported from the Haman Formation (Falk et al., 2010). This association of traces and tracks suggests that the bird was hunting the invertebrate, and perhaps captured it.

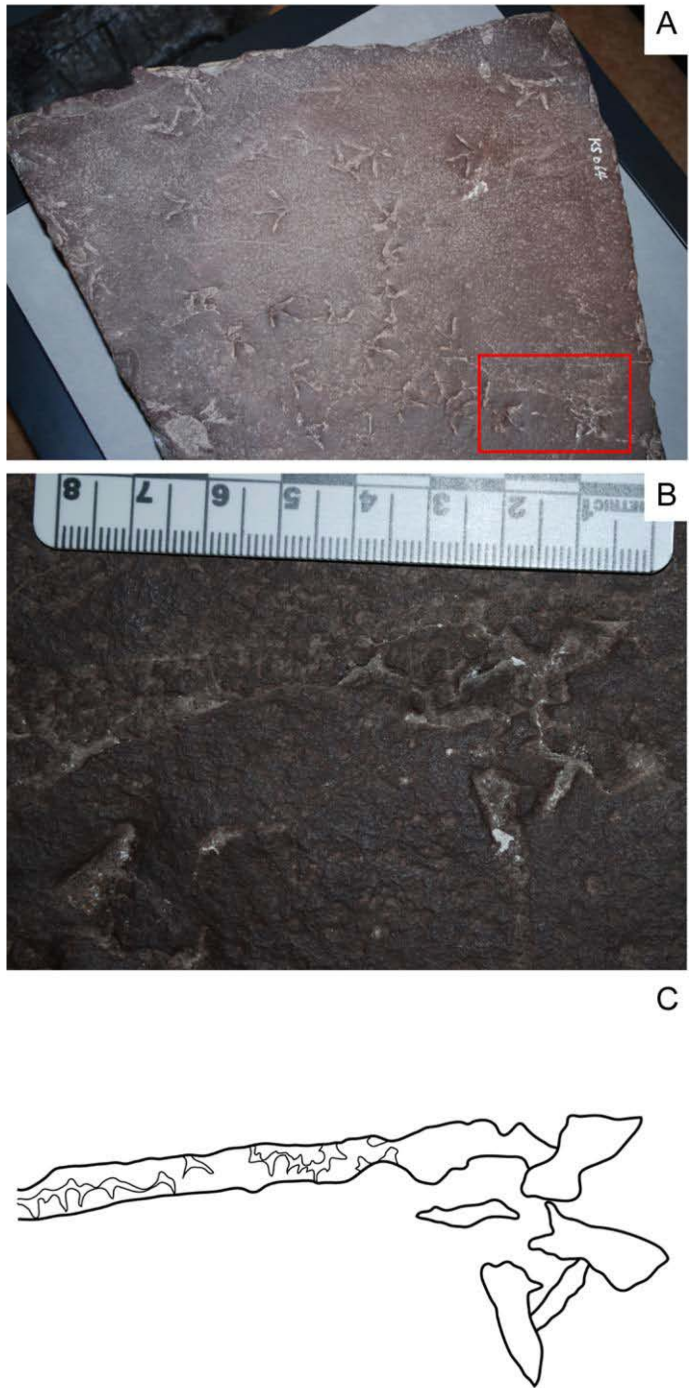

Figure 20: Intersection of an invertebrate trace (?*Steinichnus*) and a bird track. A.) Photograph of KS064, with area of B boxed in red. B.) Intersection of cf. *Steinichnus* and bird track, which may indicate predatory behavior on the part of the bird. C.) Line drawing of B.

The tracks from KS019 were not measured due to extreme track density (Fig. 21), however, KS019 does show an important behavior. Probe marks have been reported from the Haman Formation and from Upper Cretaceous deposits from northern North America (Falk et al., 2010; Fiorillo et al., 2011). The probe marks previously reported from the Haman Formation, however, were isolated, indicative of a different pattern of feeding than the type seen from the Upper Cretaceous Cantwell Formation, which show the probe marks in more of a cluster or a group (Fiorillo et al., 2011, fig. 13). Elbroch and Marks (2001) illustrate several different kinds of probing, from isolated probes, to clustered probing, to linear probing. Isolated and clustered probes are usually performed while the bird has paused; linear probing is a continuous action while the bird walks. KS019 shows several areas of probe clusters (Fig. 21B–C), a phenomenon previously unreported from Lower Cretaceous rocks.

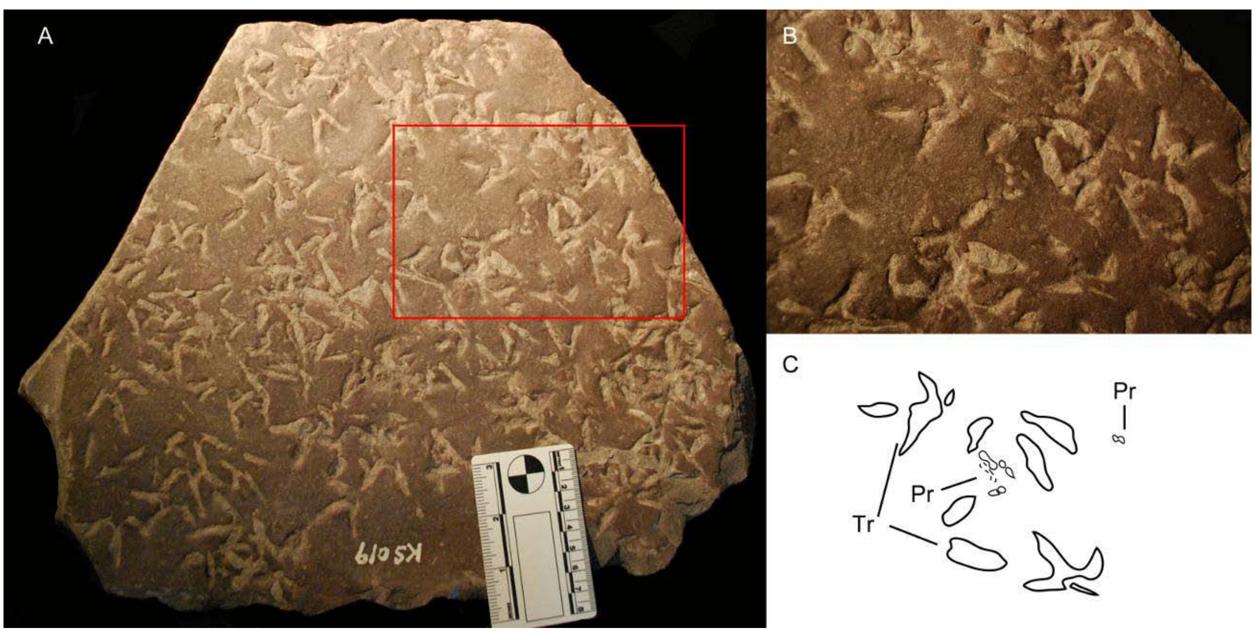

Figure 21: KS019. A.) Photograph of the specimen. Red box indicates area defined in B. B.) Close up of a probe cluster (arrow). C.) Line drawing from B. Tr-track, Pr-probe.

Other specimens of *Koreanaornis* sp. (NHC-IC-003a, NHC-IC-002A) show a variety of behaviors. NHC-IC-002A contains a series of paired to triplet parallel to subparallel traces that may or may not be slightly curved (Fig. 11). There are two possible interpretations for these marks. (1) These enigmatic traces may be the drag marks of feathers, either primary feathers or tail feathers. The bird that produced them might have been injured, although there is no evidence in the trackway of a limp or any sort of other injury. There are several behaviors that may cause a bird to drag its feathers; one of the well-known behaviors is the broken-wing-defense commonly seen in plovers. The male or female will feign a broken wing in order to draw a predator away from the vulnerable offspring. (2) These marks may represent swimming traces of a reptilian trackmaker the size of a small lizard. Reptile swim traces are often preserved as 3–5 thin, decurved lines following a central track midline (Hunt et al., 1990; Melchor and Sarjeant, 2004; Milner et al., 2006). Invertebrates were not likely responsible for these traces; they are discontinuous, and are dissimilar from any other invertebrate trace reported from the fossil record.

NHC-IC-002a also contains tracks that represent atypical shorebird track morphology (Fig. 11C). The exact behavioral cause of this morphology is unknown, as this morphology has not yet been observed in modern bird tracks. These types of tracks may represent a landing trackway, or a very fast running trackway, based on a similar morphology seen on KS064. The trackway seen on NHC-IC-002a is only four tracks long and terminates due to the broken edge of the slab. This atypical trackway morphology is unlikely to be due to the presence of a different type of bird, based on comparisons to trackways from KS064.

NHC-IC-003a contains an oval-shaped, slightly depressed area, bounded on one side by a crescent-shaped indentation and on the other by what appears to be a small linear trough (Fig. 22). Interpretation of these features is difficult without multiple examples.

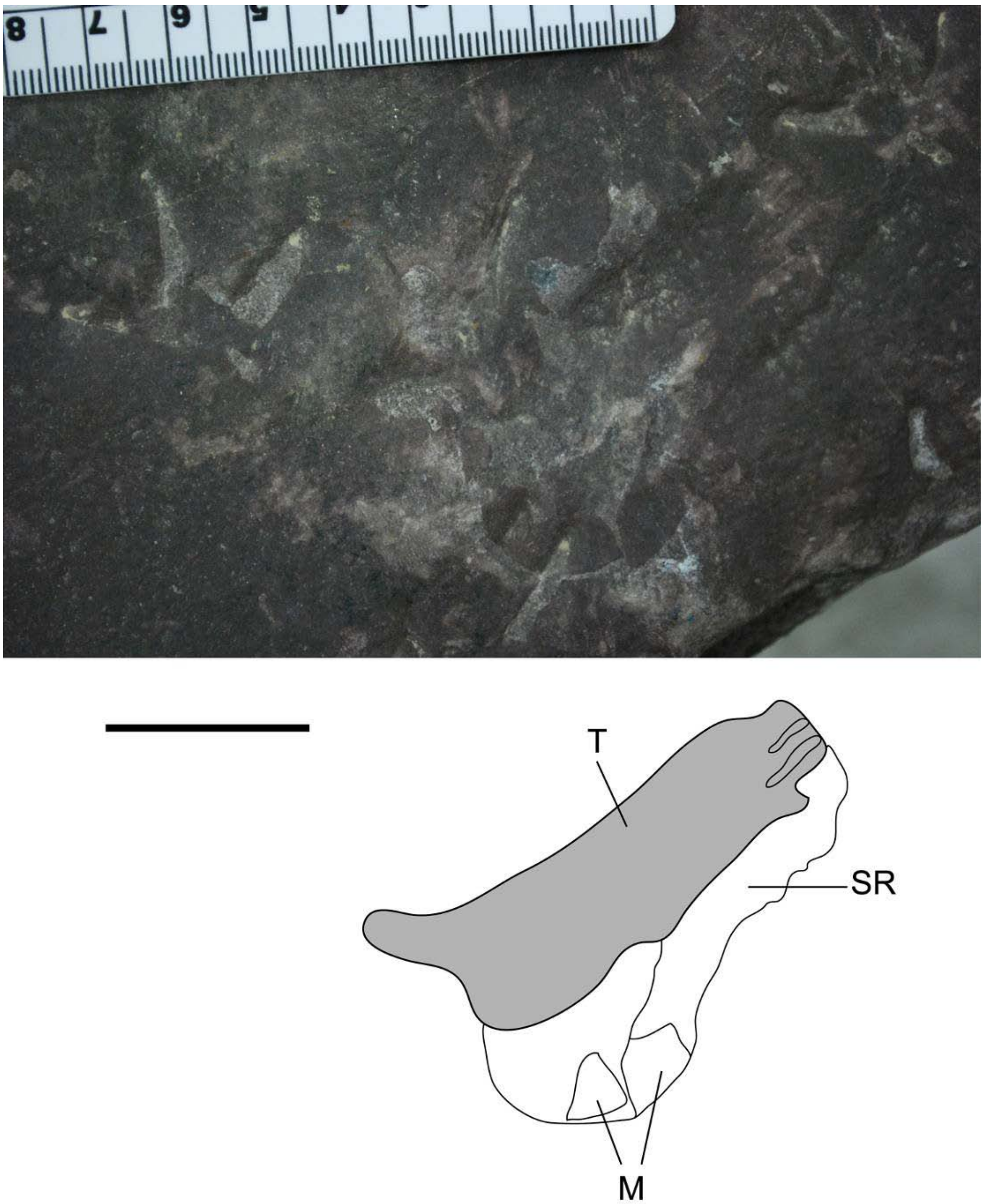

Figure 22: Enigmatic trough-like trace on NHC-IC-003a. Line drawing represents enigmatic trough (T), a displaced ridge of sediment (SR) and clasts of displaced mud (M). Line drawing scale bar 3 cm.

Implications for the depositional environment

The presence of several kinds of invertebrate trace fossils (*Steinichnus*, *Treptichnus*, and cf. *Naktodemasis*) indicates an alternating shallow, freshwater and subaerial environment. The Haman Formation has always been interpreted as an alluvial succession. The presence of current ripples on the EH1 floor slab (Fig. 7A) support this interpretation. The presence of the bird tracks and other invertebrate traces, however, likely indicates a short periods of standing water and subaerial exposure. *Steinichnus* indicates that the water table was near the sediment-air interface (Hasiotis, 2002, 2004). Subaerial exposure with algal or cyanobacterial growth as a sediment binder would preserve the tracks (e.g. Noffke and Krumbein, 1999). The lack of pedogenic features suggests that sedimentation rates were much higher than pedogenic rates (Hasiotis and Platt, 2012).

The presence of the *Ignotornis gajinensis* spoonbill-like traces and their overall complete similarity to modern black-faced spoonbill *Palatea minor* traces allows for a more specific interpretation of the depositional environment. Spoonbills feed using extrasensory electromagnetic organs on the bill (Swennen and Yu, 2004). Spoonbills do not feed on subaerially exposed sediment due to the uses of these extrasensory organs; therefore, there spoonbill-like feeding traces are strong evidence for the presence of water at the time of trackway production. Modern *P. minor* trackways with paired arcuate traces nearly identical in morphology to the trackways with arcuate marks from the Haman Formation were made in very shallow water that was < 6–7 cm deep (Swennen and Yu, 2005). The spoonbills were observed feeding in deeper waters, and footprints were observed from these foraging sessions, but no arcuate scything traces were found alongside them when the spoonbills foraged in waters deeper than 6 cm (Swennen and Yu, 2005, fig 2b). This is due to the varying positions of the head in relation to depth of the water during feeding (Swennen and Yu, 2005, fig 1). The Haman Formation trackways were produced by something that had a very similar morphology to *P. minor* based on stride length and foot parameters and, therefore, the length of the bill and leg of the Early Cretaceous spoonbill-like bird were slightly smaller than the modern *P. minor.* The water level must have been similar, but slightly more shallow, to that recorded by Swennen and Yu (2005) in order to leave the arcuate traces.

Implications for avian evolution based on behavioral evidence

The behavioral evidence shown in this the study area of the Lower Cretaceous Haman Formation indicates a high diversity of birds (Table 4). Ornithurine birds likely produced these tracks, as they are the dominant water birds of the Early Cretaceous (Zhou and Zhang, 2007). The presence of scything traces, peck marks, and probe marks also indicate that several modern feeing behaviors had evolved by the Early Cretaceous. The high morphologic variation (at least 7 different morphologies at the GISE site) in the Haman Formation supports these interpretations.

Formation	Location	Age	Diversity	Ichnogenera
Dakota	Colorado,	Late Cretaceous	High	*Ignotornis,*
	USA			*Koreanaornis*
				Aquatilavipes
Lakota	South Dakota,	Early Cretaceous	Low	*Aquatilavipes*
	USA			
Gething	British Colombia,	Early Cretaceous	Low	*Aquatilavipes*
	Canada			
Haman	Republic of	Early Cretaceous	Very High	*Koreanaornis*
	Korea			*Geoseongornipes*
				Ignotornis, more
Jindong	Republic of	Late Cretaceous	Low	*Jindongornipes*
	Korea			*Koreanaornis*
Uhangri	Republic of	Late Cretaceous	Low	*Uhangrichnus*
	Korea			
Itsuki	Japan	Early Cretaceous	Low	*Aquatilavipes*
Jingchuan	China	Early Cretaceous	Low	*Tatarornipes*
Tugulu	China	Early Cretaceous	Very High	*Koreanaornis*
(Group)				*Aquatilavipes*
				Moguiornipes, more
Jinhua	China	Late Cretaceous	Low	*Dongyangornipes*
				Koreanaornis

Table 4: Examples of rock units with low diversity, high diversity, and very high diversity of fossil birds.

This diversity of morphologies and behaviors suggests that ornithurine birds had a radiation that may have rivaled the enantiornithine birds for its diversity during the Early Cretaceous. Enantiornithines were the dominant terrestrial birds during the Cretaceous (Zhang et al., 2004), and filled the niches of terrestrial birds. The ornithurine birds were much smaller in diversity according to the body fossil record (Zhou and Wang, 2010); however, they dominate the avian trace-fossil record, with no known tracks of enantiornithines preserved. Ornithurine birds dominate the water-margin environments of the Early Cretaceous, which is where all Early

Cretaceous bird tracks are preserved (Lim et al., 2002). This lack of enantiornithine tracks may be an artifact of the lifestyle of these birds, as they were mainly arboreal (i.e., tree dwelling).

Recent studies of avian molecular clocks suggest that the origin of modern bird families took place during the Cretaceous (Pereira et al., 2007; Brown et al., 2008; Pacheco et al., 2011). Some Late Cretaceous fossil birds have been assigned to modern or Cenozoic orders and/or even Cenozoic families (Chiappe and Dyke, 2002; Kurochkin et al., 2002), but no Early Cretaceous birds are thought to belong to extant families or genera. The likelihood of the spoonbill-like tracemaker belonging to the Threskiornithidae is very small, and these tracks are probably the traces of a spoonbill ecomorph—a shallow-water-feeding bird with a spoon-shaped bill.

The majority of Mesozoic avian tracksites are monospecific with relatively few tracks (Lockley et al., 2001, 2009; Anfinson et al., 2009); however, an increasing number of in multi-ichnotaxa sites with high track density are being identified in East Asia (Xing et al., 2011; Lockley et al., 2012; Kim et al., 2012). This may be evidence that East Asia was the center of early avian evolution as suggested by Zhou et al. (2003).

CONCLUSIONS

The fossil bird tracks of the Lower Cretaceous Haman Formation at the GSIE site show at least seven different morphotypes. Associated with these tracks are a variety of feeding behaviors, from isolated probe marks and clustered probing, to pecking, and complex arcuate traces associated with web-footed tracks that are identical to similar traces produced by modern Black-faced Spoonbills. Other behaviors include landing traces, walking and foraging, and traces of predator-prey interaction. The environment of this locality is interpreted as extremely shallow water (~5–6 cm deep) based on comparison of the Cretaceous traces to similar modern avian traces and their environment. The webbed-footed bird tracks and traces were produced under water based on the presence of the arcuate traces, the conditions under which these traces are produced by modern spoonbills, and the lack of mudcracks indicative of subaerial exposure. The incredible morphologic and behavioral diversity of the GSIE site and at other localities from the Lower Cretaceous Haman Formation suggests that the Mesozoic ornithurine radiation was, perhaps, as diverse as the enantiornithine radiation; however, the ornithurines were confined to the water-margin environments, whereas the enantiornithines dominated terrestrial niches. Many of the bird tracks seen at the GISE site are yet undescribed, in part, due to the sheer amount of material that still needs to be examined. Also, this locality is only one of many bird tracksites in the Cretaceous of South Korea and other outcrops still need to be examined for bird tracks.

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A MORPHOMETRIC APPROACH TO USING BONES AS A PROXY FOR TRACKS: IS RETRODICTING AVIAN TRACEMAKER MORPHOLOGY POSSIBLE?

ABSTRACT

Reconstructing the soft tissue of modern and ancient bird feet from osteology alone has not been previously performed. Similarly, retrodicting trace-fossil morphology from body fossils has not been attempted for birds. This study takes a series of morphometric measurements from osteological, soft tissue, and ethanol-preserved specimens of birds from the University of Kansas ornithological collections. Tissue volume and general morphology is thought to be well preserved in ethanol, making the morphological measurements aquired in this work representative of living birds. The relative length of phalangeal pads varies between life-habit groups—the phalangeal pads of passeriform (perching) birds tend to be fleshy, and relatively large in regards to the bony phalanx. The phalangeal pads of ground birds are also fleshy, but reduced in relation to the bony phalanx, whereas the interphalangeal pad is expanded. The phalangeal pads of wading birds and shorebirds are thin and lack fleshiness, and are reduced in regards to the bony phalanx, whereas the interphalangeal pad is expanded. Webbed-footed birds and lobed-footed birds lack clearly defined toe pads. Fleshiness and expansion of the interphalangeal pads may be correlated with the consistency of the media with which the bird often interacts. Results indicate that soft tissue and ethanol-preserved specimens are not significantly different from osteological specimens with regard to toe length, indicating that soft tissue does not factor into toe length in track production. Toe width, especially width at more proximal joints, often varies significantly between osteology and soft tissue and, therefore, is not a practically applied measurement when dealing with tracks. Furthermore, footprint toe width is

influenced by media consistency. Based on this evidence, ancient bird tracks can be retrodicted strictly from fossil bird feet directly.

INTRODUCTION

A recurring concept in invertebrate and vertebrate ichnology is the difficulty of thoroughly linking tracemaker and trace. In very rare cases, deceased animals are found in, alongside, or at the end of their trace—e.g., Solnhofen horseshoe crabs at the end of their trackways (Lomax and Racay, 2012), crayfish burrows with body fossils (Hasiotis and Mitchell, 1993), and a purported protoceratopsian track alongside a skeleton (Niedzwiedzki et al., 2012). Fortey and Seilacher (1997) erected a series of criteria to aid in associating a trace fossil with a possible tracemaker. These criteria include a close association of body and trace in outcrop, overlapping stratigraphic range of body and trace, and minimal other fossil candidates that could produce the trace at that time. There are formations that contain both avian trace fossils and body fossils within the same formation (e.g., the Eocene Green River Formation, U.S.A.), although they are often found separated by great distance and in different beds in the same member or in different members of the same formation, and thus likely offset by as much as 10^3–10^5 years of sedimentation (Begon et al., 2006). The chances of an animal leaving a trace and then being preserved nearby are very small.

A major limiting factor in preserving the avian tracemaker and trace together is the environment. Those environments best suited to preserve body fossils are often anoxic (e.g., deep meromictic lakes) or high energy (i.e., rivers that flood and trap large quantities of articulated and/or disarticulated skeletons into a bonebed) (Martin, 1999). Production of avian tracks and trackways, on the other hand, require extremely shallow water or subaerial exposure, followed by rapid burial for preservation. If not buried rapidly, bird tracks can desiccate and become unrecognizable in 4–7 days (Cohen et al., 1991).

Gaps in the fossil record make many ichnologists reluctant to link trace to tracemaker. Another argument is that one organism may create multiple types of traces, or multiple types of animals may produce traces that all look very similar (e.g., Ekdale et al., 1984). This is also true in vertebrate traces; for example, tracks of small shorebirds are exceptionally similar in many cases, often distinguishable only by size or presence/absence of a hallux or direct observation of tracemaking (Elbroch and Marks, 2001). Modern birds can be linked to the traces they produce through direct observation; in the fossil record this is not possible.

This paper reports on morphometric analyses of the bones and soft tissues of modern birds. No study has adopted a comprehensive examination of bone and soft tissues of the feet of modern birds. Few studies have attempted to link the feet of fossil birds to the tracks they may have produced; Li et al. (2011) examined the fossil tracks of an Early Cretaceous shorebird-like ichnogenus *Tatarornipes* and compared them to the foot and hindlimb of a specimen of *Cathayornis chabuensis* found in the same formation, near Chabu, Inner Mongolia. They determined that *Cathayornis*, an arboreal perching enantiornithine bird, was not the producer of the Chabu traces, based on the skeletal morphology and the size and morphology of the track, which lacked a hallux.

BACKGROUND

There have been countless morphometric soft tissue studies using museum specimens (e.g., taxidermied museum skins or specimens in ethanol storage), however, there are no published studies linking bone to skin morphology in modern birds, nor is there information where the soft-tissue morphometrics are compared to bone morphometrics in live birds. Furthermore, the use of museum specimens has limitations—shrinkage in study skin prepared specimens has been known to occur (Greenwood, 1979; Kuczynski et al., 2003; Wilson and McCracken, 2008). Studies correcting for shrinkage in study skin prepared specimens have been conducted (Fjeldsa, 1980; Wilson and McCracken, 2008). Kuczynski et al. (2003) suggest that data on morphometric shrinkage may also be difficult to interpret due to subjectivity in the measuring process. They also suggest that the age of the skin may affect the amount of shrinkage, although this has yet to be quantified (Kuczynski et al., 2003).

Studies that reconstruct soft tissues in fossil birds have largely focused on plumage (e.g. O'Connor et al., 2012), as it is the most common soft tissue preserved. Few studies (e.g., Martin and Tate, 1976) have reconstructed the soft tissues of the feet of fossil birds which may aid in identifying avian tracemakers from their footprints. Some studies have reconstructed the soft tissues of dinosaur feet with the intention of relating foot morphology to tracks by simply expanding the lines of the osteology of the foot to account for soft tissue (e.g. Falkingham et al., 2011), however, that does not account for the amount of soft tissues to either side of the bone (i.e., the width of the toes), or the pads on the feet.

MATERIALS AND METHODS

Analyses were performed on osteological specimens, recently collected (frozen) specimens, and on specimens preserved in ethanol, in order to retrodict soft tissues of fossil bird feet so that they could be related to fossil bird tracks in future studies. Data collected from soft-tissue specimens were compared to the respective bone morphology to quantify how significant the amount of soft tissue are in contribution to total toe length and width. All materials used in this study are from the University of Kansas Ornithological Collection. One hundred and ninety osteological specimens were measured, 23 specimens in subzero storage were measured, and 17 specimens from the University of Kansas Ornithological wet lab were measured (Appendix II). Those specimens listed without numbers were measured while they were in subzero storage awaiting processing. Due to constraints on the availability of specimens, some skin and/or ethanol specimens had only one individual available for use (e.g., for skin, the Great Egret *Ardea alba*).

A series of 38 morphologic measurements were performed on every skeletal specimen, and a series of 27 morphologic measurements were performed on specimens preserved in ethanol and subzero storage specimens (see Appendix II). Birds were separated into life-habit groups (e.g., aboreal, ground-dwelling, etc.) in order to establish morphological differences between groups, as well as streamline interpretations of variation between osteology and soft tissue. Figures 1–6 present the means and standard deviations for all combinations of species and preservation types as calculated by Minitab. A General Linear Model ANOVA for each species was conducted in Minitab to test for significant variation between the means of osteological specimens, recently dead specimens, and specimens preserved in ethanol for each species. Phalangeal length (i.e., the length of the bony phalanx) cannot be accurately measured on soft-tissue and ethanol specimens, therefore, the length of the phalangeal pad was measured instead.

Tukey and Bonferroni range tests were performed alongside the ANOVA. Tukey's range test is considered more conservative when dealing with unequal sample sizes (Dunnet, 1980), therefore, Tukey's range test was used for the breakdown of trivariable ANOVA tests (i.e., those specimens with osteological, soft tissue, and ethanol components). Tukey's range test results were analyzed only with those examples that had three preservation types, although Tukey's range tests were performed on each species (see Appendix III).

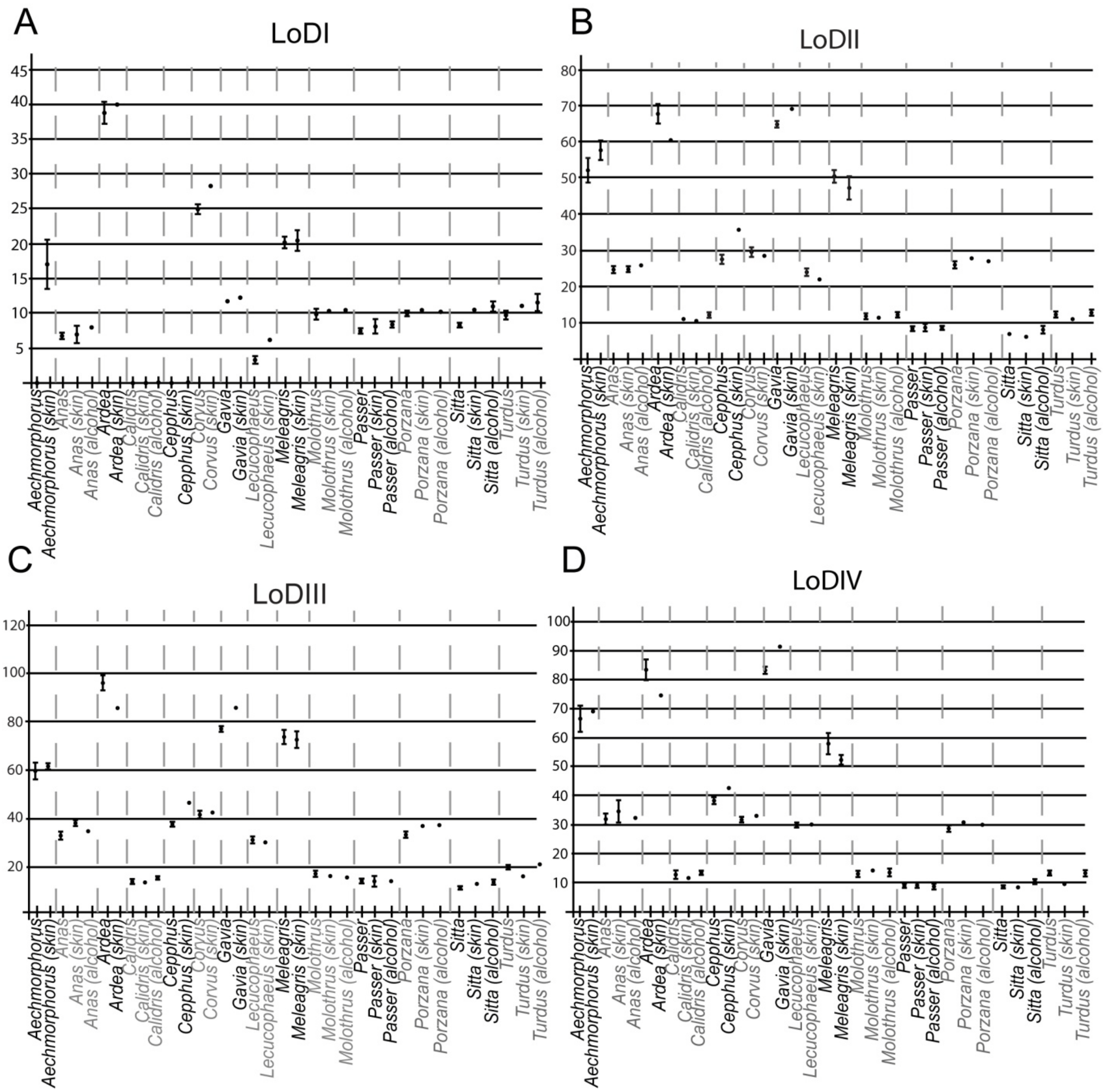


Fig. 1: Graph of ANOVA results for toe length. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this

study. LoDI= Length of digit one. LoDII= Length of digit two. LoDIII= Length of digit three. LoDIV= Length of digit four. A.) Length of digit one. B.) Length of digit two. C.) Length of digit three. D.) Length of digit four.

RESULTS

For the majority of measurements across many species, the variations between bone and skin were not significant (p-value > 0.05) (Fig. 1–6). Table 1 shows those measurements that had statistically significant results. Note that the proximal joint on all three toes is a strongly variable morphologic landmark and is often statistically significant between bone and the two soft tissue types (Fig. 2). Note also that the lengths of the phalanxes are often statistically significant between bone and soft tissue.

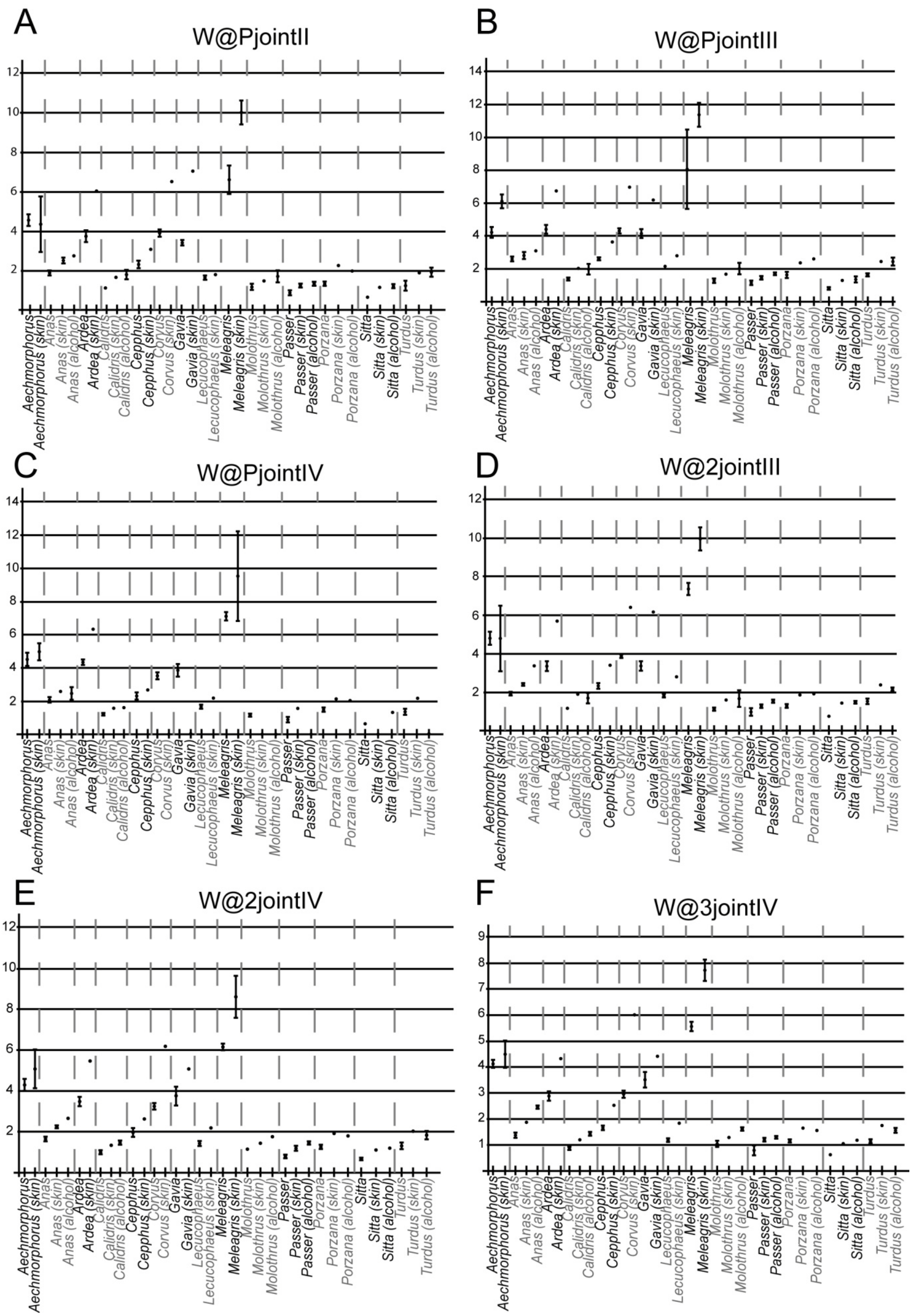

A
W@PjointII
B
W@PjointIII
C
W@PjointIV
D
W@2jointIII
E
W@2jointIV
F
W@3jointIV

Fig. 2 (Opposite page): Graph of ANOVA results of joint width. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this study. W@Pjoint II= Width at the proximal joint of toe two. W@Pjoint III= Width at the proximal joint of toe three. W@Pjoint IV= Width at the proximal joint of toe four. W@2joint III= Width at the second joint of toe three W@2joint IV= Width at the second joint of toe four. W@3joint IV= Width at the third joint of toe four. A.) Width at the proximal joint of toe two. B.) Width at the proximal joint of toe three. C.) Width at the proximal joint of toe four. D.) Width at the second joint of toe three. E.) Width at the second joint of toe four. F.) Width at the third joint of toe four.

Certain species showed a markedly—although not always significantly—longer osteological toe length than soft tissue and/or ethanol-preserved toe lengths. Many of the passeriform (perching) species (e.g., *Passer*, *Molothrus*, and *Turdus*) had longer osteological toes II, III, and/or IV. For example, the average osteological length of digit III of *P. domesticus* is 14.2 mm, whereas the average soft tissue length of digit III was 14.04 mm. The average length of digit III of *P. domesticus* ethanol-preserved specimens was 14.09. Nonpasserines with an osteological toe length greater than the soft tissue length included the Great Egret (*Ardea alba*) and the Pigeon Guillemot (*Cepphus columba*). *A. alba* had an osteological toe II length of 67.9 mm, osteological toe III length of 96.8 mm, and a osteological toe IV length of 83.4 mm. The soft tissue toe lengths for *A. alba* are: toe II, 60.5 mm; toe III, 85.9 mm; and toe IV, 74.6 mm (Appendix I). *C. columba* had a osteological toe II length of 27.6 mm and a soft tissue toe II length of 35.8 mm.

In *A. alba*, *Calidris alba*, and *Cepphus columba*, the majority of measurements between bone and soft tissue display statistically significant differences (Table 1). In *A. alba* only six measurements had p-values > 0.05; length of digit I, length of digit II, length of digit IV, foot length, length of the tarsometatarsus, and the width of the proximal end of the tarsometatarsus. In *Calidris alba*, only the length of digit III, length of digit IV, length of the tarsometatarsus, width of the tarsometatarsus at the proximal end, and width of the tarsometatarsus at the trochlea had p-values > 0.05. In *Cepphus columba*, only the width of the first and second joints of toe IV, the length of the second phalanx (or phalangeal pad) of toe II, length of the first phalanx (or phalangeal pad) of toe III, length of the third and fourth phalanxes (or phalangeal pads) of toe IV, foot length, and the width of the tarsometatarsal trochlea have p-values > 0.05.

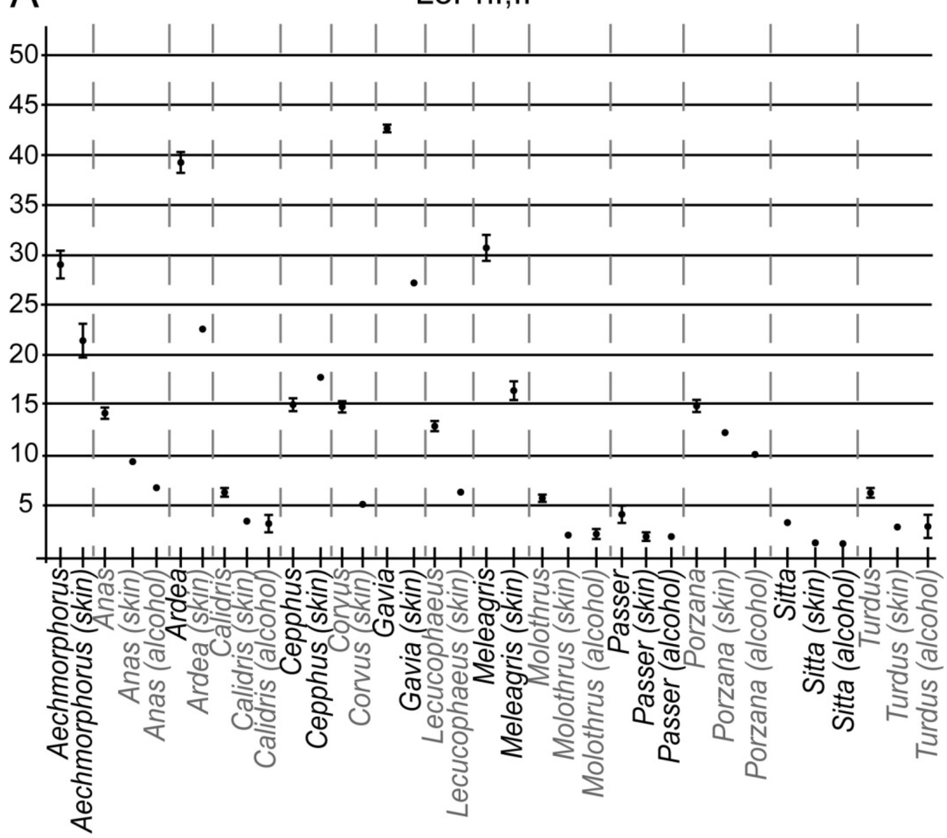
Measurement	Significant in
LoDI	*Corvus , Sitta*
LoDII	*Calidris, Cepphus, Corvus*
LoDIII	*Anas, Ardea, Cepphus, Gavia, Sitta,Turdus*
LoDIV	*Cepphus, Gavia, Sitta, Turdus*
W@PjointII	*Anas, Ardea, Calidris, Cepphus, Corvus, Meleagris, Passer, Porzana, Sitta, Turdus*
W@PjointIII	*Achemorphorus, Ardea, Calidris, Cepphus, Corvus, Gavia, Molothrus, Passer, Porzana, Sitta, Turdus*
W@PjointIV	*Ardea, Calidris, Porzana*
W@2jointIII	*Anas, Ardea, Calidris, Cepphus,Corvus, Gavia, Meleagris, Passer, Porzana, Sitta, Turdus*
W@2jointIV	*Anas, Ardea, Calidris, Corvus, Meleagris, Molothrus, Passer, Porzana, Sitta, Turdus*
W@3jointIV	*Anas, Ardea, Calidris, Cepphus, Corvus, Meleagris, Molothrus, Passer, Porzana, Sitta, Turdus*
LoPhI,II	*Achemorphorus, Anas, Ardea, Calidris, Cepphus, Corvus, Gavia, Meleagris, Molothrus, Passer, Porzana, Sitta, Turdus*
LoPhII,II	*Ardea, Calidris, Lecucophaeus, Meleagris, Molothrus, Sitta, Turdus*

Measurement	Significant in
LoPhI,III	*Achemorphorus, Anas, Ardea, Calidris, Corvus, Gavia, Meleagris, Passer, Porzana, Sitta, Turdus*
LoPhII,III	*Anas, Ardea, Calidris, Cepphus, Corvus, Meleagris, Molothrus, Passer, Porzana, Sitta, Turdus*
LoPhIII,III	*Ardea, Calidris, Cepphus, Corvus, Gavia, Molothrus, Passer, Sitta, Turdus*
LoPhI,IV	*Anas, Ardea, Calidris, Cepphus, Gavia, Meleagris, Porzana, Sitta, Turdus*
LoPhII,IV	*Ardea, Calidris, Cepphus, Gavia, Meleagris, Molothrus, Porzana, Sitta, Turdus*
LoPhIII,IV	*Aechmorphorus, Ardea, Calidris, Corvus, Passer, Porzana*
LoPhIV,IV	*Ardea, Calidris, Corvus, Gavia, Meleagris, Molothrus, Porzana, Sitta, Turdus*
Foot Length	*Ardea, Calidris, Meleagris, Passer, Sitta, Turdus*
Lotmt	*Cepphus, Corvus, Gavia, Meleagris, Molothrus, Passer, Sitta*
Wotmt@prox	*Anas, Cepphus, Corvus, Gavia, Porzana, Sitta*
Wotmt@cond	*Ardea, Corvus, Sitta*

Table 1: (Opposite Page) Significant p-values generated in the ANOVA. Values are grouped by morphometric measurement. LoDI= Length of digit one. LoDII= Length of digit two. LoDIII= Length of digit three. LoDIV= Length of digit four. W@Pjoint II= Width at the proximal joint of toe two. W@Pjoint III= Width at the proximal joint of toe three. W@Pjoint IV= Width at the proximal joint of toe four. W@2joint III= Width at the second joint of toe three W@2joint IV= Width at the proximal joint of toe four. W@3joint IV= Width at the third joint of toe four. LoPhI, II= Length of phalanx one, toe two. LoPhII, II= Length of phalanx two, toe two. LoPhI, III= Length of phalanx one, toe three. LoPhII, III= Length of phalanx two, toe three. LoPhIII, III= Length of phalanx three, toe three. LoPhI, IV= Length of phalanx one, toe four. LoPhII, IV= Length of phalanx two, toe four. LoPh III, IV= Length of phalanx four, toe four. Lotmt= Length of tarsometatarsus. Wotmt@prox= Width of the tarsometatarsus at the proximal end. Wotmt@cond= Width of the tarsometatarsus at the condyles (distal end). These abbreviations will remain the same throughout the paper.

For many specimens, the joint width was significantly greater in soft-tissue specimens than in osteological specimens (Fig. 2), whereas the overall toe length may not statistically vary between osteological and soft-tissue specimens (Table 1). In soft tissue specimens, distal joint width often did not vary significantly with respect to bone, however, proximal joint width did (Table 1).

A


LoPhI,II
50
45
40
35
30
25
20
15
10
5
Aechmorphorus
Aechmorphorus (skin)
Anas
Anas (skin)
Anas (alcohol)
Ardea
Ardea (skin)
Calidris
Calidris (skin)
Calidris (alcohol)
Cepphus
Cepphus (skin)
Corvus
Corvus (skin)
Gavia
Gavia (skin)
Lecucophaeus
Lecucophaeus (skin)
Meleagris
Meleagris (skin)
Molothrus
Molothrus (skin)
Molothrus (alcohol)
Passer
Passer (skin)
Passer (alcohol)
Porzana
Porzana (skin)
Porzana (alcohol)
Sitta
Sitta (skin)
Sitta (alcohol)
Turdus
Turdus (skin)
Turdus (alcohol)

B

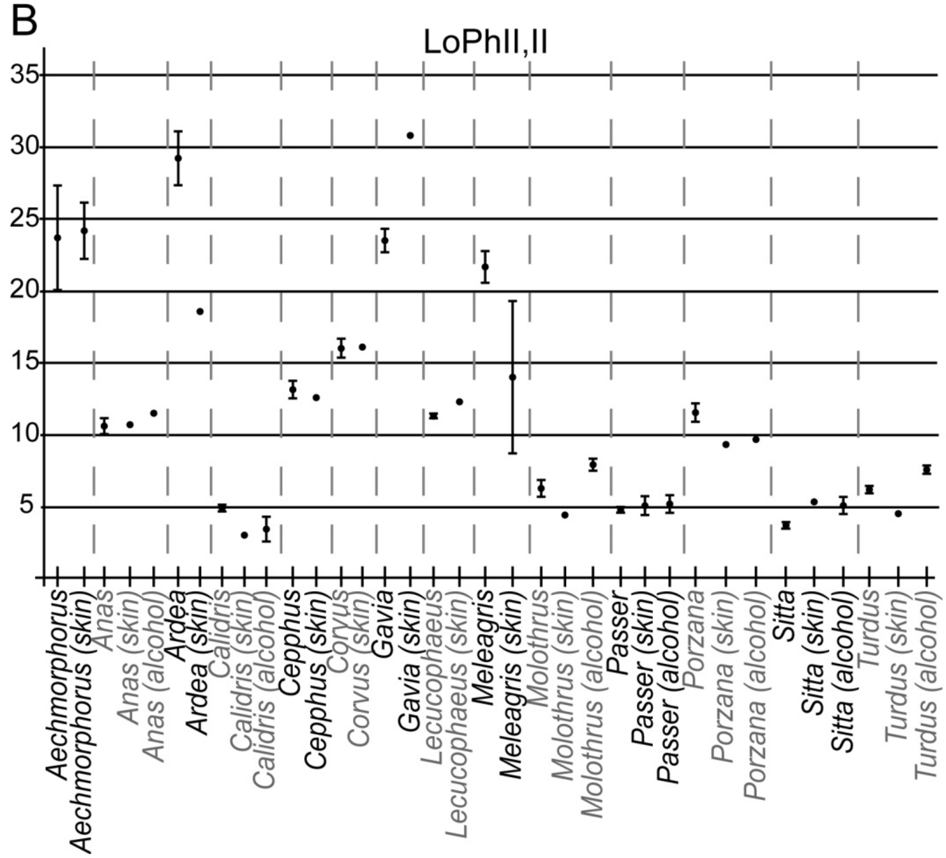

LoPhII,II
35
30
25
20
15
10
5
Aechmorphorus
Aechmorphorus (skin)
Anas
Anas (skin)
Anas (alcohol)
Ardea
Ardea (skin)
Calidris
Calidris (skin)
Calidris (alcohol)
Cepphus
Cepphus (skin)
Corvus
Corvus (skin)
Gavia
Gavia (skin)
Lecucophaeus
Lecucophaeus (skin)
Meleagris
Meleagris (skin)
Molothrus
Molothrus (skin)
Molothrus (alcohol)
Passer
Passer (skin)
Passer (alcohol)
Porzana
Porzana (skin)
Porzana (alcohol)
Sitta
Sitta (skin)
Sitta (alcohol)
Turdus
Turdus (skin)
Turdus (alcohol)

Fig. 3 (Opposite page): Graph of ANOVA results of phalanx and phalangeal pad length for digit II. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this study. LoPhI= Length of phalanx one. LoPhII= Length of phalanx two. A.) Length of phalanx (or phalangeal pad) one. B.) Length of phalanx (or phalangeal pad) two.

Skin and ethanol specimens did not vary significantly for the majority of measurements. In a few species, certain measurements (e.g., in *Molothrus*, the width of the proximal joint of toe IV) showed significant variation between osteological, soft tissue, and ethanol specimens (see Table 2 for a complete list). In other cases, certain measurements indicated that bone and soft tissue did not vary significantly, however, ethanol specimens did (e.g., in *Molothrus*, the length of phalanx-phalangeal pad II on digit II). In few cases, osteological specimens and ethanol specimens did not vary significantly, however, soft-tissue specimens did (e.g., in *Sitta,* the length of phalanx-phalangeal pad II on digit III). Note that these variations in statistical significance between osteological, soft tissue, and/or ethanol specimens are not necessarily constant between or within life-habitat groups, and each individual species can display any level of statistical significance between the three variables.

Aechmorphorus occidentalis	Osteology	Soft-tissue	Ethanol
LoDI	N/A	N/A	N/A
LoDII	A	A	N/A
LoDIII	A	A	N/A
LoDIV	A	A	N/A
W@PjointII	A	A	N/A
W@PjointIII	A	B	N/A
W@PjointIV	A	A	N/A
W@2jointIII	A	A	N/A
W@2jointIV	A	A	N/A
W@3jointIV	A	A	N/A
LoPhI,II	A	B	N/A
LoPhII,II	A	B	N/A
LoPhI,III	A	B	N/A
LoPhII,III	A	A	N/A
LoPhIII,III	A	A	N/A
LoPhI,IV	A	A	N/A
LoPhII,IV	A	A	N/A
LoPhIII,IV	A	B	N/A
LoPhIV,IV	A	A	N/A
Foot Length	A	A	N/A
Lotmt	A	A	N/A
Wotmt@prox	A	A	N/A
Wotmt@cond	A	A	N/A
Anas discors	Osteology	Soft-tissue	Ethanol
LoDI	A	A	A
LoDII	A	A	A
LoDIII	A	AB	B
LoDIV	A	A	A
W@PjointII	A	A	B
W@PjointIII	A	A	A
W@PjointIV	A	A	A
W@2jointIII	A	B	C
W@2jointIV	A	B	C
W@3jointIV	A	B	C
LoPhI,II	A	B	C
LoPhII,II	A	A	A
LoPhI,III	A	B	B
LoPhII,III	A	A	A
LoPhIII,III	A	A	A
LoPhI,IV	A	B	B
LoPhII,IV	A	A	A
LoPhIII,IV	A	A	A
LoPhIV,IV	A	A	A
Foot Length	A	A	A
Lotmt	A	A	A

Wotmt@prox	A	A	B
Wotmt@cond	A	A	A
Ardea alba	Osteology	Soft-tissue	Ethanol
LoDI	A	A	N/A
LoDII	A	A	N/A
LoDIII	A	B	N/A
LoDIV	A	A	N/A
W@PjointII	A	B	N/A
W@PjointIII	A	B	N/A
W@PjointIV	A	B	N/A
W@2jointIII	A	B	N/A
W@2jointIV	A	B	N/A
W@3jointIV	A	B	N/A
LoPhI,II	A	B	N/A
LoPhII,II	A	B	N/A
LoPhI,III	A	B	N/A
LoPhII,III	A	B	N/A
LoPhIII,III	A	B	N/A
LoPhI,IV	A	B	N/A
LoPhII,IV	A	B	N/A
LoPhIII,IV	A	B	N/A
LoPhIV,IV	A	B	N/A
Foot Length	A	B	N/A
Lotmt	A	A	N/A
Wotmt@prox	A	A	N/A
Wotmt@cond	A	B	N/A
Calidris alba	Osteology	Soft-tissue	Ethanol
LoDI	N/A	N/A	N/A
LoDII	A	A	A
LoDIII	A	A	A
LoDIV	A	A	A
W@PjointII	B	A	A
W@PjointIII	B	AB	A
W@PjointIV	B	A	A
W@2jointIII	B	A	A
W@2jointIV	B	A	A
W@3jointIV	C	B	A
LoPhI,II	A	B	B
LoPhII,II	A	AB	B
LoPhI,III	A	B	B
LoPhII,III	A	B	B
LoPhIII,III	A	B	B
LoPhI,IV	A	AB	B
LoPhII,IV	A	B	B
LoPhIII,IV	A	B	B
LoPhIV,IV	A	B	B
Foot Length	A	A	A

Lotmt	A	A	A
Wotmt@prox	A	A	A
Wotmt@cond	A	A	A
Cepphus columba	Osteology	Soft-tissue	Ethanol
LoDI	N/A	N/A	N/A
LoDII	B	A	N/A
LoDIII	B	A	N/A
LoDIV	B	A	N/A
W@PjointII	B	A	N/A
W@PjointIII	B	A	N/A
W@PjointIV	A	A	N/A
W@2jointIII	B	A	N/A
W@2jointIV	A	A	N/A
W@3jointIV	B	A	N/A
LoPhI,II	B	A	N/A
LoPhII,II	A	A	N/A
LoPhI,III	A	A	N/A
LoPhII,III	A	B	N/A
LoPhIII,III	B	A	N/A
LoPhI,IV	A	B	N/A
LoPhII,IV	A	A	N/A
LoPhIII,IV	A	A	N/A
LoPhIV,IV	A	A	N/A
Foot Length	A	A	N/A
Lotmt	B	A	N/A
Wotmt@prox	B	A	N/A
Wotmt@cond	A	A	N/A
Corvus corax	Osteology	Soft-tissue	Ethanol
LoDI	B	A	N/A
LoDII	A	A	N/A
LoDIII	A	A	N/A
LoDIV	A	A	N/A
W@PjointII	B	A	N/A
W@PjointIII	B	A	N/A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	B	A	N/A
W@2jointIV	B	A	N/A
W@3jointIV	B	A	N/A
LoPhI,II	A	B	N/A
LoPhII,II	A	A	N/A
LoPhI,III	A	B	N/A
LoPhII,III	A	B	N/A
LoPhIII,III	B	A	N/A
LoPhI,IV	N/A	N/A	N/A
LoPhII,IV	A	A	N/A
LoPhIII,IV	A	B	N/A
LoPhIV,IV	B	A	N/A

Foot Length	A	A	N/A
Lotmt	B	A	N/A
Wotmt@prox	B	A	N/A
Wotmt@cond	B	A	N/A
Gavia pacifica	Osteology	Soft-tissue	Ethanol
LoDI	N/A	N/A	N/A
LoDII	N/A	N/A	N/A
LoDIII	B	A	N/A
LoDIV	B	A	N/A
W@PjointII	B	A	N/A
W@PjointIII	B	A	N/A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	B	A	N/A
W@2jointIV	A	A	N/A
W@3jointIV	A	A	N/A
LoPhI,II	A	B	N/A
LoPhII,II	N/A	N/A	N/A
LoPhI,III	A	B	N/A
LoPhII,III	A	A	N/A
LoPhIII,III	B	A	N/A
LoPhI,IV	A	B	N/A
LoPhII,IV	A	B	N/A
LoPhIII,IV	A	A	N/A
LoPhIV,IV	B	A	N/A
Foot Length	A	A	N/A
Lotmt	B	A	N/A
Wotmt@prox	B	A	N/A
Wotmt@cond	A	A	N/A
Lecucophaeus pipixcan	Osteology	Soft-tissue	Ethanol
LoDI	A	A	N/A
LoDII	A	A	N/A
LoDIII	A	A	N/A
LoDIV	A	A	N/A
W@PjointII	A	A	N/A
W@PjointIII	A	A	N/A
W@PjointIV	A	A	N/A
W@2jointIII	A	A	N/A
W@2jointIV	A	A	N/A
W@3jointIV	A	A	N/A
LoPhI,II	A	A	N/A
LoPhII,II	B	A	N/A
LoPhI,III	A	A	N/A
LoPhII,III	A	A	N/A
LoPhIII,III	A	A	N/A
LoPhI,IV	A	A	N/A
LoPhII,IV	A	A	N/A
LoPhIII,IV	A	A	N/A

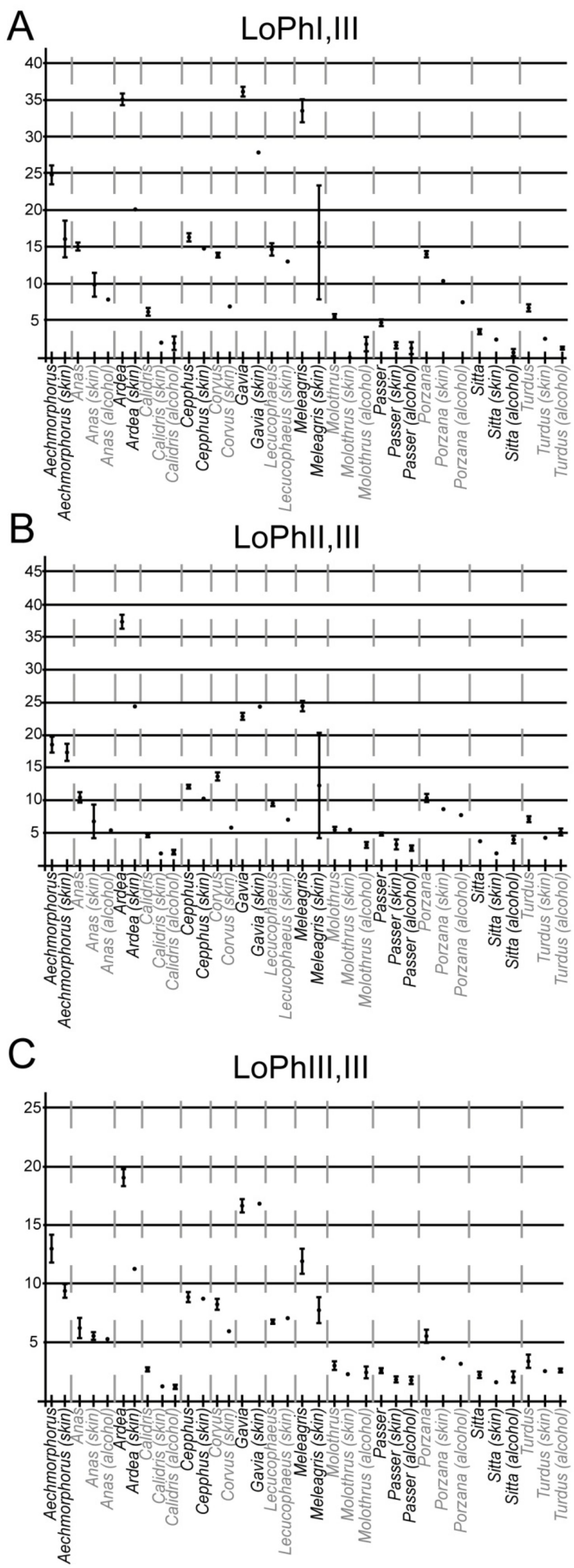
LoPhIV,IV	A	A	N/A
Foot Length	A	A	N/A
Lotmt	A	A	N/A
Wotmt@prox	A	A	N/A
Wotmt@cond	A	A	N/A
Meleagris gallopavo	Osteology	Soft-tissue	Ethanol
LoDI	A	A	N/A
LoDII	A	A	N/A
LoDIII	A	A	N/A
LoDIV	A	A	N/A
W@PjointII	B	A	N/A
W@PjointIII	A	A	N/A
W@PjointIV	A	A	N/A
W@2jointIII	B	A	N/A
W@2jointIV	B	A	N/A
W@3jointIV	B	A	N/A
LoPhI,II	A	B	N/A
LoPhII,II	A	B	N/A
LoPhI,III	A	B	N/A
LoPhII,III	A	B	N/A
LoPhIII,III	A	A	N/A
LoPhI,IV	A	B	N/A
LoPhII,IV	A	B	N/A
LoPhIII,IV	A	A	N/A
LoPhIV,IV	B	A	N/A
Foot Length	A	B	N/A
Lotmt	A	B	N/A
Wotmt@prox	A	A	N/A
Wotmt@cond	A	A	N/A
Molothrus ater	Osteology	Soft-tissue	Ethanol
LoDI	A	A	A
LoDII	A	A	A
LoDIII	A	A	A
LoDIV	A	A	A
W@PjointII	A	A	A
W@PjointIII	B	AB	A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	A	A	A
W@2jointIV	C	B	A
W@3jointIV	B	AB	A
LoPhI,II	A	B	B
LoPhII,II	B	B	A
LoPhI,III	N/A	N/A	N/A
LoPhII,III	A	A	B
LoPhIII,III	B	AB	A
LoPhI,IV	N/A	N/A	N/A
LoPhII,IV	A	AB	B

LoPhIII,IV	A	A	A
LoPhIV,IV	B	AB	A
Foot Length	N/A	N/A	N/A
Lotmt	B	A	AB
Wotmt@prox	A	A	A
Wotmt@cond	A	A	A
Passer domesticus	Osteology	Soft-tissue	Ethanol
LoDI	A	A	A
LoDII	A	A	A
LoDIII	A	A	A
LoDIV	A	A	A
W@PjointII	B	A	A
W@PjointIII	C	B	A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	B	B	A
W@2jointIV	C	B	A
W@3jointIV	B	A	A
LoPhI,II	A	B	B
LoPhII,II	A	A	A
LoPhI,III	A	B	B
LoPhII,III	A	AB	B
LoPhIII,III	B	A	AB
LoPhI,IV	N/A	N/A	N/A
LoPhII,IV	A	A	A
LoPhIII,IV	A	B	B
LoPhIV,IV	A	A	A
Foot Length	B	A	A
Lotmt	B	A	B
Wotmt@prox	A	A	A
Wotmt@cond	A	A	A
Porzana carolina	Osteology	Soft-tissue	Ethanol
LoDI	A	A	A
LoDII	A	A	A
LoDIII	A	A	A
LoDIV	A	A	A
W@PjointII	B	A	A
W@PjointIII	B	AB	A
W@PjointIV	B	A	A
W@2jointIII	B	A	A
W@2jointIV	B	A	A
W@3jointIV	B	A	A
LoPhI,II	A	B	B
LoPhII,II	A	A	A
LoPhI,III	A	B	C
LoPhII,III	A	AB	B
LoPhIII,III	A	A	A
LoPhI,IV	A	B	B

LoPhII,IV	A	B	B
LoPhIII,IV	A	A	A
LoPhIV,IV	A	A	A
Foot Length	A	A	A
Lotmt	N/A	N/A	N/A
Wotmt@prox	B	AB	A
Wotmt@cond	A	A	A
Turdus migratorius	Osteology	Soft-tissue	Ethanol
LoDI	A	A	A
LoDII	A	A	A
LoDIII	A	B	A
LoDIV	A	B	A
W@PjointII	B	AB	A
W@PjointIII	B	A	A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	B	A	A
W@2jointIV	B	A	A
W@3jointIV	B	A	A
LoPhI,II	A	B	B
LoPhII,II	B	C	A
LoPhI,III	A	B	C
LoPhII,III	A	B	B
LoPhIII,III	B	C	A
LoPhI,IV	A	AB	B
LoPhII,IV	A	AB	B
LoPhIII,IV	A	A	A
LoPhIV,IV	B	B	A
Foot Length	A	B	A
Lotmt	A	A	A
Wotmt@prox	A	A	A
Wotmt@cond	A	A	A
Sitta canadensis	Osteology	Soft-tissue	Ethanol
LoDI	B	A	A
LoDII	A	A	A
LoDIII	B	AB	A
LoDIV	B	AB	A
W@PjointII	B	A	A
W@PjointIII	B	A	A
W@PjointIV	N/A	N/A	N/A
W@2jointIII	B	A	A
W@2jointIV	B	A	A
W@3jointIV	C	B	A
LoPhI,II	A	B	B
LoPhII,II	B	A	A
LoPhI,III	A	A	B
LoPhII,III	A	B	A
LoPhIII,III	C	B	A

LoPhI,IV	A	B	B
LoPhII,IV	A	B	C
LoPhIII,IV	A	A	A
LoPhIV,IV	B	A	A
Foot Length	B	A	A
Lotmt	B	A	AB
Wotmt@prox	B	B	A
Wotmt@cond	B	A	A

Table 2: The groups interpreted by Tukey's range test produced in Minitab. A is significantly different from B, which is significantly different from C. Any groups with AB indicates that A and B are significantly different from each other, but that the AB group overlaps both of these distributions.



A
LoPhI,III
40
35
30
25
20
15
10
5
Aechmorphorus
Aechmorphorus (skin)
Anas
Anas (skin)
Anas (alcohol)
Ardea
Ardea (skin)
Calidris
Calidris (skin)
Calidris (alcohol)
Cepphus
Cepphus (skin)
Corvus
Corvus (skin)
Gavia
Gavia (skin)
Lecucophaeus
Lecucophaeus (skin)
Meleagris
Meleagris (skin)
Molothrus
Molothrus (skin)
Molothrus (alcohol)
Passer
Passer (skin)
Passer (alcohol)
Porzana
Porzana (skin)
Porzana (alcohol)
Sitta
Sitta (skin)
Sitta (alcohol)
Turdus
Turdus (skin)
Turdus (alcohol)
B
LoPhII,III
45
40
35
30
25
20
15
10
5
Aechmorphorus
Aechmorphorus (skin)
Anas
Anas (skin)
Anas (alcohol)
Ardea
Ardea (skin)
Calidris
Calidris (skin)
Calidris (alcohol)
Cepphus
Cepphus (skin)
Corvus
Corvus (skin)
Gavia
Gavia (skin)
Lecucophaeus
Lecucophaeus (skin)
Meleagris
Meleagris (skin)
Molothrus
Molothrus (skin)
Molothrus (alcohol)
Passer
Passer (skin)
Passer (alcohol)
Porzana
Porzana (skin)
Porzana (alcohol)
Sitta
Sitta (skin)
Sitta (alcohol)
Turdus
Turdus (skin)
Turdus (alcohol)
C
LoPhIII,III
25
20
15
10
5
Aechmorphorus
Aechmorphorus (skin)
Anas
Anas (skin)
Anas (alcohol)
Ardea
Ardea (skin)
Calidris
Calidris (skin)
Calidris (alcohol)
Cepphus
Cepphus (skin)
Corvus
Corvus (skin)
Gavia
Gavia (skin)
Lecucophaeus
Lecucophaeus (skin)
Meleagris
Meleagris (skin)
Molothrus
Molothrus (skin)
Molothrus (alcohol)
Passer
Passer (skin)
Passer (alcohol)
Porzana
Porzana (skin)
Porzana (alcohol)
Sitta
Sitta (skin)
Sitta (alcohol)
Turdus
Turdus (skin)
Turdus (alcohol)

Fig. 4: (Opposite page) Graph of ANOVA results of phalanx and phalangeal pad length for digit III. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this study. A.) Length of phalanx (or phalangeal pad) one. B.) Length of phalanx (or phalangeal pad) two. C.) Length of phalanx (or phalangeal pad) three.

Some specimens display overlapping significance. For instance, for a test with three means, Tukey test results will give two significantly different means, however, one mean will be placed in both categories (A, B, and AB, see Appendix III). This indicates that two means appear significantly different from each other, and one of three means overlaps the ranges of standard deviation of the other two means.

The ratio of bone:skin did not provide conclusive results of correlation (Table 3). Bone:skin ratio of toe length did seem to have some correlation in passeriform birds (values 0.9–1.1), with the exception of *Turdus* (values 0.7–1.1), but only for toes I and III (r^2=0.1336 and r^2=0.2697, respectively). Toes II and IV had very low r^2 values (0.00006 and 0.0569, respectively). The width at the joints showed the strongest >1 for bone:skin ratios across all life habit groups, with only one individual (*Achemorphorus)* with values <1. These values, however, still do not show strong correlation (e.g., width at the proximal phalanx of toe II, r^2=0.0264), even within a life history group (e.g., width at the proximal phalanx of toe II, Passeriformes, r^2=0.0002).

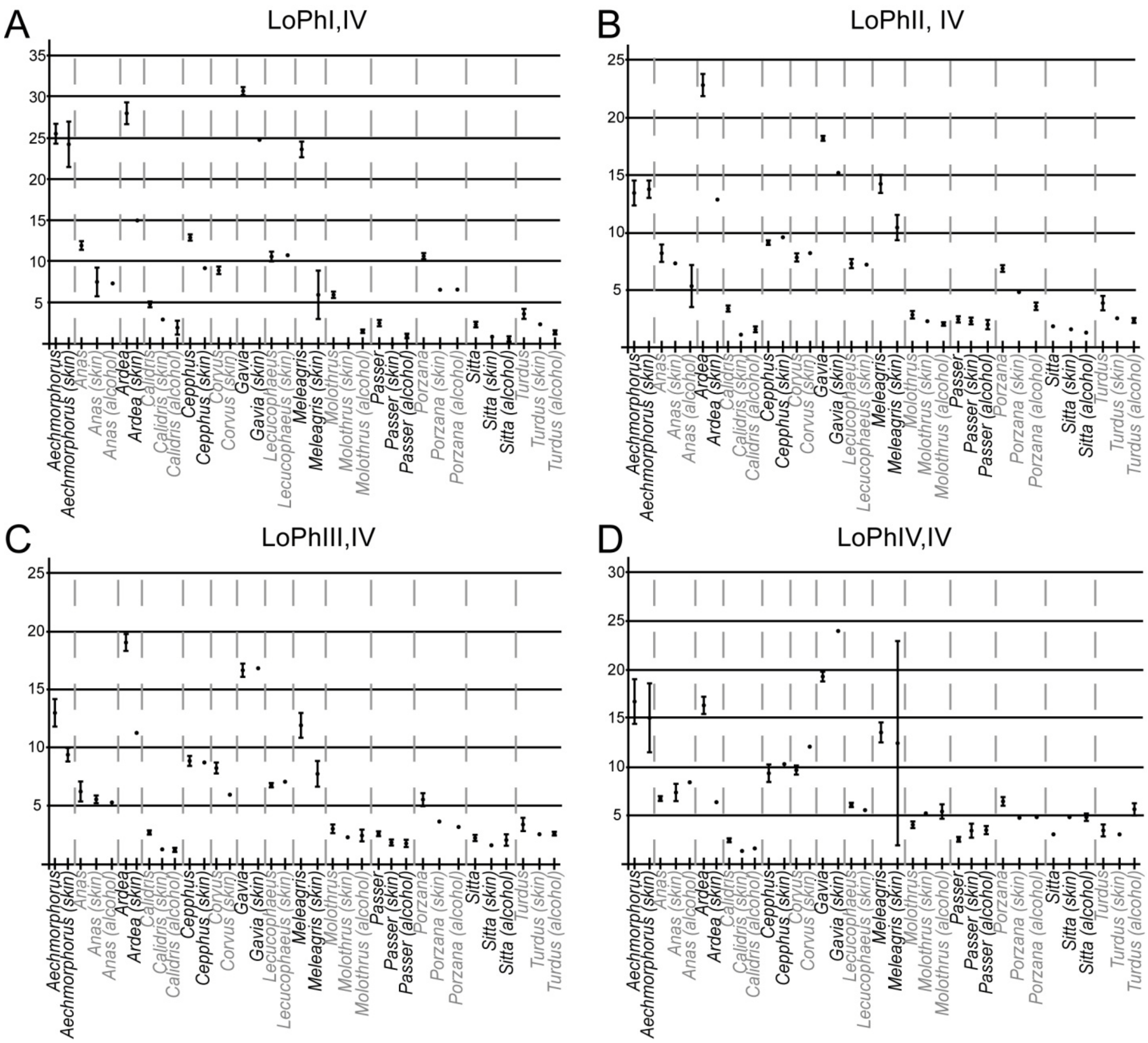


Fig. 5: Graph of ANOVA results of phalanx and phalangeal pad length for digit IV. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this study. A.) Length of phalanx (or phalangeal pad) one. B.) Length of phalanx (or phalangeal pad) two. C.) Length of phalanx (or phalangeal pad) three. D.) Length of phalanx (or phalangeal pad) four.

Name	*Anas discors*	*Porzana*	*Calidris alba*	*Turdus*	*Molothrus*	*Passer*	*Sitta*
LoDI	1.03030303	1.04674	0	1.13582778	1.044489383	1.08801	1.263475
LoDII	1.00404449	1.06928	0.94967276	0.8961171	0.960134993	1.03617	0.897781
LoDIII	1.15720888	1.10909	0.9733214	0.80944012	0.943741823	0.99083	1.144369
LoDIV	1.08298237	1.07437	0.9105314	0.72200557	1.09352518	1.01489	0.984
W@Pjoint II	1.32982917	1.68577	1.47045952	1.51888668	1.252609603	1.40947	1.726937
W@Pjoint III	1.08030593	1.44681	1.45974955	1.49090909	1.305019305	1.25894	1.573574
W@Pjoint IV	1.23990499	1.42574	1.29292929	1.58844765	0	0.28962	0
W@2joint III	1.24358974	1.43238	1.61684211	1.5483871	1.417943107	1.30326	1.883871
W@2joint IV	1.36048265	1.51969	1.33995037	1.54253308	1.252699784	1.49948	1.647059
W@3joint IV	1.36116152	1.42549	1.37931034	1.53172867	1.237410072	1.5184	1.686747
LoPhI,II	0.65762115	0.82106	0.53876898	0.44802579	0.34790287	0.44978	0.37037
LoPhII,II	1.01035294	0.80761	0.61538462	0.72903226	0.703541584	1.06095	1.440324
LoPhI,III	0.65461181	0.73958	0.32161616	0.37662821	0	0.34433	0.690544
LoPhII,III	0.64638237	0.83422	0.39934534	0.5959845	0.915486524	0.66944	0.496626
LoPhIII,III	1.42890579	0.84507	0.51712089	0.82145282	1.358615004	1.25725	1.403944
LoPhI,IV	0.63012552	0.61741	0.61634565	0.65205479	0	0	0.369819
LoPhII,IV	0.89341026	0.70315	0.33406593	0.66024406	0.803478261	0.94399	0.860963
LoPhIII,IV	0.89191353	0.65887	0.46494465	0.75128393	0.758450124	0.71081	0.717149
LoPhIV,IV	1.09184803	0.75183	0.55409505	0.88378766	1.28992629	1.34434	1.575365
Foot Length	1.04164062	1.06839	1.42890902	0.84076148	1.266023432	1.95993	1.208366
Lotmt	1.10992266	1.04911	1.00134486	0.98424606	1.296384585	0.93891	1.4105
Wotmt@prox	1.21232306	1.09777	0.95554081	1.12729426	1.092284418	0.80649	0.855792
Wotmt@cond	1.09242298	1.20611	1.17174515	1.18577075	1.285008237	1.23462	2.340094

Table 3: Bone:skin ratios calculated from the average measurements.

The ratio of ethanol:skin showed slightly better correlation overall (Table 4). Many values ranged between 0.8 and 1.1, with only one value >2 (*Turdus*, length of phalanx I, toe III) and only a few values of 0.7 and two values of 0.5 (*Turdus* and *Molothrus*, length of phalanx II, toe II). Within Passeriformes, the correlation of toe length as relates to life habitat was slightly better. Toe I had an r^2 value of 0.06, however, toe II had an r^2 value of 0.0731, toe III had an r^2 value of 0.286, and toe IV had an r^2 value of 0.045.

Name	*Anas discors*	*Porzana*	*Calidris alba*	*Turdus*	*Molothrus*	*Passer*	*Sitta*
LoDI	0.87234043	1.02547	0	0.95765	0.98381	0.96798	0.95421
LoDII	0.95775463	1.03033	0.86584362	0.86184	0.93126	1.00932	0.76267
LoDIII	1.0969549	0.99036	0.88018135	0.76458	1.039718	0.99645	0.94606
LoDIV	1.06947012	1.02892	0.86575208	0.72429	1.054399	1.05146	0.81663
W@Pjoint II	0.9133574	1.14	0.92307692	0.98285	0.867052	0.93358	0.94865
W@Pjoint III	0.90836013	0.9084	1.02341137	1.00136	0.832512	0.8552	0.9562
W@Pjoint IV	1.04819277	1.04854	0.97759674	0	0	0	0
W@2joint III	0.71533923	0.96907	1.1184466	1.10599	0.95858	0.83601	0.97333
W@2joint IV	0.84456929	1.0663	0.91216216	1.10469	0.819209	0.82279	0.92818
W@3joint IV	0.76219512	1.05769	0.83916084	1.1194	0.798762	0.92921	0.88732
LoPI,II	1.38839286	1.21791	1.07897545	0.97887	0.944844	0.99591	1.05882
LoPII,II	0.93185764	0.96388	0.87705712	0.59578	0.557026	0.97675	1.04912
LoPI,III	1.25508906	1.38585	1.03645833	2.03485	0	1.72622	3.74611
LoPII,III	1.25371747	1.11788	0.9	0.82563	1.595541	1.21624	0.46426
LoPIII,III	1.02175732	0.9342	0.73901465	0.62371	0.925843	1.00801	0.87664
LoPI,IV	1.0244898	0.99697	1.49747049	1.70406	0	0	1.45
LoPII,IV	1.36964618	1.34349	0.71101871	1.08135	1.115942	1.15286	1.21662
LoPIII,IV	1.0509434	1.14734	1.03846154	0.97834	0.936864	1.04466	0.78029
LoPIV,IV	0.87573964	1.0167	0.83877551	0.54321	0.965074	0.98413	1.00275
FLw/out hal	0.99808291	1.06379	1.02370203	0.78612	0.916895	0.82959	1.01695
Lotmt	0.98438412	0	1.03769578	0.98756	1.118232	0.91258	1.26155
Wotmt@prox	0.95789474	0.92308	0.94158675	1.11563	0.956291	0.78025	0.67286
Wotmt@conc	0.95072464	1.00363	1.06459732	1.02506	0.803296	0.95844	1.05239

Table 4: Ethanol:skin ratios calculated from the average measurements.

The length of the bony phalanx (Ph) was compared to the fleshy pad length (P) and treated as the same measurement. The phalangeal length in Passeriform birds was considerably more than the fleshy pad length in proximal phalanxes (e.g. toe II, phalanx I, average ratio of bone:skin 2.6), whereas wading birds and shorebirds had proximal phalanxes that were relatively smaller but still longer than the fleshy pad (e.g. toe II, phalanx I, average bone:skin ratio 1.6). Webbed-footed birds showed high variation in their proximal phalangeal bone:skin ratio, with the smallest being 0.846 in *Cepphus* (toe II, phalanx I), and the largest being 3.96 in *Meleagris* (toe IV, phalanx I). This trend is mostly reversed in more distal phalanxes, especially in those of the shorebird *Calidris alba* (Table 3).

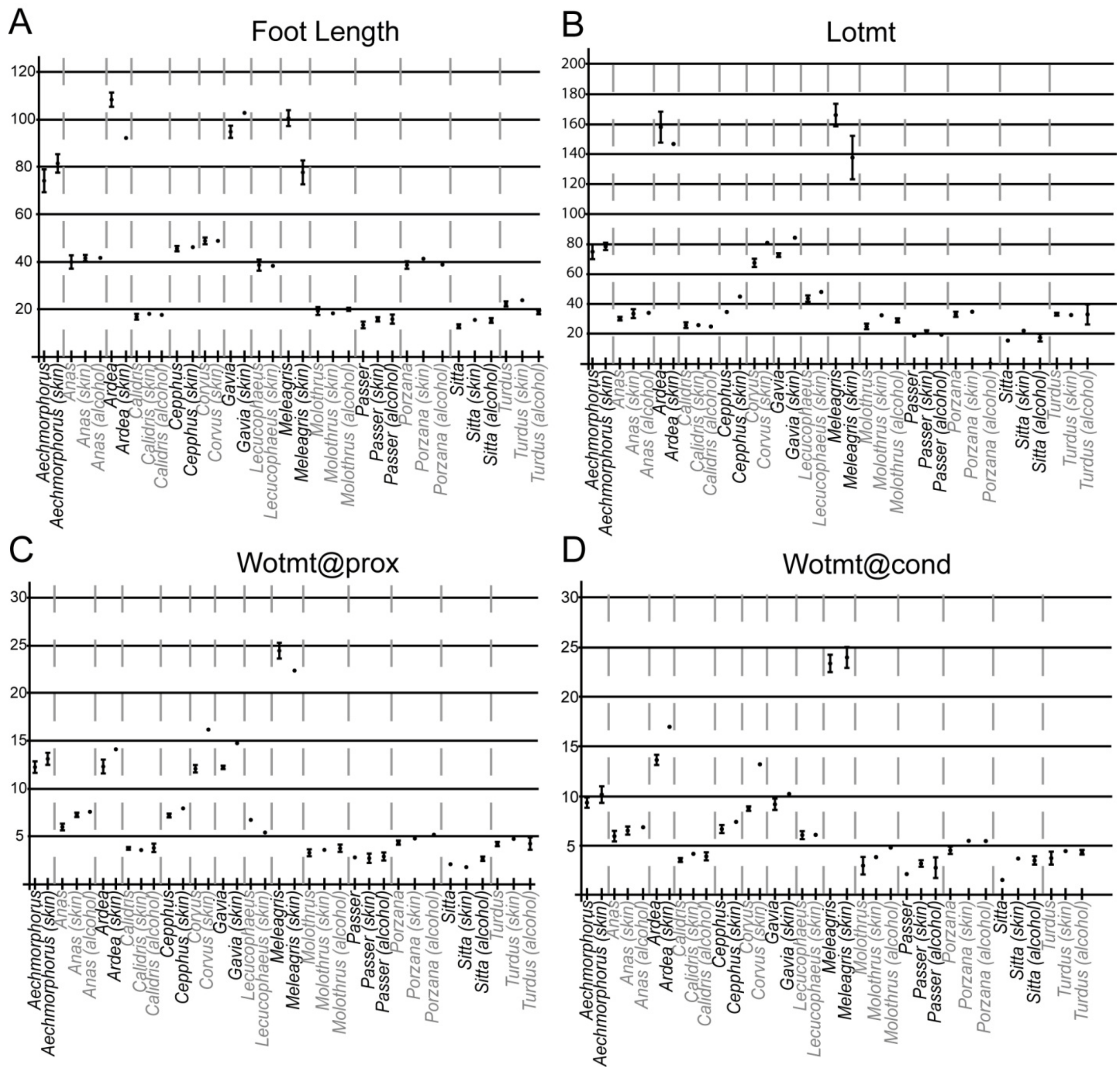


Fig. 6: Graph of the ANOVA results of foot length and the three tmt measurements. Dots represent the mean value, with the black bars above and below representing standard error. Where bars overlap, there is no significant difference between means. Genus name only represents osteological specimens, (skin) represents subzero storage specimens, and (alcohol) represents ethanol-preserved specimens. Dashed lines and alternating black and grey text delinate the different species used in this study. A.) Foot length. B.) Length of the tarsometatarsus. C.) Width of the tarsometatarsus at the proximal end. D.) Width of the tarsometatarsus at the distal condyles.

DISCUSSION

What is significant?

Few measurements were statistically significant across multiple life-habitat groups. The width at the proximal joint of toe II was significant for 10 of 14 species, with the exceptions being *Lecucophaeus pipixcan*, *Aechmorphorus occidentalis*, *Gavia pacifica*, and *Molothrus ater* (Table 1). The length of toe II, however, was only significant for 3 of 14 species—*Corvus corax*, *Cepphus columba*, and *Sitta canadensis*. Similarly, the length of toe III was significant only in 6 of 14 species, whereas the width of the proximal joint was significant in 11 of 14 species. The width at the second (more distal) joint was also significant for 11 of 14 species. Ten of the 14 species have significant p-values for both the width at the proximal joint and second joint of toe III; *Aechmorphorus occidentalis* has a significant p-value only for the proximal joint, *Meleagris gallopavo* has a significant p-value only for the second joint, the remaining two species do not have significant p-values for either measurement. The fourth toe shows a similar trend, with 4 of 14 species showing significant difference in the length of toe IV between bone and skin. When the width at the joints is examined, the proximal joint shows only 3 of 14 significantly different—this is because passeriform birds nearly incorporate the proximal joint into the metatarsal pad (Fig. 7), which makes the joint impossible to measure accurately. This measurement was, therefore, discarded in passeriform birds. The width at the second joint shows 11 of 14 species with a significant p-value, which is identical to the distal-most third joint. This indicates that the width at the joints is a fairly reliably stable and significant difference between bone and skin. Joint width, therefore, is an important parameter to measure when reconstructing the soft tissues of birds from their osteology.

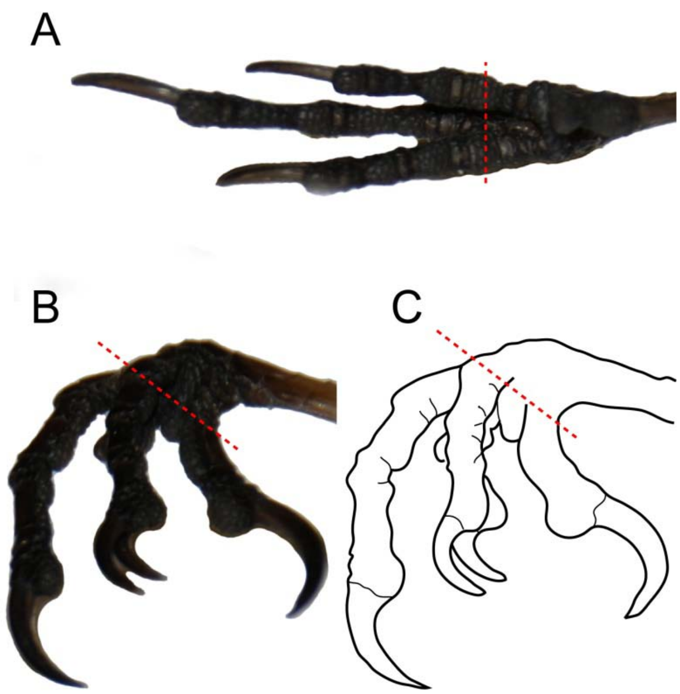


Fig. 7: Photo and line drawing of a passeriform foot showing the incorporation of the proximal phalanxes/joints into the metatarsal pad. A.) Ventral view of the foot. Dashed line is the approximate demarcation of the metatarsal pad. B.) Lateral view of the foot. Dashed line is the approximate demarcation of the metatarsal pad. Note that all to almost all of phalanx I, toe IV is incorporated into the metatarsal pad. C.) Line drawing of the lateral view of the foot.

Comparison of phalangeal length to phalangeal pad length indicates most species show significant variation between the length of the phalanx itself and the length of the phalangeal pad. In general the more proximal phalangeal pads are more often significantly different (Table 1), however, this is not always the case (e.g., length of phalanx-pad IV, toe IV). The phalangeal pad is almost always shorter than the underlying bone. A few noticeable exceptions to the rule are *Cepphus columbus* (Phalanx I, digit II) and some passeriform birds at the distal phalanxes (see Fig. 3).

Some values that may be significant are missing from Table 1 because the phalangeal pad was not measureable in some individuals (<1–2 mm long), especially with the proximal phalangeal pad on digit IV. This is due to the tendency of passeriform birds to incorporate much of or the entire proximal phalanx of the fourth toe into the metatarsal pad. This results in a highly reduced or absent (in extreme cases) proximal phalangeal pad for the fourth toe, which may be related to life habit, taxonomy, or both.

Why are the toe length values not significant but joint width is?

Toe lengths of many individuals, especially passeriform birds, are not statistically significant between bone, skin, and ethanol. Birds, in general, do not have enough soft tissue between bones to make any significant difference in toe length. As long as the ungual (i.e., claw) is disregarded, the soft-tissue toe lengths are not significantly different than the osteological toe lengths.

Joint width, on the other hand, is often statistically significant. Even in birds that have relatively thin toes without large fleshy pads and minimal soft tissue on the feet (e.g., webbed-footed birds, waders), the proximal joints are significantly different. In most species the width of the distal joints is also significant.

The myology of the bird foot is extremely simple. There is a very small relative amount of soft tissue (Vanden Berge and Zweers, 1993). Only ten muscles, most of which are ligamentous in form, are known from the feet (Table 5). Of these ten, two are absent in most groups of birds (Vanden Berge and Zweers, 1993). Tendons are found on the ventral side of the foot. Each tendon splits into multiple branches that runs below each toe, and attaches onto certain phalanxes (see e.g. Vanden Berge and Zweers, 1993, fig. 6.16, 6.18). The positioning of this attachment is likely what gives a joint its significantly fleshy morphology. According to Baumel et al. (1993), the distal portion of the ligamentous *M. flexor digitus longus* and the *M. flexor hallucis* insert on the proximal portion of each phalanx. On the dorsal side of the foot, the *M. extensor digitus longus* broadens and inserts on the distal portion of the proximal phalanx and the proximal portion of the distal phalanx, covering the joint area (e.g., Hudson et al., 1959; Berman and Raikow, 1982). This broadening of the *M. extensor digitus longus* is likely another defining factor in the significant difference between the osteological joint width and the soft-tissue joint width.

Muscle name	Origin	Insertion
M. flexor perforans et perforati digit II et III; M. flexor perforati digit IV	Variable defining characteristic for taxa	Variable defining characteristic for taxa
M flexor hallucis longus	May have multiple origins	Tuberculum flexorium on the phalanx
M. flexor digitum longus	May have multiple origins	Tuberculum flexorium on the phalanx
M. extensor hallicus longus	Variable	Variable
M. flexor hallicus brevis	Shaft of the tarsometarsus	N/A
M. adductor et abductor digiti II	Medial side of distal half of tarsometarsus	Base of proximal phalanx
M. extensor proprius digiti III	Rare and irregular outside of ratites	Rare and irregular outside of ratites
M. extensor proprius et brevis digiti IV	Variable	Variable
M. adductor digiti IV	Variable; minute	Variable; minute
M. abductor digiti IV	Absent in most birds	Absent in most birds

Table 5: Muscles known from the foot of birds. All information is taken from Vanden Burge and Zweers (1993).

Several birds, especially passeriforms, show slightly longer osteological toe lengths than soft-tissue toe lengths (Fig. 1), however, this difference is rarely significant (Table 1). The explanation behind this is that many passeriforms have a relatively large and fleshy metatarsal pad in comparison to wading, webbed-footed, and some ground birds (Fig. 8). They have incorporated portions of their proximal phalanxes—or, in the case of the fourth toe, the majority or entirety of their proximal phalanx—into the metatarsal pad. This is certainly reflected in their trackways as low angles of divarication (Falk et al., 2011). This effect likely increases the power and ease of gripping branches. The incorporation of portions of phalanxes into the metatarsal pad, however, results in the difficulty of measuring the total toe length. In many cases, the entire osteological toe is not measured. This result may be slightly mediated by the incorporation of a portion of the bony ungual into the apparent (soft-tissue) toe length.

Fig. 8: Photographs of the fleshy pads of the feet of modern birds. A.) A shorebird, *Calidris*. B.) A ground bird, the Prairie Chicken, *Tympanuchus cupido*. C.) A lobed-footed bird, Western Grebe, *Acheomorphorus occidentalis*. D.)

A webbed-footed bird, Franklin's Gull, *Leucophaeus pipixcan*. E.) A perching bird, white-breasted nuthatch, *Sitta carolinensis*.

The bony ungual and the keratinous claw sheaths were not included in this study. If the keratinous claw sheath was to be included in the soft tissue toe length, then the soft tissue toe length may be considered significantly different from the osteological toe length. Since claw impressions, however, are not always preserved in the trace fossil record, claw length was not included in this study.

Influences on variation

Three variables influence the difference between osteology and soft tissue: 1) the presence or absence of extra skin around the toes—i.e., lobing or webbing; 2) the life habitat and/or morphology of the specific bird (e.g., perching, shorebird); 3) in rare cases, the type of preservation of the specimen being measured (i.e., ethanol vs. subzero storage). All specimens are fixed (preserved) with 10% formaldehyde immediately after collection, but are transferred to ethanol for long-term storage (M. Robbins, pers comm). Ethanol, however, has not always been used as a long-term storage preservative.

The presence or absence of webbing or lobing is a significant factor in foot morphology. Webbed- and lobed-footed birds seem to have less flesh on the toe than other species, and do not seem to possess real pads. The width at the joint is significantly different for 2 of the 3 webbed-footed birds in this study, with the only exception being the distal-most joint of toe IV, in which all three species are significantly different. The only significantly different joint width in *Aechmorphorus*, the lobed-footed bird measured, is the proximal joint of toe III. The variation between the width of the osteological joint and the fleshy joint does not seem to be standard; in some instances there is only a relatively small amount of difference, whereas in others there is a relatively large amount of difference (Fig. 2).

Life-habit and morphology also influences the variation of the toes, mainly in the differences between phalangeal pad length and osteological phalanx length. The relative length, fleshiness, and even the presence or absence of phalangeal pads is largely dependent on which type of life habitat to which the bird belongs. Webbed- and lobed-footed birds often lack true phalangeal pads, maintaining instead a simple covering of scales with fold lines demarcating areas of movement (Fig. 8A, B). Wading birds and shorebirds have more clearly defined pads, but lack the fleshy bumps seen on the feet of ground birds and perching birds (Fig. 8C–E). Waders, shorebirds, and ground birds all have reduced phalangeal pads with expanded interphalangeal pads, whereas perching birds have expanded phalangeal pads and reduced or absent interphalangeal pads. Birds with expanded interphalangeal pads have no need to grasp branches—they are often awkward and ungainly when grasping branches (Falk et al., 2011, fig. 8). Expanded interphalangeal pads may increase the surface area of the toe, allowing for better weight distribution when moving across soft media. Perching birds, however, rely on the grasping ability of their feet more than do shorebirds and other ground-dwelling and water-margin birds; thus, freely flexing and tightly gripping toes are a necessity. A large pad between the phalanxes, covering the joint, would greatly inhibit flexion and prevent grasping.

In general, the proximal phalangeal pads are the most significantly different from the phalanxes (Appendix II). In two well-studied examples (*Calidris alba* and *Passer domesticus*) from two different life habitats (shorebird and perching bird, respectively) the p-values of the proximal pads were often <0.001 (Appendix II). The p-value tends to increase distally for *Passer*. The p-value in *Calidris* remains relatively the same, usually <0.02. This indicates that in perching birds the relative length of the pad tends to increase distally. The p-value for the distal most pad of toe IV is significant in *Turdus* and *Sitta* because the pad is significantly longer than the bony phalanx; in *Passer* this difference is not significant. Proximal pads are significantly shorter in perching birds for two reasons: 1) Some portion of the proximal phalanx is incorporated into the metatarsal pad, limiting the amount of space between the metatarsal pad and proximal joint that could be occupied by a pad, and 2) smaller proximal pads likely facilitate easier grasping, just as small or absent interphalangeal pads facilitate grasping.

The relative fleshiness of the pad also varies between life-habitat groups. Ground birds and perching birds have very fleshy pads, whereas waders and shorebirds tend to lack a fleshy protrusion. This could be a matter of surface tension response—the fleshy pad is more likely to punch through the surface of muddy sediment, which would result in the bird being more likely to sink. A more level surface, however, would result in a bird that would be less likely to break the surface layer of mud.

Sources of Error

The soft-tissue, and, to a lesser extent, the ethanol-preserved specimens used in this study were limited in number. This is due to two main issues: 1) the wet lab size bias and 2) subzero storage bias. The wet lab size bias refers to the fact that large birds do not fit in small jars. There is a limited amount of storage space in any wet lab, and fewer numbers of large-bodied birds (e.g., *Meleagris* and *Ardea*) are preserved. Subzero storage is limited by whatever birds have recently been collected, whether by active collection (e.g., hunting) or scavenge collecting (e.g., window kills). Birds are not actively stored in subzero storage in most institutions—rather it is temporary storage before the birds are prepared, either as osteological specimens or taxidermied skin specimens. This small sample size may cause an overabundance of significantly different variables, however, the individuals in this study were mainly from the same geographic area, which would lessen the impact of body size variation.

The combination of these two biases often results in small sample size. A notable exception in this study is the European House Sparrow (*Passer domesticus*), which has been the focus of a large collection project at the University of Kansas (Johnson and Selander, 1973 and references therein). The issue of small sample size in most species in this study, however, suggests that not all significant variation seen across osteological, subzero, and ethanol specimens may be truly significant. Significant differences may, in some cases, be a result of body size variation across a species that is only apparent due to small sample size.

Some species show radical differences in certain measurements that are not reflected in other species, even in the same or similar life habitat. Two specific examples are *Meleagris gallopavo* and *Ardea alba*. Some measurements taken on *Meleagris* skin specimens, for example, show standard deviation and error bars far larger than recorded for any other specimen (Fig. 3, Appendix I). This could be due to sexual size dimorphism—male wild turkeys are significantly larger than females. Male and female osteological specimens were measured, however, and did not show the same amount of difference (Fig. 3), although overall the osteological measurements did show greater variation than many other species. The variation between soft-tissue specimens may also be indicative that one of the specimens measured was a juvenile and one was an adult. *Ardea* shows a similar situation; the majority of the measurements show skin as significantly smaller than bone, some by a large margin (Fig. 1–6). This is likely due to measuring a subadult specimen. Many subadult or first winter plumages of birds look similar to adult plumages or adult wintering or nonbreeding plumages (e.g., Sibley, 2000), which may make identifying subadult specimens from adult specimens—without dissection or observation of osteological features (e.g., tarsometatarsal fusion)—difficult or impossible.

Sources of error also arise based on the type of foot morphology measured. One of the difficulties in measuring the width of webbed- and lobed-footed toes is determining where, exactly, the joint ends (Fig. 8). The demarcation of the lateral edges of the joint is not always clear, and when it is, there may be difficulty in performing accurate measurements. The webbing does not allow actual measurement of the joint at its widest point (the midpoint of the bone itself), which may influence the data collected. Difficulty in manipulation of the toes may also result in toe rotation or other sources of data error.

In some cases (e.g., *Sitta*) ethanol specimens are significantly different than skin specimens in regard to pad length which is contra to the majority of results shown. Many of these specimens predate the ethanol storage requirement and were originally preserved in formaldehyde. Studies describing the differences in wet lab tissue preservation have mostly focused on stable isotope or molecular studies (e.g., Sarakinos et al., 2002; Nagy, 2010). Kristoffersen and Salvanes (1998) examined ethanol and formaldehyde storage in fish and fish otoliths. They found that body weight loss was higher in ethanol, and ethanol tended to be slightly acidic, and could etch the surface of otoliths, however, length of either type of specimen did not significantly decrease (Kristoffersen and Salvanes, 1998). Specimens preserved in formaldehyde also lose flexibility in the feet, making accurate measurements difficult. Any significant variation between ethanol and soft tissue specimens may, therefore, be attributed to: 1) age of the specimen (i.e., how long it has been in wet lab storage); or 2) original type of preservation, whether it was formaldehyde or ethanol. If the flexibility of the foot is lost, the pad may lose its elasticity and remain compressed. A second possibility is that weight loss indicates water loss, suggesting the flesh itself undergoes shrinkage; however, that is difficult to interpret, as there is no evidence of length change reported previously (Kristoffersen and Salvanes, 1998).

Retrodicting soft tissue and tracks of fossil birds: can it be done?

Certain trends can be observed within life habitat groups (Fig. 1—4), however, the trends are difficult or impossible to correlate across all life-habitat groups. This result indicates that the feet of birds are too widely variable to draw widespread conclusions in regards to soft-tissue reconstructions. Birds are strongly limited by the adaptations necessary for flight—one of the few relatively plastic body parts on a bird is, in fact, the feet. The feet, therefore, are one of the most highly variable structures across class Aves, although they are highly conserved within some groups (e.g., Passeriformes). Any soft-tissue reconstruction would first need to be narrowed down to a life habit group based on osteology, and perhaps whole-body anatomy, if necessary. After that, certain steps can be taken to retrodict the gross anatomy of the foot—e.g., fleshiness of pads, relative length of phalangeal and interphalangeal pads, etc.

Retrodicting trace fossils from body fossils is a difficult task that has rarely been performed (e.g., Fortey and Seilacher, 1997) and has only been performed once in avian traces (Li et al., 2011). The most common single-track measurements used in fossil bird track research are toe length, foot length, foot width, and angle of divarication. Toe length and foot length can both be derived from osteological specimens with relative consistency (Fig. 9) and can, therefore, be reconstructed. Foot width cannot be accurately reconstructed from osteology; however, angle of divarication can be retrodicted from the arc angle of the trochlea of the tarsometatarsus (Falk et al., 2011). This may allow for foot width to be reconstructed based on the estimated angle of divarication and toe length. Toe length can be retrodicted directly from osteology, as soft-tissue toe lengths are often not significantly different (Table 1) and, therefore, any tracks produced by fossil birds can be retrodicted directly from the available anatomy. The width of toes from tracks has been collected (see Chapter 1, Appendix I), however, the media consistency (i.e., grain size and moisture content) can have a strong influence on the toe widths of a track (see Chapter 5). Soft-tissue reconstructions are not necessary in order to retrodict the tracks of fossil birds, based on the measurements important for track reconstruction (i.e., toe length and foot length).

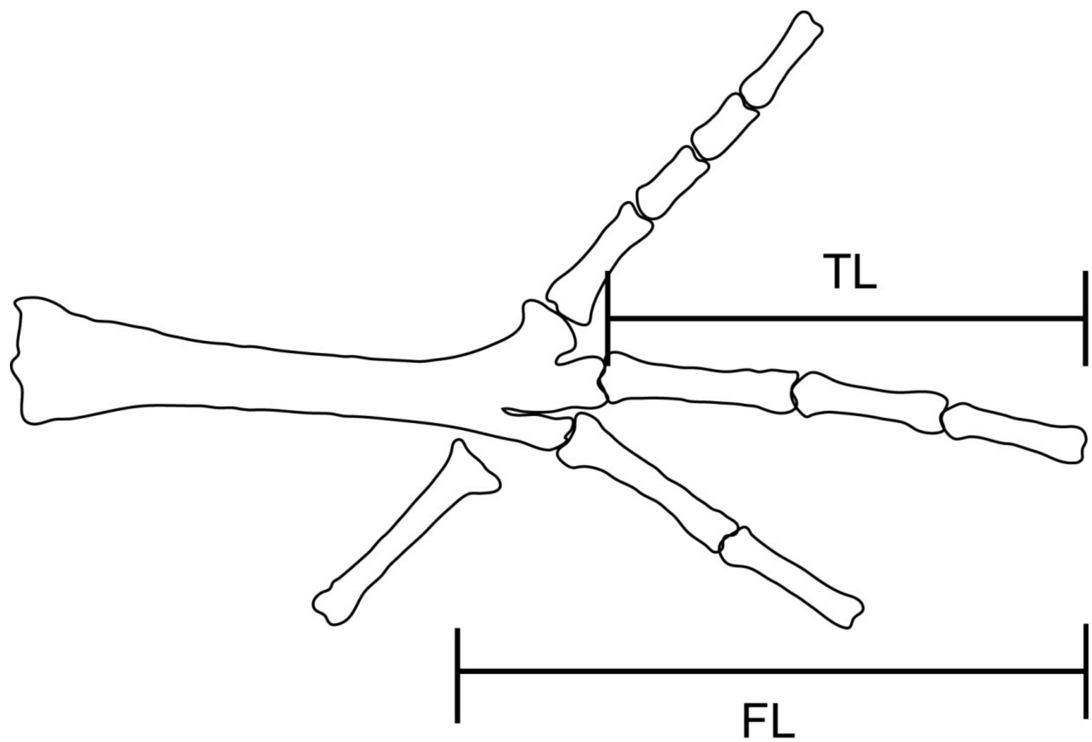


Fig. 9: How to measure toe length and foot length on modern bird osteological specimens. Note that this specimen was disarticulated and has been reconstructed.

CONCLUSIONS

This is the first study to compare the foot morphometrics among osteological, subzero, and ethanol-preserved avian specimens. Previous studies have examined shrinkage rates in museum skins, or various properties of ethanol and formaldehyde preservation, but never combining all three into a integrated study. The length of the toes between osteological, subzero, and ethanol specimens was rarely significantly different, and significant differences may be due to comparing subadult soft-tissue and/or ethanol specimens to adult osteological specimens. The width of the joints, however, are significantly different in many species, especially the more proximal joints, and is likely due to tendons surrounding the joint surface. Webbing or lobing increases the likelihood of error during measuring and may also impact joint width. Phalanx length and phalangeal pad length are significantly different across most life-habitat groups, especially shorebirds, waders, ground birds, and perching birds. Shorebirds and waders tend to exhibit a decrease in the fleshiness of their phalangeal pads, and reduce the phalangeal pad itself while increasing the size of the interphalangeal pad. Perching birds, however, exhibit a strong reduction or elimination of the interphalangeal pad and an increased length of the phalangeal pad. Perching and ground birds tend to have fleshier pads than those of waders and shorebirds, which is likely an adaptation for walking across soft media. Osteology and soft tissue morphology can be related, but a broad, sweeping correlation across all life-habitat groups is difficult to establish. When attempting to reconstruct soft tissue in fossil birds, the best methodology is to determine which life-habitat group it belongs to based on osteology, and then begin the reconstruction based on the parameters for that particular group.

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AN IN-DEPTH ANALYSIS OF THE FEET OF BIRDS FROM THE JEHOL BIOTA: BONES REFLECTING TROPHIC SPECIALIZATIONS AND EVOLUTIONARY PATTERNS

ABSTRACT

Principal component analysis (PCA) has been used on fossil birds to help determine life habit trends and functional morphology. This study conducts three analyses of modern avian hindlimbs, and adds several fossil birds from the Early Cretaceous of China into the three analyses to compare and contrast modern and ancient avian limb morphology. The first PCA—toe length—indicates that toe I has a strong influence on foot morphology and, in modern birds, a robust toe I is a good indicator of arboreality. Toe I is also generally a good indicator of arboreality in fossil birds, however, a primitive foot morphotype makes interpretation more difficult. The second PCA—the hindlimb elements (femur, tibiotarsus, and tarsometatarsus)—indicates that many early fossil birds, with the exception of some primitive ornithurines, had a different posture and leg position than their modern relatives. The femur was not bound to the body wall with muscle, as in modern birds, and the relative proportions and influences of the hindlimb elements were different with respect to modern birds. The third PCA—combined toe and hindlimb element lengths—indicates that the majority of variation seen among fossil and modern birds is actually represented in feet, not in the elements of the hindlimb. Although the hindlimb positioning has clearly shifted through time, it has remained relatively more stable and with a smaller amount of relative variation compared to the toes. These results are supported by a NPMANOVA test, which shows that 21 morphotypes in the toe length analysis have p-values <0.01 in comparison to other morphotypes, whereas only 9 morphotypes in the hindlimb analysis have p-values <0.01, most of which are enantiornithines.

INTRODUCTION

The birds of the Lower Cretaceous Yixian and Jiufotang formations from northeastern China are among the most complete and spectacularly preserved fossils in the world. These specimens are often found with soft tissues preserved, including feathers and/or other soft tissues (e.g., Xu et al., 2003; Zhou et al., 2003). The excellent preservation of these fossils has given paleontologists a rare insight into the avian ecosystems of the Lower Cretaceous. Fossil birds are rarely well preserved and any remains found are often larger, exceptionally fragmentary long bones. This makes the study of whole-body morphology extremely difficult.

Preservation of the very small and delicate phalanges is even more rare. Often bird skeletons disarticulate, and although the tarsometatarsus is often preserved, the toes are very rare; notable non-Jehol Group exceptions are the German Upper Jurassic Solnhofen Limestone, the Upper Cretaceous Niobrara Chalk of the western U.S.A., the Eocene Messel Formation in Germany, the Eocene Green River Formation, U.S.A., and the Eocene–Oligocene Florissant Formation, U.S.A. (e.g., Martin and Tate, 1976; Chandler, 1999; Mayr, 2006; Wellnhofer, 2009).

The birds of the Jehol Group are very diverse. As of 2010 there are 13 orders, 14 families, 33 genera, and 39 species known (Zhou and Wang, 2010), with more new species and genera being found every year. The Jehol Group has also produced fossils of the four-winged glider *Microraptor*, an animal that has been argued as either a dinosaur or a bird (e.g., Xu et al., 2003, Gong et al., 2012). Regardless of phylogenetic placement, many scientists suggest that *Microraptor* was an arboreal animal that glided between trees, and only the interpretation of the configuration of the hindlimb varies between studies (e.g., Chatterjee and Templin, 2007; Alexander et al., 2010).

The diversity of the Jehol Group birds is reflected in the number of both enantiornithine and ornithurine birds. Enantiornithines Walker, 1981, are an entirely extinct subclass of birds that were first discovered in Europe (Walker, 1981). Enantiornithines were the dominant terrestrial birds in the Cretaceous (Zhang et al., 2004), and were generally small and arboreal in the Early Cretaceous, although exceptions do exist (Zhou et al., 2008). Enantiornithines differ from ornithurine (modern-type) birds by having a scapular boss on the coracoid that fits into a cup on the scapula; ornithurine birds have a scapular boss on the scapula that fits into a cup on the coracoid (Walker, 1981). The metatarsals of enantiornithines also fuse proximal-to-distal, the opposite of ornithurine birds (Martin, 1983).

The feet of birds often reflect their life habits. The tarsometatarsus influences the toes, causing the toes to either splay widely for walking on soft media, or narrowly for grasping and perching (Falk et al., 2011). Elongation of the terminal phalanx of each toe and shortening of the proximal phalanges indicates an arboreal lifestyle (Fisher, 1946; Zhou and Farlow, 2001). The degree of curvature of the keratinous sheath covering the claws can also indicate arboreality (Feduccia, 1993). Modifications to the trochlea of the tarsometatarsus can cause different toe positions, which are preserved in the fossil record; i.e., the protrusion of a *trochlea accessoria* on trochlea IV causes the fourth toe to rotate and face caudally, resulting in zygodactyly (Baumel and Whitmer, 1993).

Unlike many fossils, the birds of the Jehol Group are often preserved as articulated or nearly articulated skeletons, which allows for very precise identification of each phalanx. In many cases, especially that of toe IV where the phalanges are reduced and very short with little identifying characteristics, if the toes are disarticulated, reconstruction of the foot is almost impossible. The birds of the Jehol Group, in many cases, also have multiple specimens of each species available for study.

The purpose of this paper is to examine the foot morphology of a wide range of the birds of the Jehol Group and compare them to the foot morphologies of modern birds. This includes those specimens currently described as theropod dinosaurs (i.e., *Microraptor*). In doing so a better understanding of the life habits of the Jehol Group birds and their ecological position will be attained. Results presented here can be used to eventually reconstruct the soft tissue anatomy of fossil birds.

INSTITUTIONAL ABBREVIATIONS

IVPP—Institute of Vertebrate Paleontology and Paleoanthropology; DNHM—Dalian Natural History Museum; PLOM—Paleontological Museum of Liaoning.

MATERIALS AND METHODS

Fossil materials used in this study are from the Lower Cretaceous Yixian and Jiufotang formations (~125 Mya) that comprise the bulk of the Jehol Group (Jiang and Sha, 2006), as well as from the Xiagou Formation in Gansu Province, northwest China. Other such fossils as *Anchiornis* and *Epidexipteryx* are from Upper Jurassic rocks (i.e., Tiaojishan Formation in Liaoning Province and Daohugou, Inner Mongolia, respectively). Only maniraptorans that closely resembled birds (e.g., dromaeosaurids) were chosen. The modern avian osteological data was collected from the University of Kansas ornithological collections. The complete dataset of modern and fossil birds is in Appendices II (modern birds) and IV (fossil birds).

A total of 48 measurements, 42 of which relate strictly to the feet and hindlimb bones, were performed on each fossil specimen when a complete hindlimb (i.e., femur, tibiotarsus, and tarsometatarsus + all four digits) was present (Table 1). A total of 38 measurements were taken on the hindlimb of modern bird specimens. There are four more measurements taken on fossil specimens—lengths of the unguals. This was not measured in modern birds due to disarticulation of the specimens. As is often the case, many of the fossil specimens were incomplete, lacking forelimbs, portions of hindlimbs, or lacked hindlimbs entirely. Some specimens, most notably those of *Gansus*, consisted only of feet and/or hindlimb elements. The data was log-adjusted to remove skew related to small body size in the majority of specimens (Fig. 1).

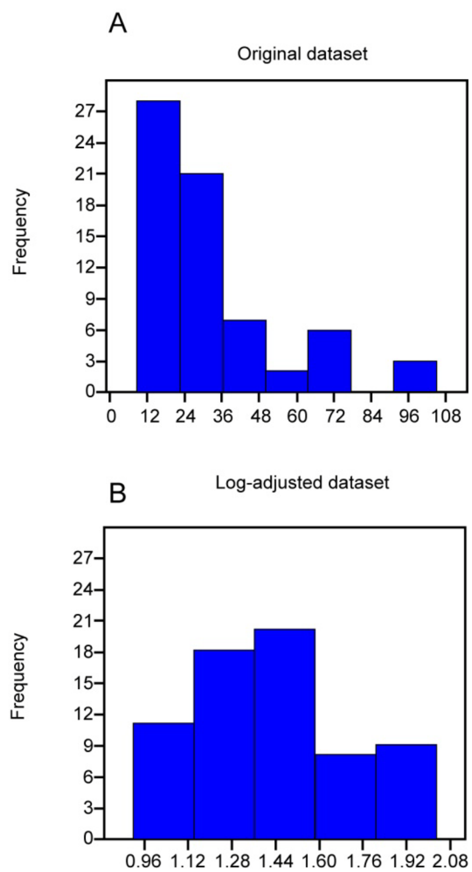


Figure 1: Histogram plotting toe III length of the combined modern+fossil bird dataset, illustrating skew in the original dataset and the more even distribution of the log-adjusted data. A.) Histogram of original dataset, with a strong skew towards smaller body size. B.) Normalized histogram after log-adjustment.

Modern	Fossil
LoDI	LoDI
LoDII	LoDII
LoDIII	LoDIII
LoDIV	LoDIV
W@Pjoint II	W@Pjoint II
W@Pjoint III	W@Pjoint III
W@Pjoint IV	W@Pjoint IV
W@2joint III	W@2joint III
W@2joint IV	W@2joint IV
W@3joint IV	W@3joint IV
LoPhI,II	LoPhI, II
LoPhII,II	LoPhII, II
LoPhI,III	LoPhI, III
LoPhII,III	LoPhII, III
LoPhIII,III	LoPhIII, III
LoPhI,IV	LoPhI, IV
LoPhII,IV	LoPhII, IV
LoPhIII,IV	LoPhIII, IV
LoPhIV,IV	LoPhIV, IV
WoPhI,II	WoPhI, II
WoPhII,II	WoPhII, II
WoPhI,III	WoPhI, III
WoPhII,III	WoPhII, III
WoPhIII,III	WoPhIII, III
WoPhI,IV	WoPhI, IV
WoPhII,IV	WoPhII, IV
WoPhIII,IV	WoPhIII, IV
WoPhIV,IV	WoPhIV, IV
Foot Length	Foot length
Lotmt	Lotmt
Lott	Lott
LoFem	Lofem
Wotmt@prox	Wotmt@prox
Wotmt@cond	Wotmt@cond
Wott@prox	Wott@prox
Wott@mid	Wott@mid
Wott@cond	Wott@cond
Wofem@cond	Wofem@cond
Not measured	LoUngI
Not measured	LoUngII
Not measured	LoUngIII
Not measured	LoUngIV

Table 1: A table of all measurements performed on modern and fossil bird skeletons. LoDI= Length of digit one. LoDII= Length of digit two. LoDIII= Length of digit three. LoDIV= Length of digit four. W@Pjoint II= Width at

the proximal joint of toe two. W@Pjoint III= Width at the proximal joint of toe three. W@Pjoint IV= Width at the proximal joint of toe four. W@2joint III= Width at the second joint of toe three W@2joint IV= Width at the proximal joint of toe four. W@3joint IV= Width at the third joint of toe four. LoPhI, II= Length of phalanx one, toe two. LoPhII, II= Length of phalanx two, toe two. LoPhI, III= Length of phalanx one, toe three. LoPhII, III= Length of phalanx two, toe three. LoPhIII, III= Length of phalanx three, toe three. LoPhI, IV= Length of phalanx one, toe four. LoPhII, IV= Length of phalanx two, toe four. LoPh III, IV= Length of phalanx four, toe four. Lotmt= Length of tarsometatarsus. Lott=Length of tibiotarsus. Lofem=Length of femur. Wotmt@prox= Width of the tarsometatarsus at the proximal end. Wotmt@cond= Width of the tarsometatarsus at the condyles (distal end). Wott@prox=Width of the tibiotarsus at the proximal end. Wott@cond=Width of the tibiotarsus at the condyles. Wofem@cond=Width of the femur at the condyles. LoUngI=Length of ungual 1. LoUngII=Length of ungual 2. LoUngIII=Length of ungual 3. LoUngIV=Length of ungual 4. These abbreviations remain the same throughout the manuscript.

The fossil specimens were compared to a range of modern specimens from the University of Kansas Ornithology collections. A Principal Component Analysis (PCA) was performed on the modern bird dataset using Palaeontological Statistics (PAST) in order to establish distinct life habits in a hypothetical morphospace; these groups were perching (arboreal), wading, ground foraging (gruiform–galliform and cloumbiform), aquatic palmate, aquatic totipalmate, foot-propelled diver, lobed, semipalmate, and shorebird. For some life habits (i.e., lobed and semipalmate) only one species from each morphotype was available. After these analyses were performed on modern birds, fossil birds were entered into the dataset. The PCA dataset sorted fossil birds into life habits based on the hypothetical morphospace generated from modern bird analyses. A separate PCA was also performed on the fossil birds alone to test for any variance in the components. The values generated by the PCA were tested using a non-parametric multiple analysis of variance (NPMANOVA) to test for significant variation between life-habit groups.

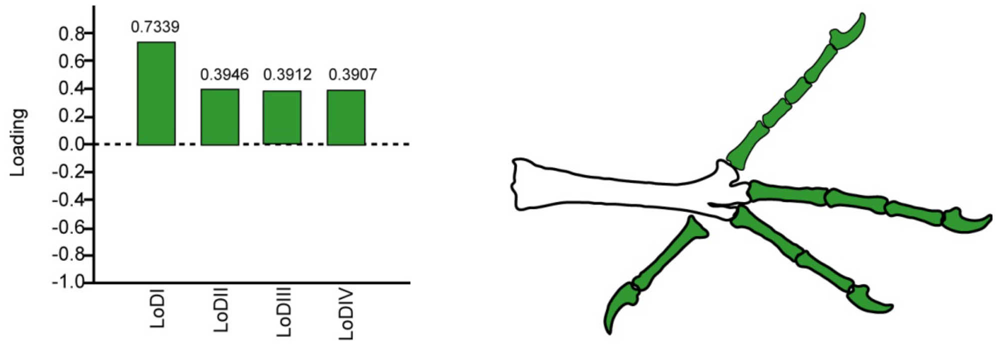
Jack-knifed rarefaction analyses were performed to better visualize variation between life-habit groups in the modern and ancient datasets.

RESULTS

Only seven measurements, divided into three distinct tests, proved significantly useful to define life-habit groups in all datasets. The first group of measurements was individual toe lengths (toes I–IV) and the second group was individual hindlimb elements. For both modern and fossil birds, these two analyses were combined to produce a third analysis that included toe lengths and hindlimb element lengths.

Four principal components (PC) resulted from the analysis on the toe length of modern birds. Principal component 1 (PC1) accounted for 68% of the variation in the data and had all positive loadings (Fig. 2A). PC2 accounted for 32% of the variation in the data and shows toe I had a strong negative loading, whereas toes II–IV had positive loadings of medium strength (Fig. 2B). PC3 accounted for 0.14% of the variation in the data and shows toe I had very weak negative loading, whereas toes II and III had strong positive loadings. Toe IV had very strong negative loading (Fig. 2C). PC4 accounted for 0.07% of the variation in the data and shows that toes I and IV did not have a strong influence (weakly negative and weakly positive, respectively), whereas toes II and III had very strong loadings. Toe II is very strongly negative, whereas toe III is very strongly positive (Fig. 2D).

A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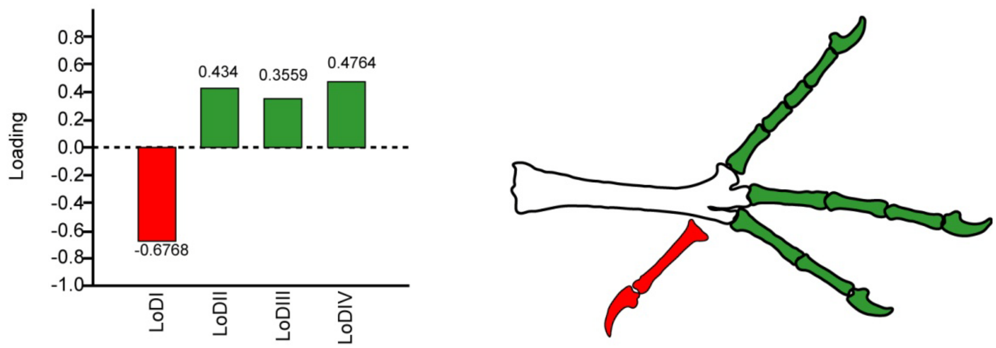
LoDI
LoDII
LoDIII
LoDIV

B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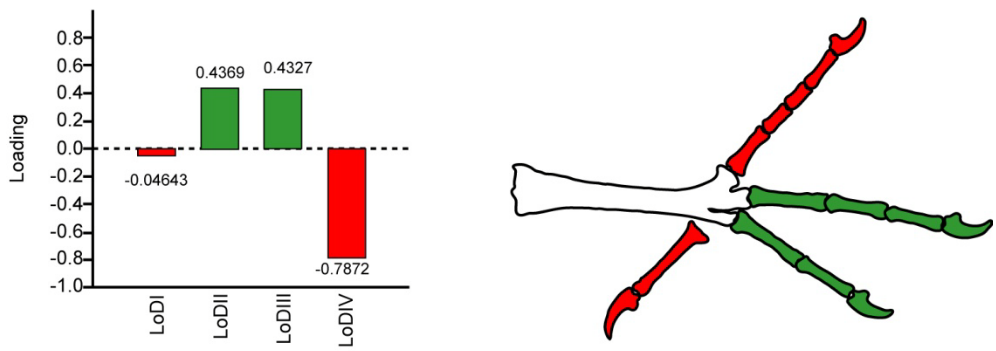
LoDIII
LoDIV

C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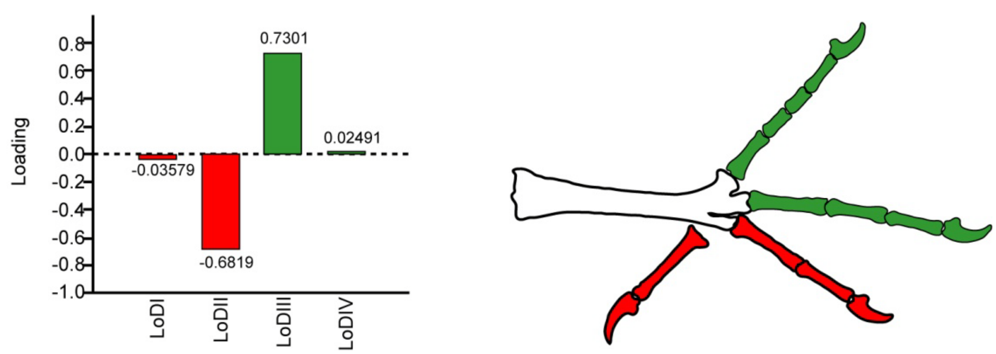
LoDI
LoDII
LoDIII
LoDIV

D


Loading
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-0.6819
0.7301
0.02491
LoDI
LoDII
LoDIII
LoDIV

Fig. 2: (Opposite page) Graphs of the loadings for PC1–4 for the modern-only toe length analysis. Each graph is accompanied by a line drawing of the hindlimb of a bird with the positive elements highlighted in green and the negative elements highlighted in red. A.) Loadings of PC1. B.) Loadings of PC2. C.) Loadings of PC3. D.) Loadings of PC4.

When the toe length PCA PC1 was graphed as a scatterplot in conjunction with PC2, PC1 drew the clusters towards the center axis (Fig. 3A). Due to log-adjusted normalization, , other combinations of PCs for each subsequent analysis were also examined as well as the combination of PC1–PC2. The toe length PC2-PC3 scatterplot showed strong separation of webbed-footed birds (palmate birds and foot-propelled divers) into one cluster, a cluster of shorebirds, ground birds, and wading birds, and a more separate cluster of zygodactyl and perching birds (Fig. 3B). The results of the NPMANOVA generally seem to support these clustering of life-habit groups (Table 2).

	Waders	Lobed-footed	Foot-propelled	Webbed-footed	Semipalmate	Ground	Zygodactyl	Perching	Dove
Waders	0	0.3677	0.0952	0.514	0.0127	0.3081	0.0138	0.0003	0.0404
Lobed-foot	0.3677	0	0.606	0.3517	0.025	0.4024	0.0951	0.0231	0.3277
Foot-prope	0.0952	0.606	0	0.5532	0.0335	0.1481	0.0306	0.0014	0.0691
Webbed-fo	0.514	0.3517	0.5532	0	0.262	0.4228	0.4284	0.5314	0.3497
Semipalmat	0.0127	0.025	0.0335	0.262	0	0.016	0.0068	0.0306	0.0578
Ground	0.3081	0.4024	0.1481	0.4228	0.016	0	0.2083	0.0113	0.297
Zygodactyl	0.0138	0.0951	0.0306	0.4284	0.0068	0.2083	0	0.0823	0.6941
Perching	0.0003	0.0231	0.0014	0.5314	0.0306	0.0113	0.0823	0	0.2234
Dove	0.0404	0.3277	0.0691	0.3497	0.0578	0.297	0.6941	0.2234	0

Table 2: Results of the NPMANOVA for the modern-only toe length analysis. Significantly different values are highlighted in yellow.

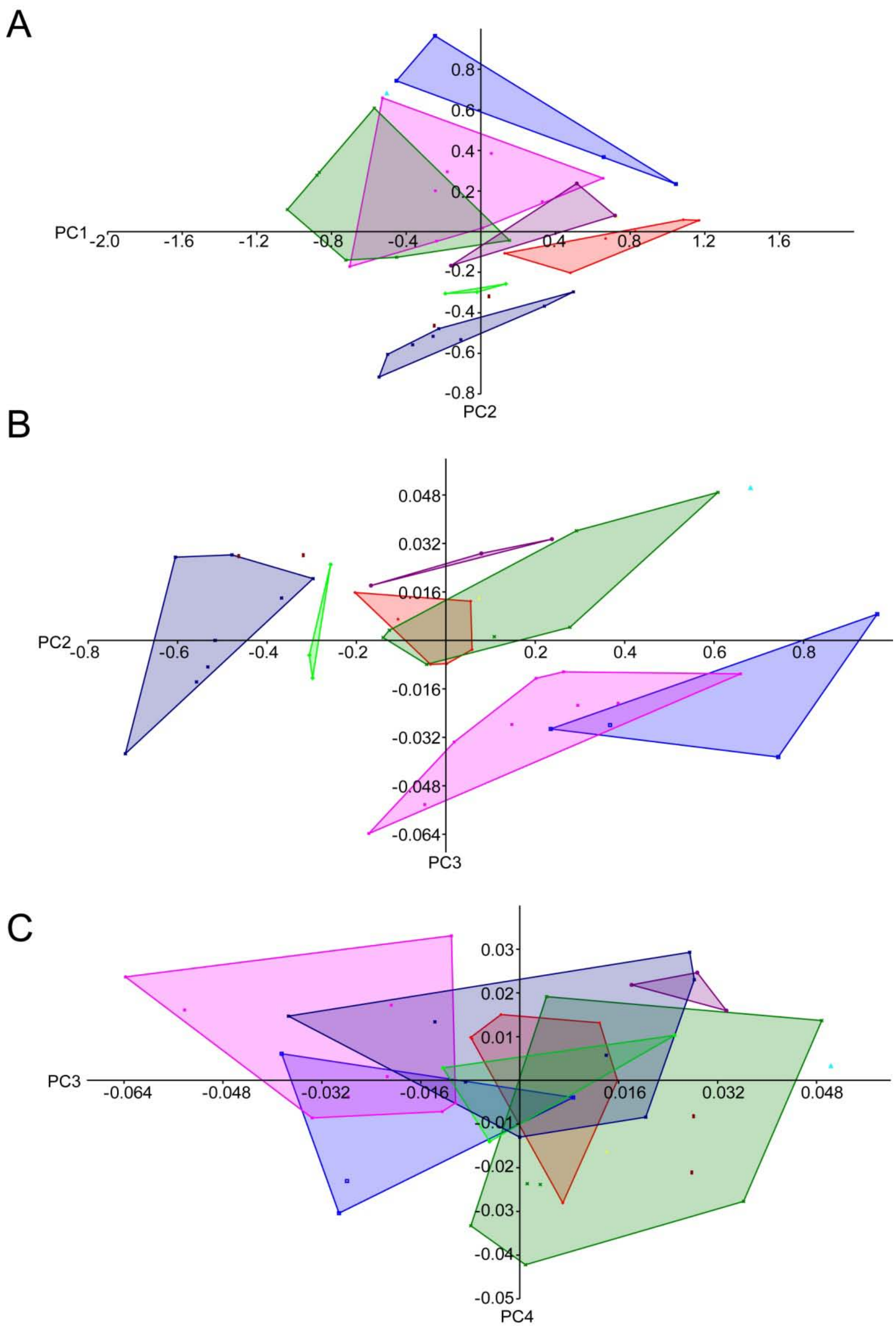


Fig. 3: PC1-PC2 and PC2-PC3 scatterplots of the modern-only toe length analysis. In all modern-only analyses, pink polygons represent webbed-footed birds, sky blue dots represents semipalmate birds, yellow dots represent lobed-

footed birds, light blue polygons represent foot-propelled divers, dark blue polygons represent perching birds, red polygons represent wading birds, burgundy rectangles represent doves, purple polygons represent ground birds, light green polygons represent zygodactyl birds, and dark green polygons represent shorebirds. A.) PC1-PC2 scatterplot. B.) PC2-PC3 scatterplot.

The modern-only hindlimb-element-length analysis contained three PCs. PC1 again accounted for the majority of the variance (96%) and all variables had positive loadings. PC2 accounted for only 3.4% of the variance, and showed that the tarsometatarsus had strongly negative loading, whereas the femur had strongly positive loading. The loading for the tibiotarsus was very weakly negative (Fig. 4). PC3 accounted for a very small portion of the total variance (0.07%), and showed the tarsometatarsus and femur with somewhat strong positive loadings, and the tibiotarsus with strongly negative loading (Fig. 4C).

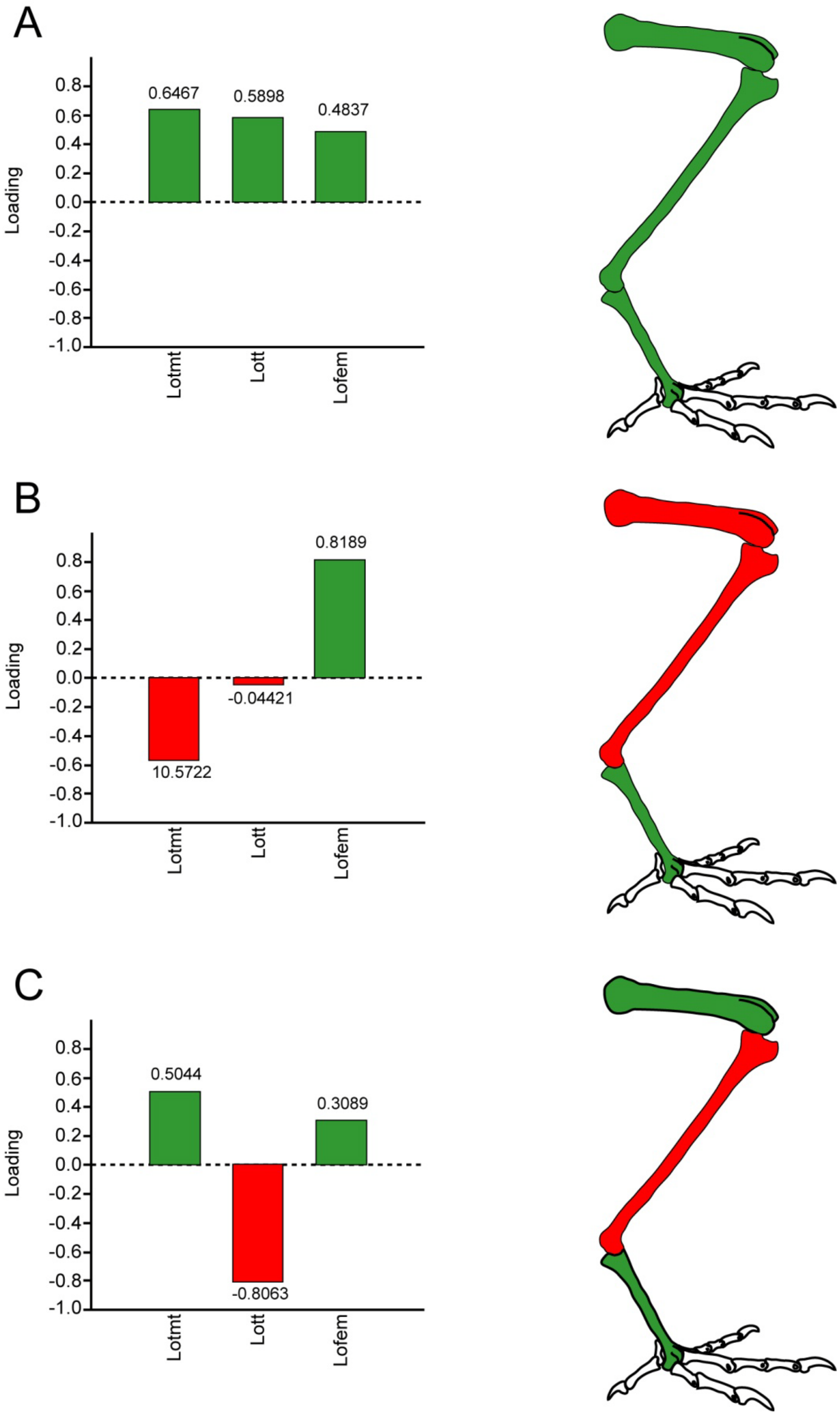


Fig. 4: Graph of the loadings of the modern-only hindlimb analysis. A.) Loadings of PC1 B.) Loadings of PC2 C.) Loadings of PC3.

The PC1–PC2 scatterplot for the modern-only hindlimb-element-length analysis does not show any strong clustering. The more arboreal birds, however, trend towards the left side of the scatterplot (more negative PC1), whereas ground birds and waders trend towards the right side of the scatterplot (more positive PC1). Shorebirds cover a particularly large area on this scatterplot, and are mostly negative with regards to PC2 (Fig. 5A). On the PC2-PC3 scatterplot the clusters are somewhat better defined (Fig. 5B). There is still some overlap between ground birds (particularly *Colinus virginianus*) and perching birds along the PC2 axis, as well as waders and zygodactyl birds along the PC2 axis. Shorebirds still cover a relatively large area along the scatterplot. Along the PC3 axis there is more significant clustering, with webbed-footed birds and foot-propelled divers on the negative side of the axis, and other morphotypes on the positive side. The results of the NPMANOVA support the lack of distinct clustering, with only two instances of p-values <0.05 (Table 3).

	Waders	Lobed-footed	Foot-propelled	Webbed-footed	Semipalmate	Ground	Zygodactyl	Perching	Dove
Waders	0	0.3909	0.9255	0.6057	0.6179	0.8061	0.4555	0.1787	0.1856
Lobed-footed	0.3909	0	0.864	0.4918	0.4198	0.7989	0.1989	0.0462	0.3304
Foot-propelled	0.9255	0.864	0	0.5304	0.4113	0.7708	0.6041	0.5607	0.737
Webbed-footed	0.6057	0.4918	0.5304	0	0.3971	0.6498	0.455	0.6575	0.4581
Semipalmate	0.6179	0.4198	0.4113	0.3971	0	0.9196	0.6066	0.7695	0.6712
Ground	0.8061	0.7989	0.7708	0.6498	0.9196	0	0.2056	0.8666	0.1033
Zygodactyl	0.4555	0.1989	0.6041	0.455	0.6066	0.2056	0	0.1241	0.202
Perching	0.1787	0.0462	0.5607	0.6575	0.7695	0.8666	0.1241	0	0.2911
Dove	0.1856	0.3304	0.737	0.4581	0.6712	0.1033	0.202	0.2911	0

Table 3: Results of the NPMANOVA for the modern-only hindlimb analysis. Significantly different values are highlighted in yellow.

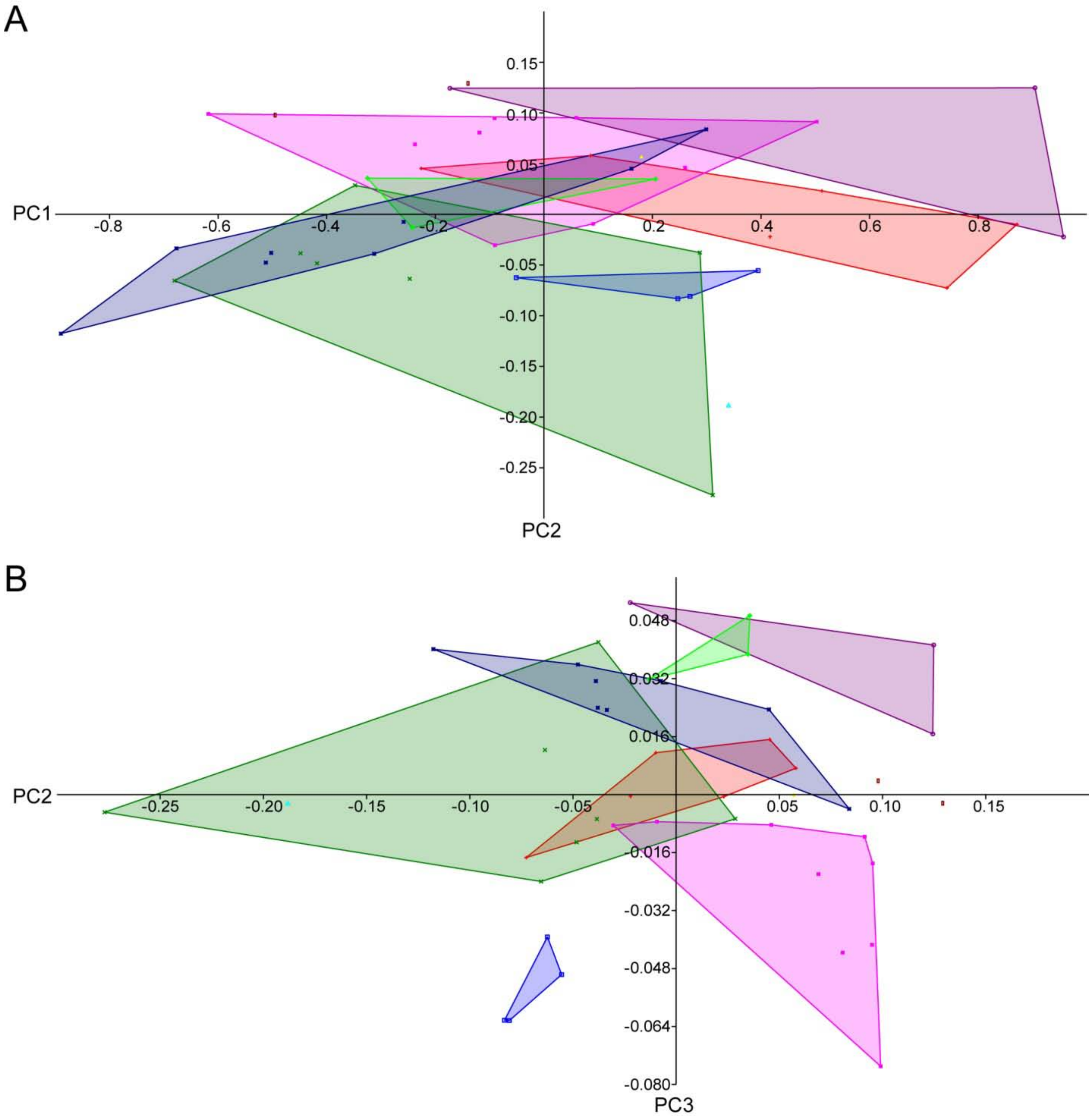


Fig. 5: Scatterplots of the modern-only hindlimb analysis. A.) PC1-PC2 scatterplot. B.) PC2-PC3 scatterplot.

Using the modern bird dataset, these two analyses were combined into one, the toe length+hindlimb analysis. The loadings for PC1 are all positive despite normalization. PC1 accounts for 69% of the variance of the data. PC2 accounts for 27% of the variance of the data, and shows toe I length is the dominant factor, with a very strongly negative loading, whereas the other variables have strong to moderately strong positive loadings (Fig. 6). PC3 accounts for 3.2% of the variation in the data and shows the toe lengths with weak to strong negative loadings, and shows hindlimb element lengths with strong positive loadings (Fig. 6C). PC4–PC7 account for 1% of the variation in the data when combined, and show a varied mix of positive and negative loadings between toe length and hindlimb elements (Fig. 6D–F). The PC1-PC2 and PC2-PC3 scatterplots look similar to the scatterplots produced by the modern-only toe-length analysis (Fig. 7).

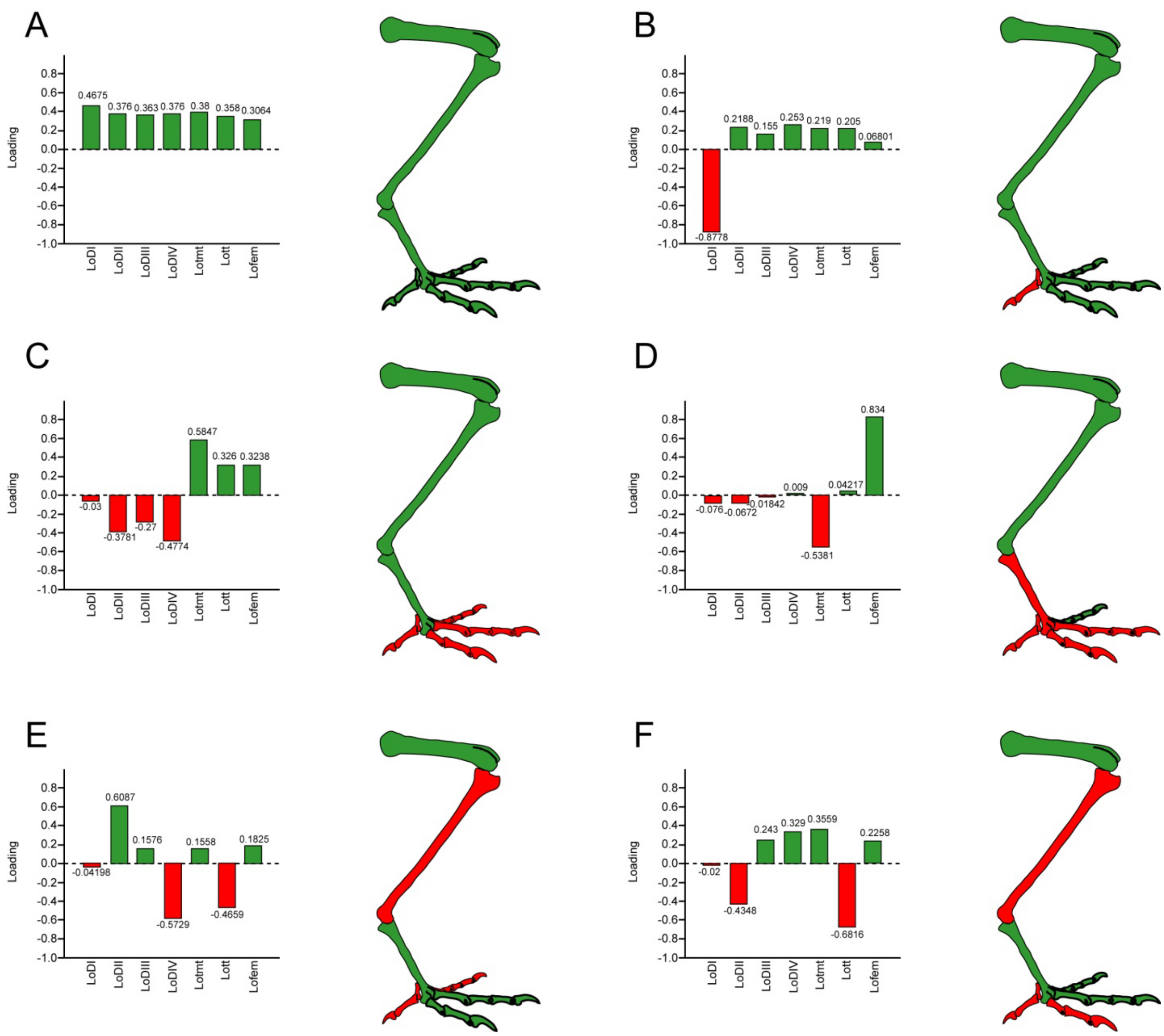


Fig 6: Graph of the loadings of the modern-only toe+hindlimb analysis. A.) Loadings of PC1 B.) Loadings of PC2 C.) Loadings of PC3 D.) Loadings of PC4 E.) Loadings of PC5 F.) Loadings of PC6.

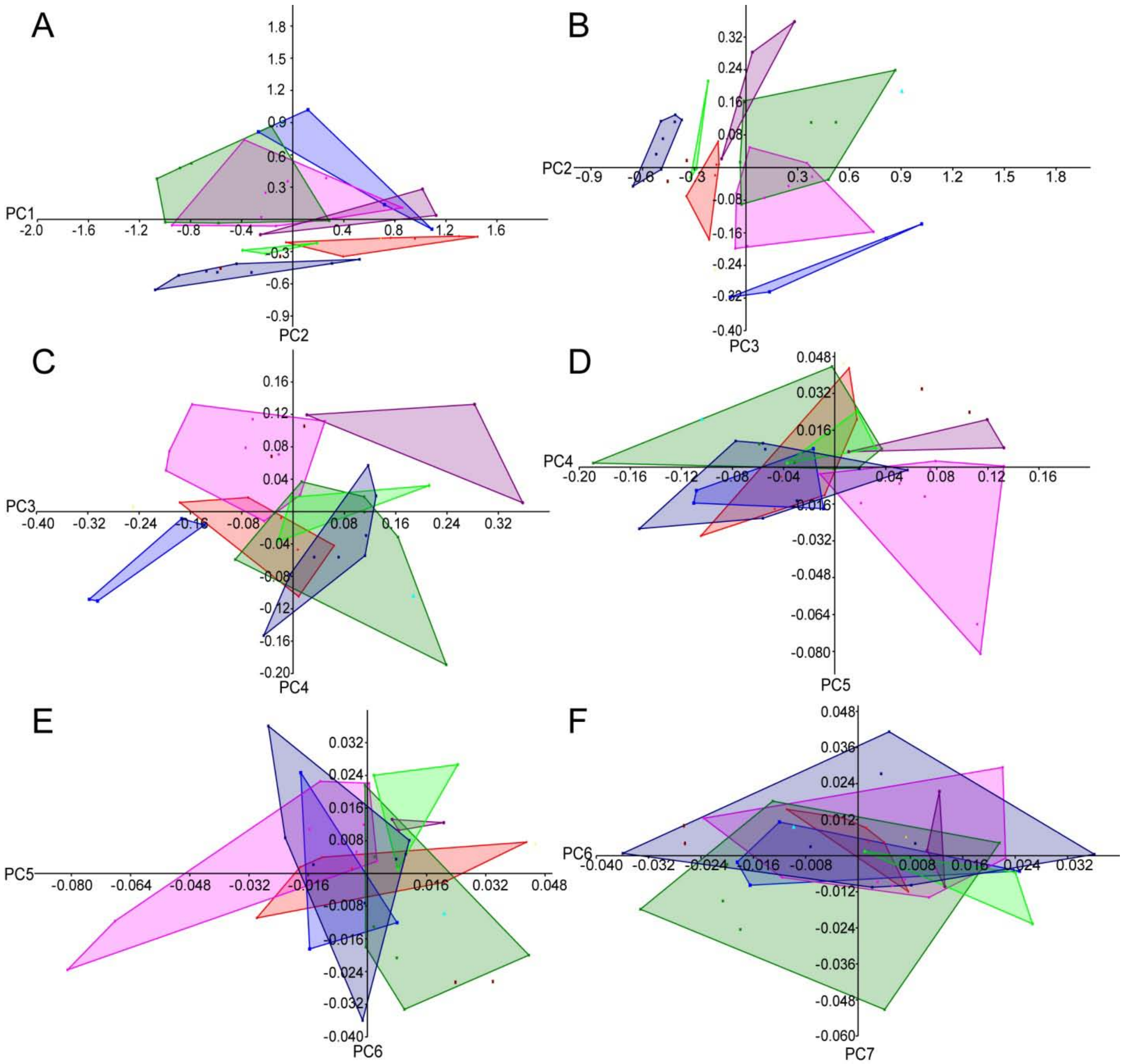
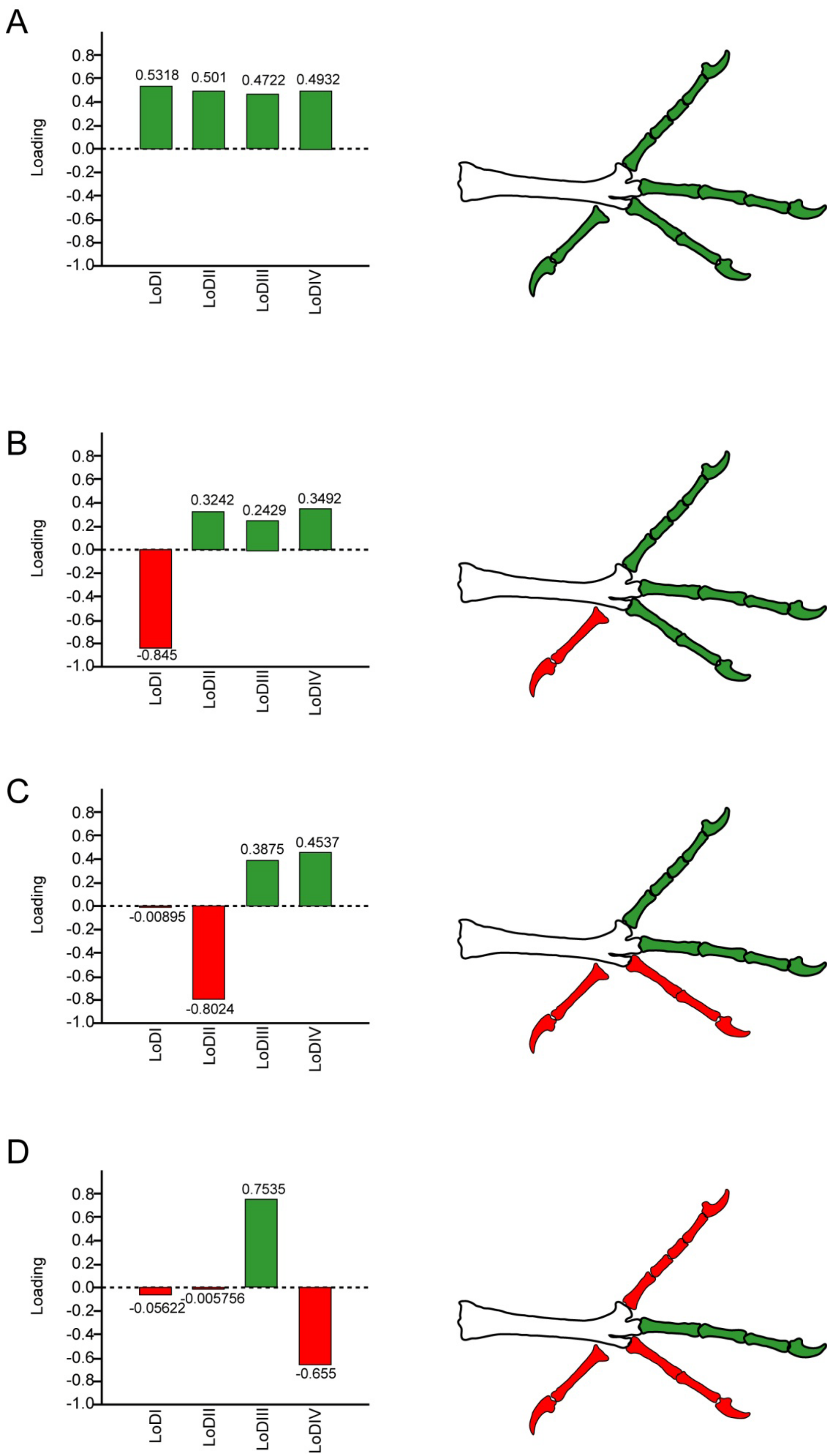


Fig. 7: Scatterplots of the modern-only toe+hindlimb analysis. A.) PC1-PC2 scatterplot. B.) PC2-PC3 scatterplot. C.) PC3-PC4 scatterplot D.) PC4-PC5 scatterplot E.) PC5-PC6 scatterplot F.) PC6-PC7 scatterplot.

After the modern-only analyses were performed, fossil data were added to the dataset and the analyses were redone. In the toe-length analysis, the loadings for PC1 were still all positive (Fig. 8A). PC1 accounted for 72% of the variance in the data. PC2 showed toe I with a very strongly negative loading, whereas toes II–IV had somewhat strongly positive loadings (Fig. 8B), and accounted for 27% of the variance in the data. PC3 (Fig. 8C) accounted for 0.38% of the variance in the data and showed toe II with very strong negative loading, and toe I with very weak negative loading. Toes III and IV had strong positive loadings. PC4 (Fig. 8D) accounted for 0.2% of the variation in the data and showed toe III with a very strong positive loading, whereas toe IV had very strong negative loading. Toes I–II had very weak negative loadings.


A
Loading
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0.4932
LoDI
LoDII
LoDIII
LoDIV
B
Loading
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LoDI
LoDII
LoDIII
LoDIV
C
Loading
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0.4537
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LoDI
LoDII
LoDIII
LoDIV
D
Loading
0.7535
-0.05622
-0.005756
-0.655
LoDI
LoDII
LoDIII
LoDIV

Fig. 8: (Opposite page) Graphs of the loadings for PC1–4 for the modern+fossil toe length analysis. A.) Loadings of PC1. B.) Loadings of PC2. C.) Loadings of PC3. D.) Loadings of PC4.

The PC1-PC2 scatterplot for the toe-length analysis shows similar clustering to the modern-only analysis (Fig. 9). *Archaeopteryx* plots very close to the center of the intersection of both axes and groups with long-tailed birds+microraptorines, and primitive ornithurines. Enantiornithines form their own cluster. Primitive Cretaceous birds (e.g., *Sapeornis*) also form their own cluster, which overlaps slightly with zygodactyl birds, Confuciusornithids, and long-tailed birds+microraptorines (Fig. 9A). The PC2-PC3 scatterplot (Fig. 9B) has a similar result, however, the enantiornithines and wading birds overlap on the negative side of the PC2 axis. *Archaeopteryx* is again nested with long-tailed birds+microraptorines, which overlap with primitive ornithurines. Confuciusornithids slightly overlap with wading birds due to an outlier, *Jinzhouornis*. The PC3-PC4 scatterplot shows no strong separation of individual clusters at all. The results of the NPMANOVA support this mixed clustering amongst the scatterplots (Table 4).

	Waders	Lobed-footed	Foot-propelled	Webbed-footed	Semipalmat	Ground	Zygodactyl	Perching	Dove	Primitive	Enantiornith	Long-tailed	Ornithurine	Confuciusor
Waders	0	0.3592	0.0443	0.5875	0.3887	0.6461	0.0725	0.0062	0.036	0.0507	0.0007	0.2869	0.4407	0.0108
Lobed-footed	0.3592	0	0.526	0.7975	0.9473	0.8985	0.8013	0.0472	0.3361	0.2986	0.0182	0.9525	0.932	0.0976
Foot-propelled	0.0443	0.526	0	0.8383	0.8868	0.3402	0.3667	0.1008	0.066	0.5734	0.0026	0.6534	0.9134	0.0302
Webbed-footed	0.5875	0.7975	0.8383	0	0.2126	0.5611	0.4439	0.11	0.342	0.1733	0.068	0.2445	0.2568	0.2143
Semipalmate	0.3887	0.9473	0.8868	0.2126	0	0.3231	0.0767	0.0199	0.3605	0.1245	0.4643	0.0587	0.3422	0.2667
Ground	0.6461	0.8985	0.3402	0.5611	0.3231	0	0.1984	0.05	0.1	0.1992	0.007	0.788	0.9737	0.103
Zygodactyl	0.0725	0.8013	0.3667	0.4439	0.0767	0.1984	0	0.1661	1	0.1998	0.0059	0.2122	0.1403	0.0942
Perching	0.0062	0.0472	0.1008	0.11	0.0199	0.05	0.1661	0	0.1819	0.0859	0.0099	0.0093	0.0776	0.0383
Dove	0.036	0.3361	0.066	0.342	0.3605	0.1	1	0.1819	0	0.8	0.0228	0.1357	0.1965	0.1023
Primitive	0.0507	0.2986	0.5734	0.1733	0.1245	0.1992	0.1998	0.0859	0.8	0	1	0.1781	0.1373	0.4925
Enantiornithine	0.0007	0.0182	0.0026	0.068	0.4643	0.007	0.0059	0.0099	0.0228	1	0	0.0009	0.0163	0.0063
Long-tailed	0.2869	0.9525	0.6534	0.2445	0.0587	0.788	0.2122	0.0093	0.1357	0.1781	0.0009	0	0.2512	0.0895
Ornithurine	0.4407	0.932	0.9134	0.2568	0.3422	0.9737	0.1403	0.0776	0.1965	0.1373	0.0163	0.2512	0	0.0847
Confuciusornithid	0.0108	0.0976	0.0302	0.2143	0.2667	0.103	0.0942	0.0383	0.1023	0.4925	0.0063	0.0895	0.0847	0

Table 4: Results of the NPMANOVA for the modern+fossil toe length analysis. Statistically different values are highlighted in yellow.

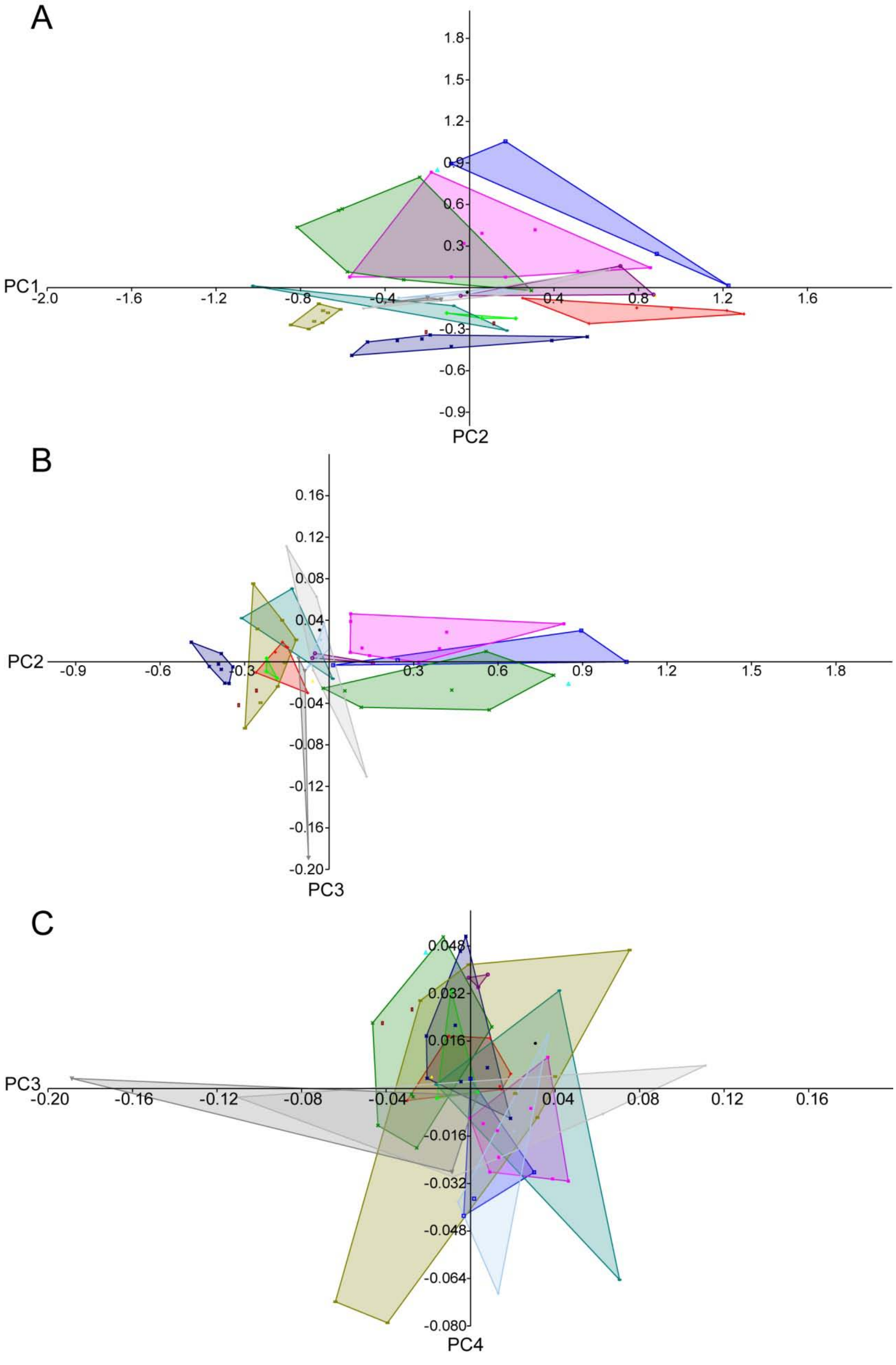
A
PC1
PC2
B
PC2
PC3
C
PC3
PC4

Fig. 9: (Opposite page) Scatterplots of the modern+fossil toe length analysis. In all modern+fossil analyses, pink polygons represent modern webbed-footed birds, sky blue dots represent modern semipalmate birds, yellow dots represent modern lobed-footed birds, light blue polygons represent modern foot-propelled divers, dark blue polygons represent modern perching birds, red polygons represent modern wading birds, burgundy rectangles represent modern doves, purple polygons represent modern ground birds, light green polygons represent modern zygodactyl birds, and dark green polygons represent modern shorebirds. Teal polygons represent primitive birds, gold polygons represent enantiornithines, maniraptorians and long-tailed birds are represented by silver polygons, pale blue polygons represent primitive ornithurines, slate grey polygons represent confuciusornithids, and *Archaeopteryx* is represented by a black dot. A.) PC1-PC2 scatterplot B.) PC2-PC3 scatterplot. C.) PC3-PC4 scatterplot.

The hindlimb analysis contained a slightly larger dataset, especially for enantiornithines. The loadings were, overall, very similar to the modern only analysis. PC1 accounted for 95% of the variance in the data and had all strongly positive loadings (Fig. 10A). PC2 accounted for 4.7% of the variance in the data and had strongly negative loading for the tarsometatarsus, very weakly negative loading for the tibiotarsus, and very strongly positive loading for the femur (Fig. 10B). PC3 only accounted for 0.4% of the variance in the data, and showed strongly positive loadings for the tarsometatarsus and femur, and very strongly negative loading for the tibiotarsus (Fig. 10C).

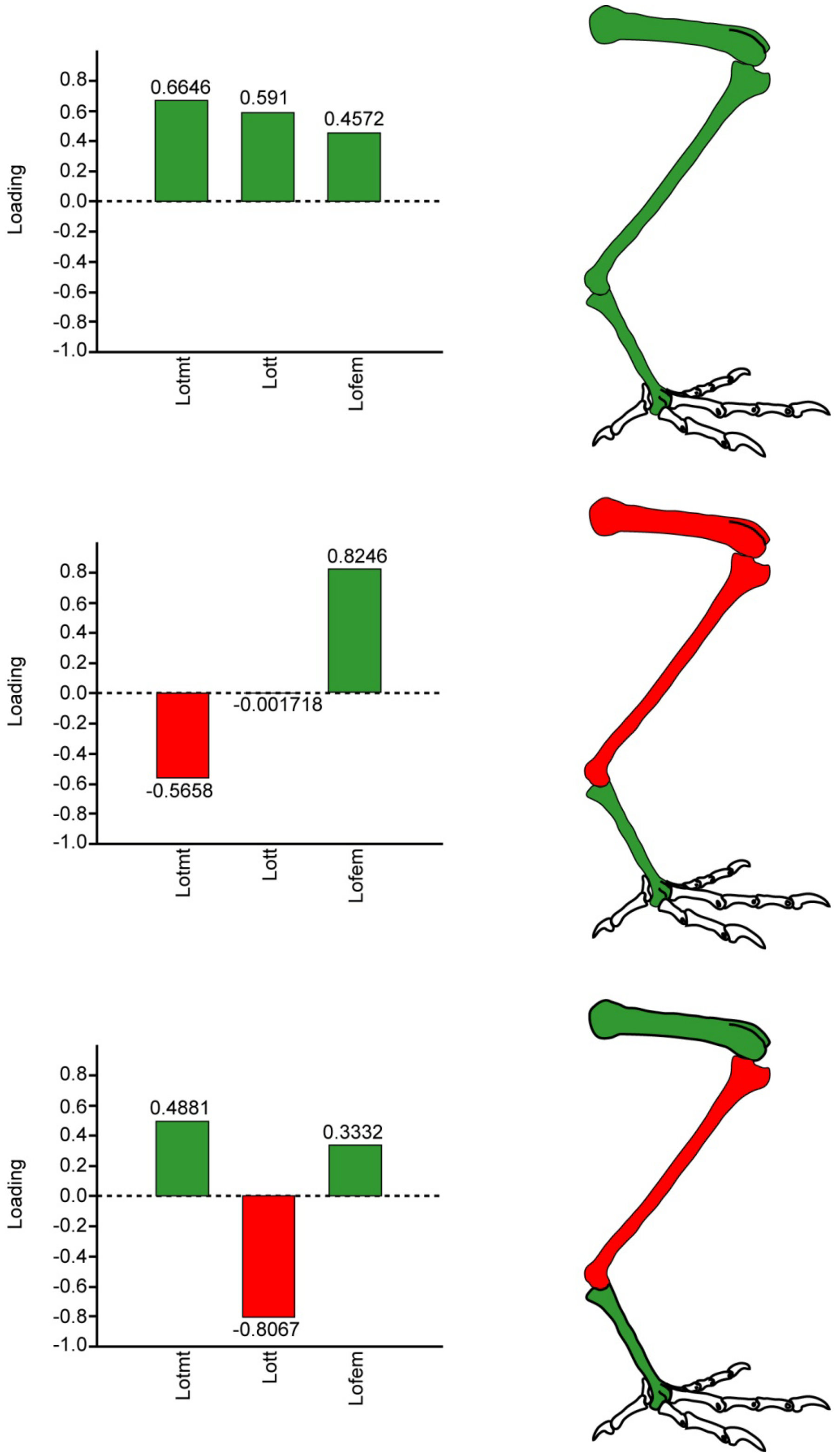

Fig. 10: Graph of the loadings of the modern+fossil hindlimb analysis. A.) Loadings of PC1 B.) Loadings of PC2 C.) Loadings of PC3.

The PC1-PC2 scatterplot of the hindlimb analysis showed some separation of fossil birds from the modern groups, with the exception of the Cretaceous ornithurines, and with one exception of webbed-footed birds (*Sterna paradisea*) overlapping with the enantiornithine cluster (Fig. 11A). Most of this separation is along the PC2 axis. The PC2-PC3 scatterplot, however, has lost much of this clustering (Fig. 11B). Primitive birds, confuciusornithids, and long-tailed birds+microraptorines do tend towards the positive side of the PC2 axis, although there is some overlap with other modern bird groups. Enantiornithines cover a very wide range in the morphospace. The results of the NPMANOVA generally support this trend. Only enantiornithines have many comparisons with p-values <0.05 (Table 5).

	Waders	Lobed-foot	Foot-prope	Webbed-fo	Semipalmat	Ground	Zygodactyl	Perching	Dove	Primitive	Enantiornith	Long-tailed	Ornithurine	Confuciuso
Waders	0	0.9267	0.5641	0.8569	0.7609	0.7865	0.5116	0.5429	0.4562	0.2181	0.3933	0.5494	0.5338	0.2056
Lobed-footed	0.9267	0	0.4792	0.3131	0.8107	0.6032	0.5904	0.4024	0.3352	0.3326	0.007	0.4268	0.268	0.0999
Foot-propelled	0.5641	0.4792	0	0.3834	0.6765	0.0582	0.0843	0.1382	0.0656	0.2634	0.0002	0.0043	0.1158	0.0263
Webbed-footed	0.8569	0.3131	0.3834	0	0.935	0.796	0.671	0.7549	0.7871	0.4063	0.0015	0.2138	0.2864	0.1921
Semipalmate	0.7609	0.8107	0.6765	0.935	0	0.8528	0.8446	0.8567	0.8298	0.7969	0.9668	0.7438	0.8113	0.86
Ground	0.7865	0.6032	0.0582	0.796	0.8528	0	0.2071	0.882	0.4024	0.8024	0.0009	0.032	0.7667	0.195
Zygodactyl	0.5116	0.5904	0.0843	0.671	0.8446	0.2071	0	0.3293	0.502	0.2046	0.0014	0.0227	0.1463	0.5005
Perching	0.5429	0.4024	0.1382	0.7549	0.8567	0.882	0.3293	0	0.7945	0.5662	0.1565	0.3458	0.8306	0.884
Dove	0.4562	0.3352	0.0656	0.7871	0.8298	0.4024	0.502	0.7945	0	0.3391	0.0113	0.0317	0.7357	0.4071
Primitive	0.2181	0.3326	0.2634	0.4063	0.7969	0.8024	0.2046	0.5662	0.3391	0	0.0006	0.883	0.2824	0.4577
Enantiornithine	0.3933	0.007	0.0002	0.0015	0.9668	0.0009	0.0014	0.1565	0.0113	0.0006	0	0.0001	0.5525	0.0011
Long-tailed	0.5494	0.4268	0.0043	0.2138	0.7438	0.032	0.0227	0.3458	0.0317	0.883	0.0001	0	0.0977	0.0123
Ornithurine	0.5338	0.268	0.1158	0.2864	0.8113	0.7667	0.1463	0.8306	0.7357	0.2824	0.5525	0.0977	0	0.1995
Confuciusornithi	0.2056	0.0999	0.0263	0.1921	0.86	0.195	0.5005	0.884	0.4071	0.4577	0.0011	0.0123	0.1995	0

Table 5: Results of the NPMANOVA for the modern+fossil hindlimb analysis. Significantly different values are highlighted in yellow.

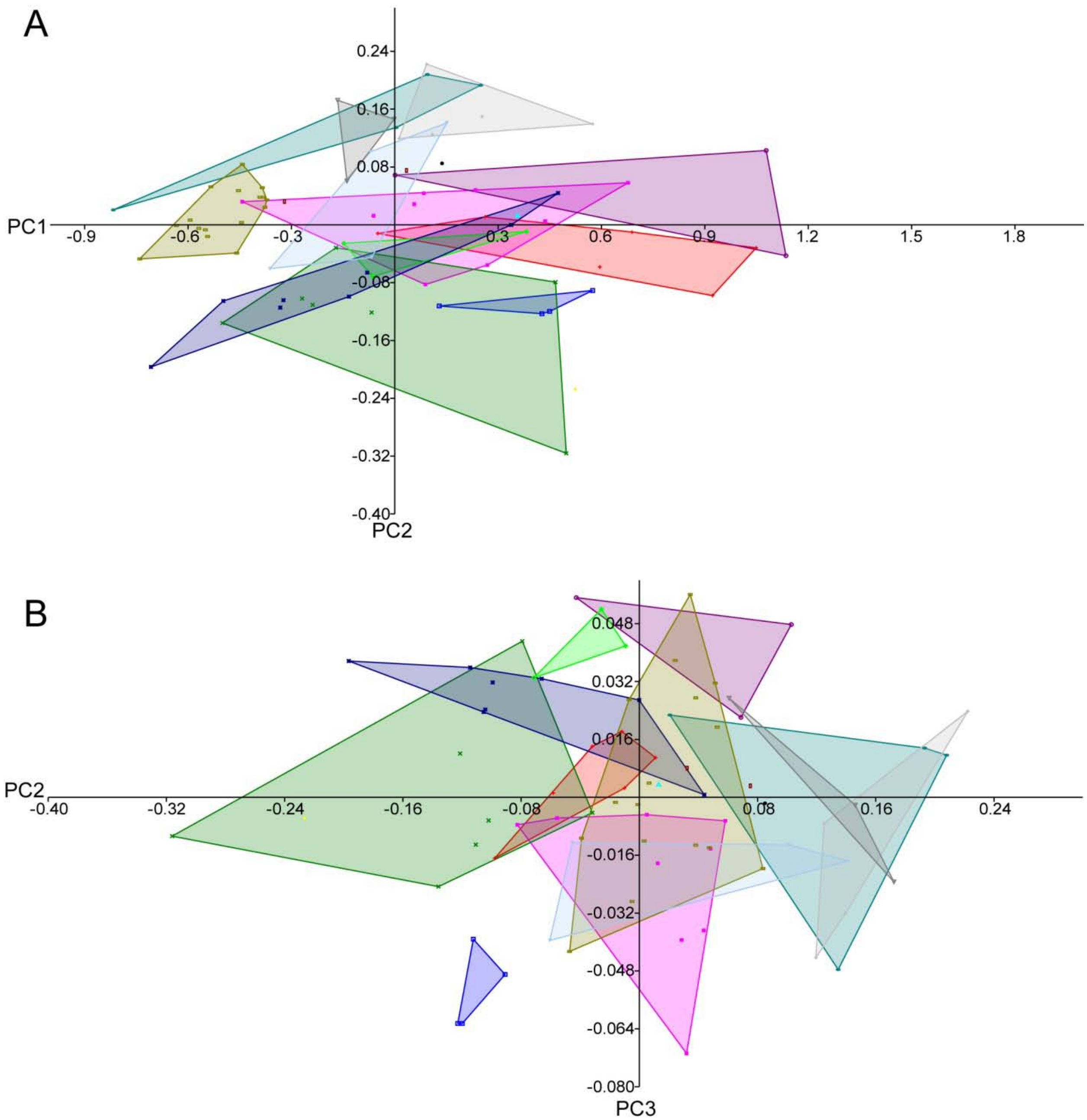

Fig. 11: Scatterplots of the modern+fossil hindlimb analysis. A.) PC1-PC2 scatterplot. B.) PC2-PC3 scatterplot.

When the toe length and hindlimb modern+fossil analyses are combined into a single analysis, the loadings do not change much in value, however, some are flipped—those that were positive in the modern-only analysis are negative, and vice versa. The loadings for PC1, however, remain positive (Fig. 12A). PC1 accounts for 76% of the variation in the data. PC2 accounts for

20% of the variation in the data and shows toe I with very strong positive loading. All other measurements have moderately strong negative loadings, except for the femur, which has very weakly positive loading (Fig. 12B). PC3 is very similar to the modern-only analysis and accounts for 3% of the variation in the data, and shows the toe length measurements with weak to strong negative loadings, and the hindlimb element measurements with strong positive loadings (Fig. 12C). PC4–PC7 account for 1.7% of the variation in the data, and show a mix of negative and positive loadings between the various measurements (Fig. 12D–F).

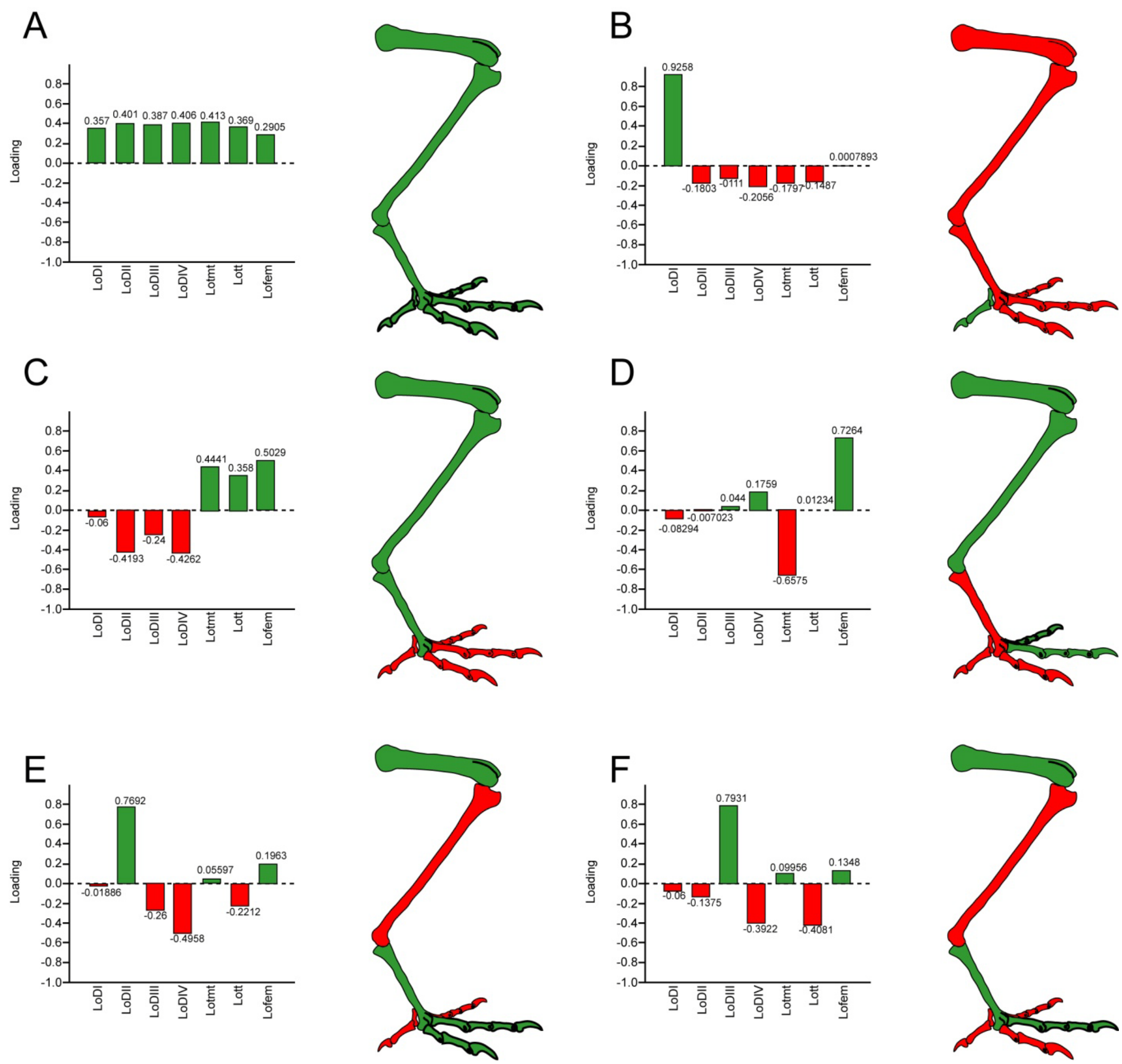

Fig. 12: (Opposite page) Graph of the loadings of the modern+fossil toe+hindlimb analysis. A.) Loadings of PC1 B.) Loadings of PC2 C.) Loadings of PC3 D.) Loadings of PC4 E.) Loadings of PC5 F.) Loadings of PC6.

The PC1-PC2 scatterplot for the toe+hindlimb analysis shows some clustering, especially those of perching birds, enantiornithines, and primitive birds. *Archaeopteryx* falls very close to the center of the morphospace (Fig. 13A). The PC2-PC3 scatterplot shows a strong separation between the arboreal birds (perching birds, zygodactyl birds, and enantiornithines) and terrestrial birds—the sole exception to this rule are the wading birds, which plot very close to perching birds (Fig. 13B). A PC2-PC4 scatterplot shows similar clustering to PC2-PC3, but strongly narrows the morphospace occupied by ground birds (Fig. 13C). Clustering begins to break down in the PC3-PC4 scatterplot with only long-tailed birds+domaeosaurs completely isolated from modern birds (Fig. 13D). Primitive birds and confuciusornithids also begin to cluster with the long-tailed birds+domaeosaurs, however, they both overlap with webbed-footed birds (Fig. 13D). The higher PC numbers result in a breakdown of clustering reflected in the results of the NPMANOVA (Fig. 14, Table 6).

	Waders	Lobed-footed	Foot-propelled	Webbed-footed	Semipalmate	Ground	Zygodactyl	Perching	Dove	Primitive	Enantiornithine	Long-tailed	Ornithurine	Confuciuso
Waders	0	0.2194	0.5095	0.2101	0.0218	0.1172	0.9434	0.1531	0.1096	0.2047	0.0009	0.0054	0.8871	0.9284
Lobed-footed	0.2194	0	0.2674	0.3581	0.0595	0.1003	0.7016	0.3564	0.3357	0.391	0.0237	0.0676	0.7376	0.7013
Foot-propelled	0.5095	0.2674	0	0.9423	0.0366	0.6968	0.9441	0.1666	0.3311	0.3414	0.0064	0.1706	0.7127	0.9431
Webbed-footed	0.2101	0.3581	0.9423	0	0.0157	0.3159	0.1731	0.0026	0.0365	0.3039	0.0003	0.0165	0.3357	0.4415
Semipalmate	0.0218	0.0595	0.0366	0.0157	0	0.5839	0.8939	0.0268	0.1635	0.0962	0.0001	0.0246	0.8688	0.9506
Ground	0.1172	0.1003	0.6968	0.3159	0.5839	0	0.8026	0.1259	0.393	0.5954	0.0056	0.1392	0.4199	0.7026
Zygodactyl	0.9434	0.7016	0.9441	0.1731	0.8939	0.8026	0	0.9085	0.8011	0.8977	0.1527	0.4883	1	0.5038
Perching	0.1531	0.3564	0.1666	0.0026	0.0268	0.1259	0.9085	0	0.1804	0.1363	0.3067	0.0102	0.1749	0.938
Dove	0.1096	0.3357	0.3311	0.0365	0.1635	0.393	0.8011	0.1804	0	0.8005	0.0222	0.1294	0.7356	0.6956
Primitive	0.2047	0.391	0.3414	0.3039	0.0962	0.5954	0.8977	0.1363	0.8005	0	0.3977	0.9164	0.7089	1
Enantiornithine	0.0009	0.0237	0.0064	0.0003	0.0001	0.0056	0.1527	0.3067	0.0222	0.3977	0	0.0015	0.4778	0.9484
Long-tailed	0.0054	0.0676	0.1706	0.0165	0.0246	0.1392	0.4883	0.0102	0.1294	0.9164	0.0015	0	0.4566	0.4707
Ornithurine	0.8871	0.7376	0.7127	0.3357	0.8688	0.4199	1	0.1749	0.7356	0.7089	0.4778	0.4566	0	0.5755
Confuciusornithid	0.9284	0.7013	0.9431	0.4415	0.9506	0.7026	0.5038	0.938	0.6956	1	0.9484	0.4707	0.5755	0

Table 6: Results of the NPMANOVA for the modern+fossil toe+hindlimb analysis. Significantly different values are highlighted in yellow.

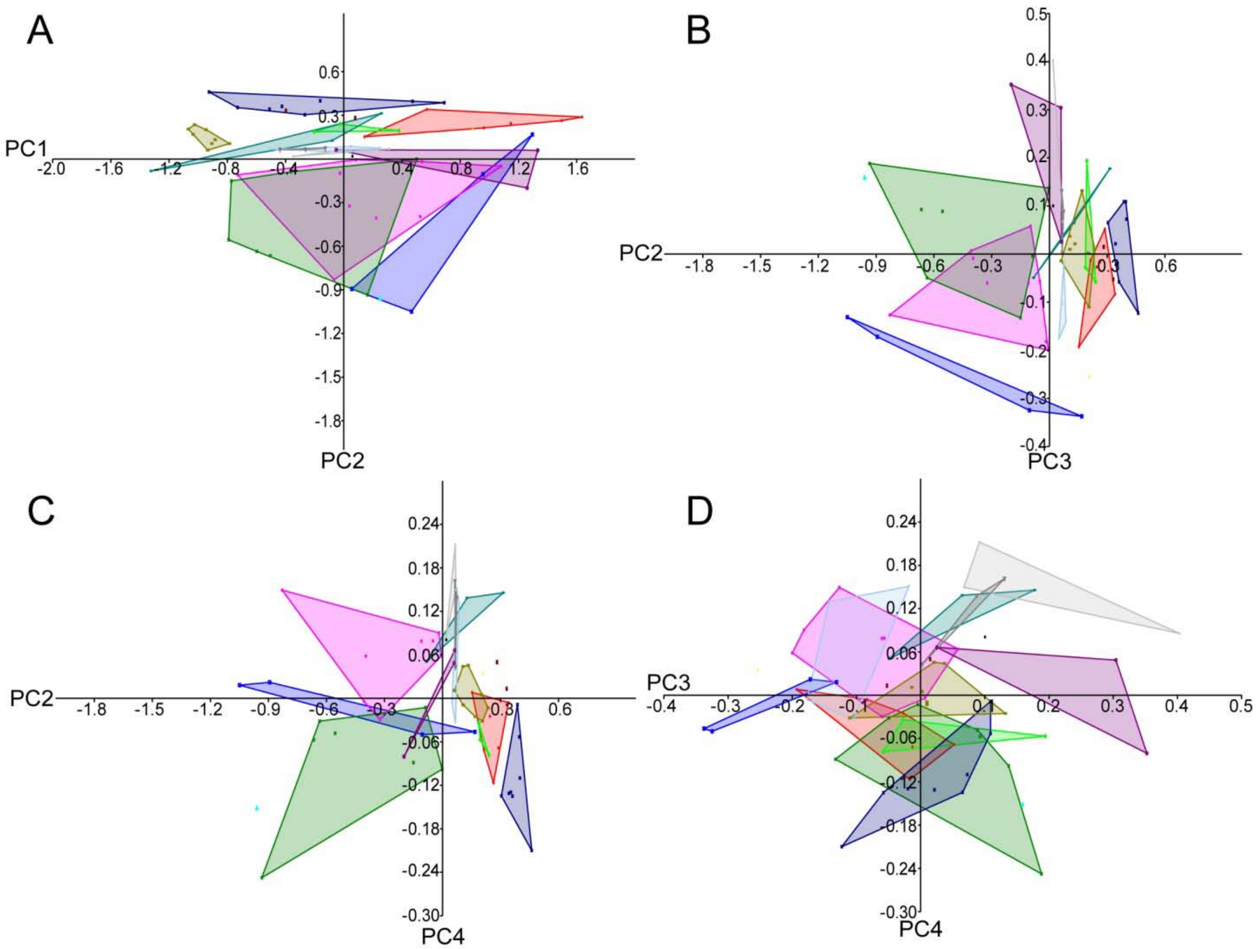

Fig. 13: Scatterplots of the fossil+modern toe+hindlimb analysis. A.) PC1-PC2 scatterplot B.) PC2-PC3 scatterplot C.) PC2-PC4 scatterplot D.) PC3-PC4 scatterplot

The results of the jacknifed rarefaction tests show that those taxa that are generally inferred as arboreal (e.g., enantiornithines and perching birds) tend to have relatively low means (Fig. 15). The variance of each life-habit group, however, overlaps in almost all cases. In the toe length analysis, enantiornithines do not overlap with semipalmate birds, foot-propelled divers, primitive birds, and long-tailed birds+microraptorines (Fig. 15A). In the hindlimb analysis, enantiornithines overlap with every other group (Fig. 15B). In the toe+hindlimb analysis, enantiornithines do not overlap with semipalmate birds and primitive birds (Fig. 15C). General trends in variance between life-habit groups remain constant between the modern-only and the modern and fossil analyses; therefore, the inclusion of fossil groups does not dramatically change or destabilize the pattern shown using modern taxa.

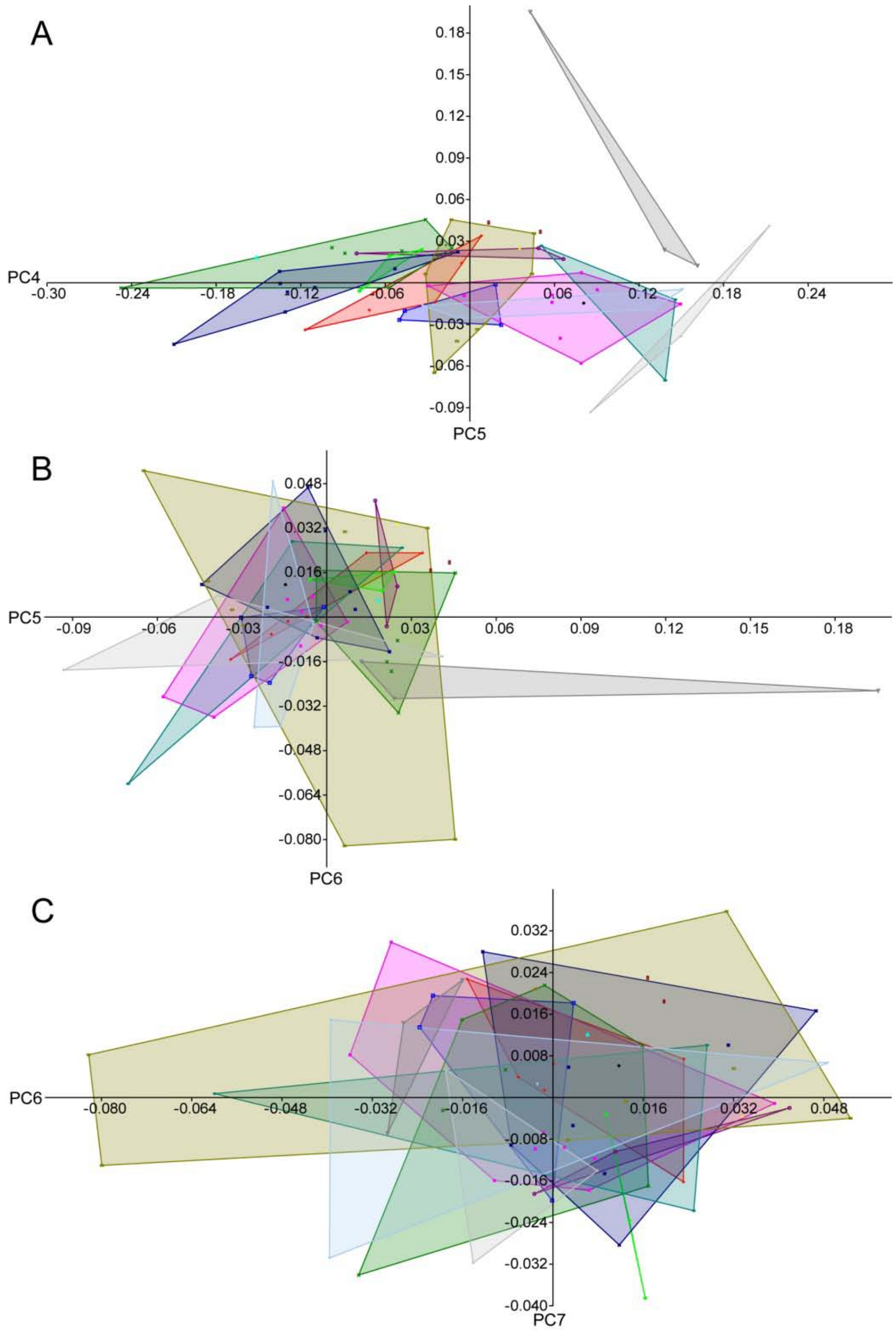

Fig. 14: Scatterplots of the fossil+modern toe+hindlimb analysis, continued. A.) PC4-PC5 scatterplot B.) PC5-PC6 scatterplot C.) PC6-PC7 scatterplot.

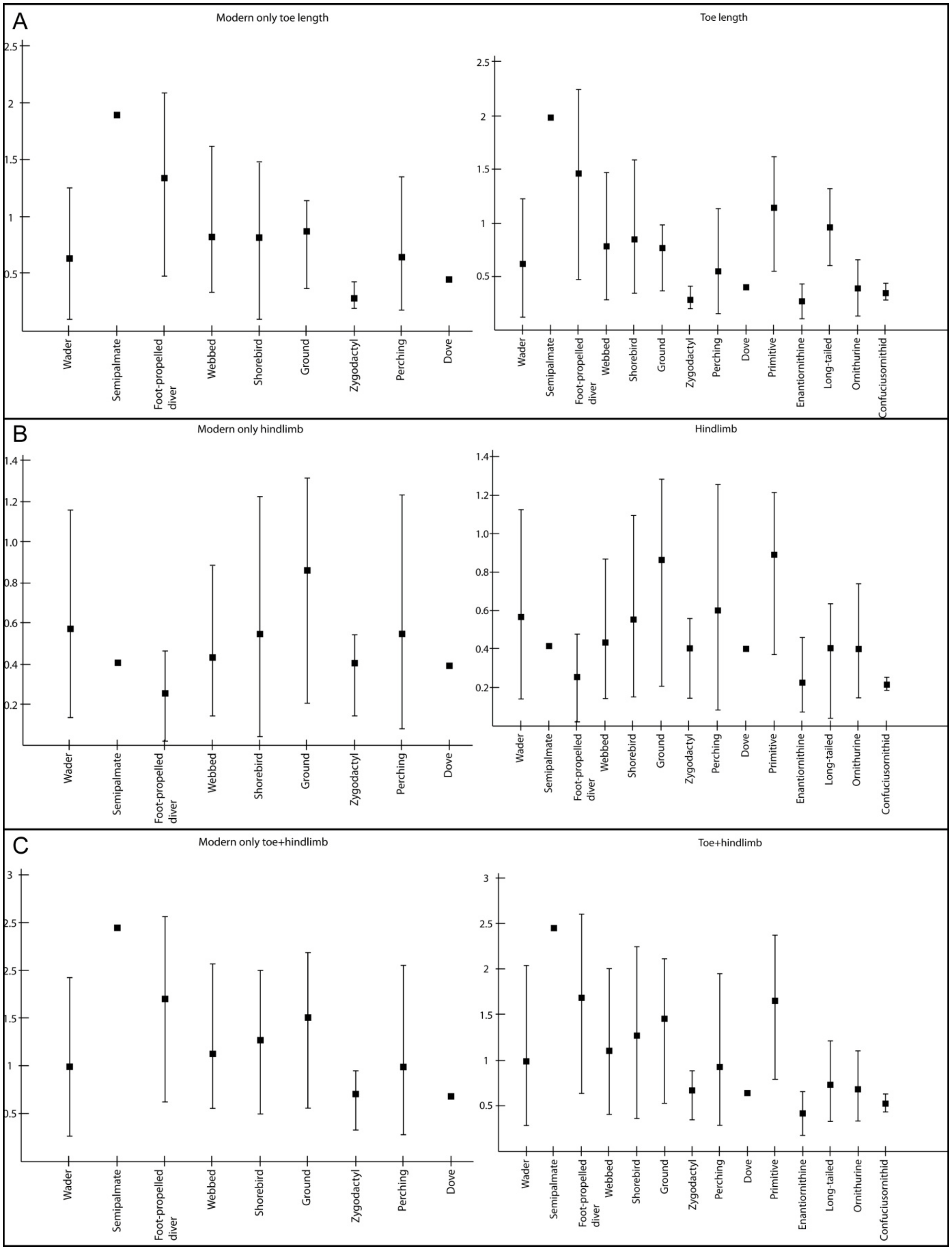

Fig. 15: Box charts with standard deviation bars representing the results of the rarefaction analysis performed on the modern-only and modern+fossil dataset. A.) Toe length B.) Hindlimb C.) Toe+hindlimb.

DISCUSSION

The use of PCA to create a hypothetical morphospace using modern and fossil birds has been previously used in avian paleontology (e.g., Livezey, 1989; Bell and Chiappe, 2011; Wang et al., 2011; Benson and Choiniere, 2013). Each study, however, looked at varying parts of the bird anatomy for their analysis. Our study focuses only on the bird hindlimb, whereas Livezey (1989) examined many different measurements beyond the limbs, Bell and Chiappe (2011) examined both fore- and hindlimbs, Wang et al. (2011) focused on the forelimb and primary feather length, and Benson and Choiniere (2013) examined the three forelimb and three hindlimb elements but did not examine the feet. Neither Livezey (1989) nor Bell and Chiappe (2011) separated out their analysis into separate body part analyses (e.g., Bell and Chiappe 2011, generated a combined fore- and hindlimb analysis but did not perform a forelimb analysis and a hindlimb analysis); rather they combined everything into one single analysis and interpreted that dataset. Benson and Choiniere (2013) did perform two separate analyses of fore- and hindlimb data, but then did not combine them. Although Benson and Choiniere (2013) presented a ternary diagram illustrating a comparison of modern bird hindlimbs to fossil bird and theropod dinosaur hindlimbs, the modern bird dataset is not included in either the PCA dataset or the resulting scatterplot. In Bell and Chiappe (2011) a modern-only dataset was developed, and then fossil taxa were superimposed onto that dataset. Wang et al. (2011) used a similar method Bell and Chiappe (2011) in their analyses for the forelimbs of modern and fossil birds.

The modern-only analysis

The analysis of the toe lengths of modern birds indicates that the length of toe I is an important factor in avian morphology. PC1, despite the log adjustment, likely represents body size, which, due to the normalization of the log-adjusted data, resulted in the data being more centralized in the scatterplot (this is true for the PC1 of all analyses), and accounts for 72% of the variability in the data. PC2—the toe I-dominated principal component—accounts for 27% of the variability in the data. In other published studies, the percent variation of PC2 is < 10% (e.g., Bell and Chiappe, 2011: 5%). This result suggests that toe I potentially correlates with life habit. An examination of the PC2-PC3 scatterplot does seem to support this interpretation (see Fig. 3B). Birds with webbed feet (webbed-footed birds and foot-propelled divers), clustered on the right (positive) side of the scatterplot, indicate that their toe I length had less influence on the overall foot morphology relative to the length of toes II–IV. Several shorebirds are also on the more positive side of the scatterplot, and many have elevated and reduced or absent hallux toes. Some shorebirds and wading birds occupy a more centralized area on the PC2 axis, along with ground birds (see Fig. 3B). This suggests that the influence of toe I and toes II–IV are approximately equal. The position of Zygodactyl birds is more negative, and perching birds even more so, indicating that toe I strongly influences foot morphology more than the other toes. PC3 has a somewhat similar pattern—toe IV is the dominant influence, and so those birds that have a long toe IV relative to toes I–III are more negative, whereas those with a relatively shorter toe IV are more positive (Fig. 3B).

The clusters seen in the toe length PC2-PC3 scatterplot clearly reflect the overall foot morphology of the bird (Fig. 3B). Interestingly, webbed-footed birds and foot-propelled divers tend to form their own cluster in the PC2-PC3 scatterplot, whereas webbed-footed birds and shorebirds showed a great deal of overlap in the PC1-PC2 scatterplot (Fig. 3A). This change is likely due to the removal of the normalized body size component (PC1) and the addition of the toe IV-dominated component (PC3). Waders, ground birds, and shorebirds all form a cluster as well, reflecting a more ground-based life habit. Perching birds, which are primarily arboreal, and zygodactyl birds form their own clusters as well (Fig. 3A). Interestingly, those perching birds with the most positive positions on the PC2 axis (*Corvus brachyrhynchos* and *C. corvax*) spend time on the ground foraging.

The hindlimb analysis shows surprisingly little variation in modern birds (Fig. 5). In the PC2-PC3 scatterplot there is some trend towards isolation of the webbed-footed birds and foot-propelled divers (Fig. 5B). Both of these bird types use their hindlimbs primarily for swimming. The two webbed-footed birds that overlap with the shorebird polygon are species of gulls, which are in the same order (Charadriiformes). The general lack of clustering of the majority of bird groups, however, indicates that the hindlimb elements for most birds do not vary much with respect to each other.

In the combined hindlimb and toe length analysis, the clustering in PC1-PC2 is generally similar to the clustering seen in the toe length PC1-PC2 analysis (Fig. 7A). This indicates that toe I dominates any other source of variation, especially that of the hindlimb. The PC2-PC3 scatterplot also reflects this dominant toe I component, as well as a difference between birds with hindlimb-dominated variation and foot-dominated variation (PC3) (Fig. 7B). For example, foot-propelled divers plot most negative on the PC3 axis, indicating the foot is the most important component because the toes are relatively long whereas the hindlimb elements are relatively short. In later scatterplots (Fig. 7C–F) the clustering breaks down, indicating that the amount that each component contributes to the overall variation is miniscule (<<1%) and are not suggestive of general morphologic or evolutionary trends.

Modern + fossil analyses

The toe length analysis combining fossil and modern data shows some interesting trends in the fossil data. *Archaeopteryx* plots very near the intersection of the PC1 and PC2 axes (Fig. 9A). Long-tailed birds+microraptorines as well as primitive ornithurines are also clustered there. Confuciusornithids are also close to the center of the morphospace. This suggests that the center of the morphospace on the PC1-PC2 scatterplot represents primitive morphology characterized by a toe I length that is approximately equal in its influence on the foot morphology to the other toes. This mid PC space of morphologic influence is likey a primitive condition. The hallux toe in *Confuciusornis*, long-tailed birds+microraptorines, and primitive ornithurine birds is not exceptionally long as in passeriform birds, waders, or zygodactyl birds, nor is it strongly reduced like that of many shorebirds, webbed-footed birds, and some ground birds (Fig. 9A). In the modern+fossil analysis, waders plot nearer to arboreal morphotypes (e.g., perching birds) based on the length of toe I, regardless of the hindlimb length. Enantiornithines also form a tight cluster, and do not overlap with any other morphogroup on the PC1-PC2 scatterplot.

Clustering in the PC1-PC2 scatterplot beings to break down on the PC2-PC3 scatterplot, where enantiornithines and waders overlap, indicating that enantiornithines have a stronger toe I influence than other primitive birds, including primitive ornithurines (Fig. 9B). The reason for the overlap in enantiornithines and waders is likely due to PC3, which is the relative relationship of toe II to toes III–IV (toe I has very weak loading and, therefore, little influence). The more negative the datapoint, the stronger the influence of toe II. There are two outliers where toe II has a very strong influence, *Jinzhouornis* and, to a lesser extent, *Sinornithosaurus*. There is also an outlier for a weak toe II influence, *Microraptor zhaoianus*. Enantiornithines have a relatively large spread along the PC3 axis, larger than any modern bird morphogroup (Fig. 9B). *Jinzhouornis* does have a long and robust toe II (Fig. 16A), and the toe of *Microraptor zhaoianus* is poorly preserved, although the second digit does appear to be much shorter than the other two digits (Fig. 16B).

Fig. 16: Photographs of *Jinzhouornis* and *Microraptor zhouianus* feet showing size and preservation of the toes. A.) *Jinzhouornis*. Note the relative robustness of toe II, and the relative fragility of toe IV. B.) *Microraptor zhouianus*. Toe II, with its large pedal claw, is overlying toes III and IV. Preservational quality is relatively poor.

The PC1-PC2 scatterplot for the hindlimb analysis shows minimal clustering. Overall, Mesozoic birds appear to cluster on the positive side of the PC2 axis, with the exceptions of enantiornithines and primitive ornithurines (Fig. 11A). This indicates that the femur of primitive birds had more of an influence on the hindlimb than did the tarsometatarsus, contrary to what is seen in most extant birds. Note that, enantiornithines overlap with modern birds on the PC2 axis, however, enantiornithines mostly form their own cluster on the PC1-PC2 scatterplot. Since the enantiornithines overlap with modern birds on the PC2 axis, the PC2-PC3 scatterplot has an almost complete breakdown of clustering (Fig. 11B). Note that most primitive birds still cluster on the positive side of the PC2 axis, away from most modern bird groups. They have a large spread along the PC3 axis, however. Enantiornithines have an even larger spread (~ -0.043–~0.05), which is comparable to almost all of the modern bird radiation, with the exception of the foot-propelled divers and some of the webbed-footed birds. The primitive ornithurine birds mainly overlap with webbed-footed birds on the PC2-PC3 scatterplot.

Similar to the modern-only combined toe length and hindlimb analysis, in the modern and fossil combined analysis toe I dominates the influence for PC2 (Fig. 12B). *Archaeopteryx* plots near the center of the morphospace, along with long-tailed birds+microraptorines, confuciusornithids, and primitive ornithurines (Fig. 13A). Enantiornithines are clustered alone in the PC1-PC2 analysis. In the combined analysis there is less overlap between enantiornithines and waders in the PC2-PC3 scatterplot (Fig. 13B), however, the overlap still occurs, likely due to the similar influence of toe I compared to toes II–IV. Primitive ornithurines plot strongly negative along the PC3 axis, indicating that the toe lengths more strongly influenced their morphology than the hindlimb. This places them closer to webbed-footed birds and foot-propelled divers, whose hindlimb has a much stronger influence than the toe lengths (Fig. 13B).

Microraptor zhaoianus is the most positive fossil outlier on the positive side of the PC3 axis, indicating that the hindlimb elements had a much stronger influence on the overall hindlimb morphology.

Long-tailed birds+microraptorines and primitive birds both have very strongly restricted wedges of morphospace in the PC2-PC3 scatterplot of the combined analysis. Primitive ornithurines and confuciusornithids are also more restricted in their morphospace than most other groups of birds (Fig. 13B). Primitive birds, however, cover a wider amount of morphospace along the PC3 axis. This indicates that the influence of the toe lengths and hindlimb with respect to each other was variable within these groups, whereas the long-tailed birds+microraptorines, primitive ornithurines, and confuciusornithids were more strongly restricted with respect to the influence of toe length and hindlimb.

Rarefaction analysis

The results of the rarefaction analyses (Fig. 15) indicate that there is significant overlap between most major life-habit groups, a result reflected in the NPMANOVA results (Table 2–6). When the toe length rarefaction analysis is examined, those birds considered arboreal tend to have means that are lower on average (generally <0.8). Interestingly, primitive birds (e.g., *Sapeornis*) and long-tailed birds (e.g., *Jeholornis*), both of which are likely arboreal based on claw morphology (Fig. 17), have very high means in the rarefaction analysis. The combined toe length and hindlimb analysis closely reflects the toe length analysis (Fig. 14A, C), which is also reflected in the scatterplots and loadings from both PCAs.

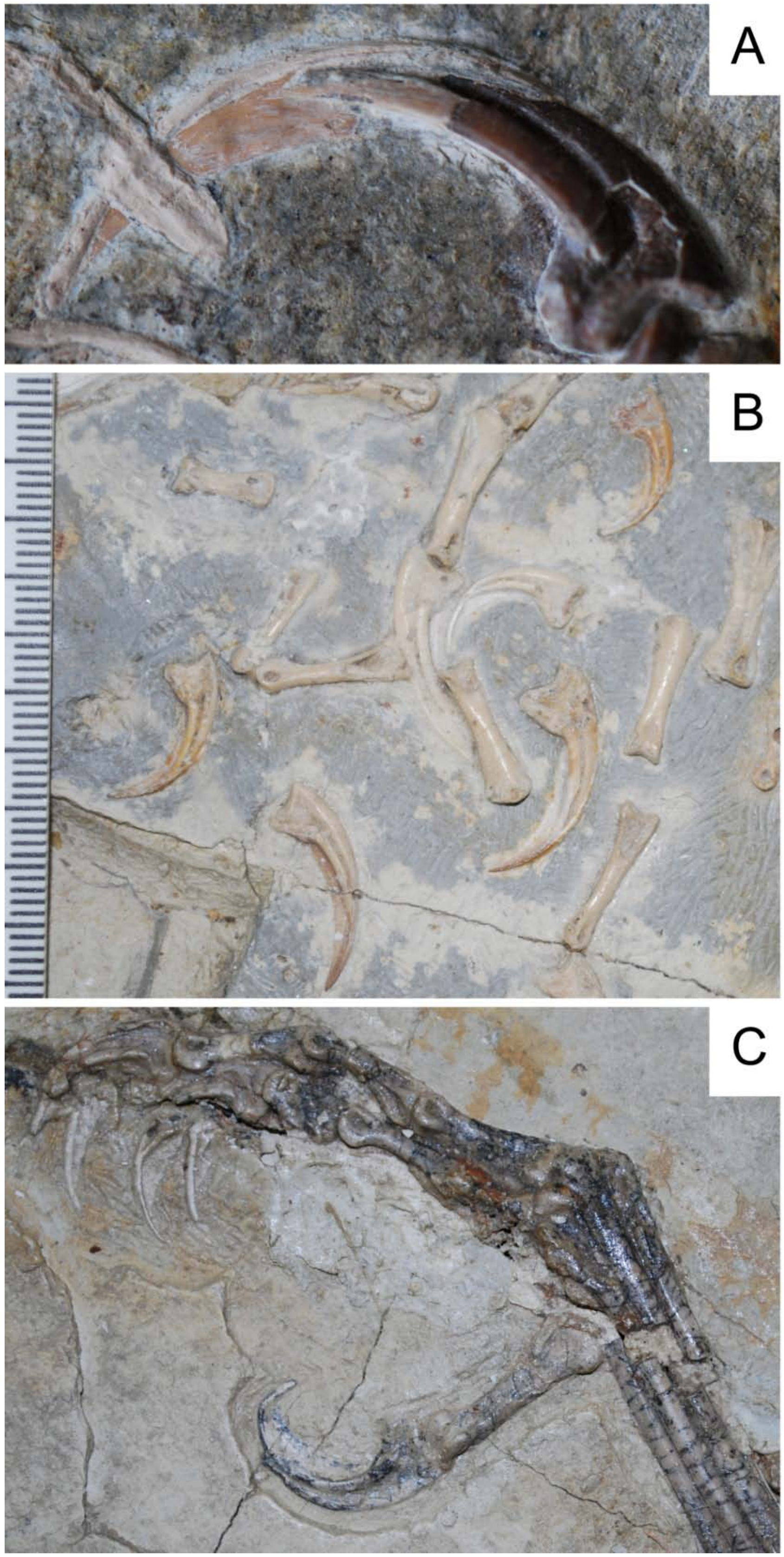
A
B
C

Fig 17: (Opposite page) Claws of aboreal primitive birds. A.) *Confuciusornis.* Pedal claw II. Bony claw core is dark brown, keratinous sheath is white. The keratinous sheath of II is partially overlapped by the keratinous sheath of III. B.) *Jeholornis*. The feet of this specimen (IVPP V 13294) are completely disarticulated, so there is no way to link claw to toe. C.) *Sapeornis*.

The hindlimb rarefaction analysis shows a different pattern than the toe length and combined rarefaction analyses. The position of the modern bird datapoints do not change, which is consistent with the other analyses, however, there seems to be no correlation between life-habit and mean (Fig. 14B). With the exception of primitive birds, Mesozoic taxa have relatively low means (0.4 or less), however, semipalmate, webbed-footed, and zygodactyl birds as well as doves also have means that are ~0.4. The PC1-PC2 scatterplot indicates separation between primitive birds and other groups with some slight overlap between enantiornithines and webbed-footed birds, and primitive ornithurine birds with other life-habit groups. This pattern, however, is not reflected in either the NPMANOVA (Table 2–6) or the rarefaction analyses (Fig. 14) because: 1) PC1 accounts for >90% of the variation and is normalized body size; and 2) the NPMANOVA and rarefaction analyses include all three principal components, and PC3 does not show strong clustering (e.g., Fig. 11B).

Scatterplot discussion

In all three combined (fossil and modern taxa) analyses, enantiornithines formed their own cluster in the PC1-PC2 scatterplots (Figs. 9A, 11A, 13A), and only in the hindlimb analysis (Figs. 11A) did it overlap with any modern taxa—a single webbed-footed bird, *Sterna paradisea*. No other fossil group is so strongly isolated in each analysis. Furthermore, in the hindlimb PC2-PC3 scatterplot, enantiornithines cover a very large morphospace, especially along the PC3 axis

(Figs. 11B). The variables influencing PC3 are the tibiotarsus (negative) and the femur+tarsometatarsus (positive) (Fig. 10C). This wide area of morphospace indicates that enantiornithines had a variable tarsometatarsus to femur+tarsometatarsus influence. Although the PC2-PC3 scatterplot of the toe length analysis also shows a wider range of variation along the PC3 axis (Fig. 9B), enantiornithines still form a relatively discrete cluster, overlapping only with webbed-footed and zygodactyl birds. In the toe length PC3-PC4 analysis, enantiornithines cover the largest range of morphospace of any other group (Fig. 9C). In the PC2-PC4 scatterplot of the combined analysis, enantiornithines still form a very discrete cluster (Fig. 13C). The PC3-PC4 scatterplot of the combined analysis, enantiornithines overlap webbed-footed birds, waders, and shorebirds, and occupy the approximate center of the morphospace (Fig. 13D). Enantiornithines are, however, still a relatively small cluster. They have simultaneously a very constrained, yet highly variable hindlimb.

Enantiornithines are unique in the amount of their variation. This, perhaps, is not surprising, given that enantiornithines represent an entire subclass of birds (Walker, 1981). The fact that their foot morphology is so very constrained is surprising. This constraint to a relatively stable foot morphotype suggests that enantiornithines, in general, had similar life habits and similar foot functions (i.e., perching or trunk climbing as in modern passeriform birds). The amount of variation in the hindlimb is less easily explained, however, evidence suggests enantiornithine hindlimb and foot anatomy is different than that of ornithurine birds.

In most modern birds, the femur has a less significant influence in the hindlimb—which is not surprising as the femur is bound to the body wall by muscle and does not contribute much to the stride (Rubenson et al., 2007). In enantiornithines, the influence of the tarsometatarsus is similar to that seen in some passeriform, several webbed-footed, ground, and some wading birds

(Fig. 11). Advanced enantiornithines, at least, possess an antitrochanter—a poorly understood articular surface on the avian pelvis—where the neck of the femur (or *facies articularis antitrochanterica*) abuts the pelvis (Hertel and Campbell, 2007 and references therein). The avian antitrochanter is different in morphology and function than the dinosaurian antitrochanter. The presence of an antitrochanter in fossil birds indicates that the femur was bound to the body wall by muscle, as in modern birds, and that some enantiornithines had a femur with limited function—i.e., knee-driven locomotion, as in modern birds. The amount of variance about the PC3 axis in the PC2-PC3 scatterplot (Fig. 11B) is approximately the same amount of variation seen in the entirety of modern (ornithurine) birds—webbed-footed birds and foot-propelled divers do have significantly more negative values than enantiornithines, but they are the only strong outliers. Enantiornithine hindlimb morphology, therefore, was approximately as varied as the hindlimb morphology of modern birds.

Enantiornithine foot morphology, on the other hand, is strongly constrained, and does not cover a large amount of morphospace in either the PC1-PC2 or the PC2-PC3 scatterplots (Fig. 9). Enantiornithines are largely constrained to terrestrial habitats (especially the arboreal realm), which may explain why they, in general, have a more confined morphospace. The PC1-PC2 scatterplot (Fig. 9A) places them in a relatively unoccupied morphospace, near Sapeornithids, Confucuisornithids, and other primitive birds. Enantiornithines do not, however, overlap any of these groups, likely due to the unusual relative proportions of the toes. In enantiornithines, the toe II is generally larger and more robust, whereas the toe IV is slender and reduced (Fig 18, see Chiappe and Walker, 2002 for examples). The PC2-PC3 scatterplot (Fig. 9B) places them near perching birds, and overlapping with zygodactyl birds and wading birds (e.g., herons) due to the presence of a relatively robust hallux, which all three groups possess.

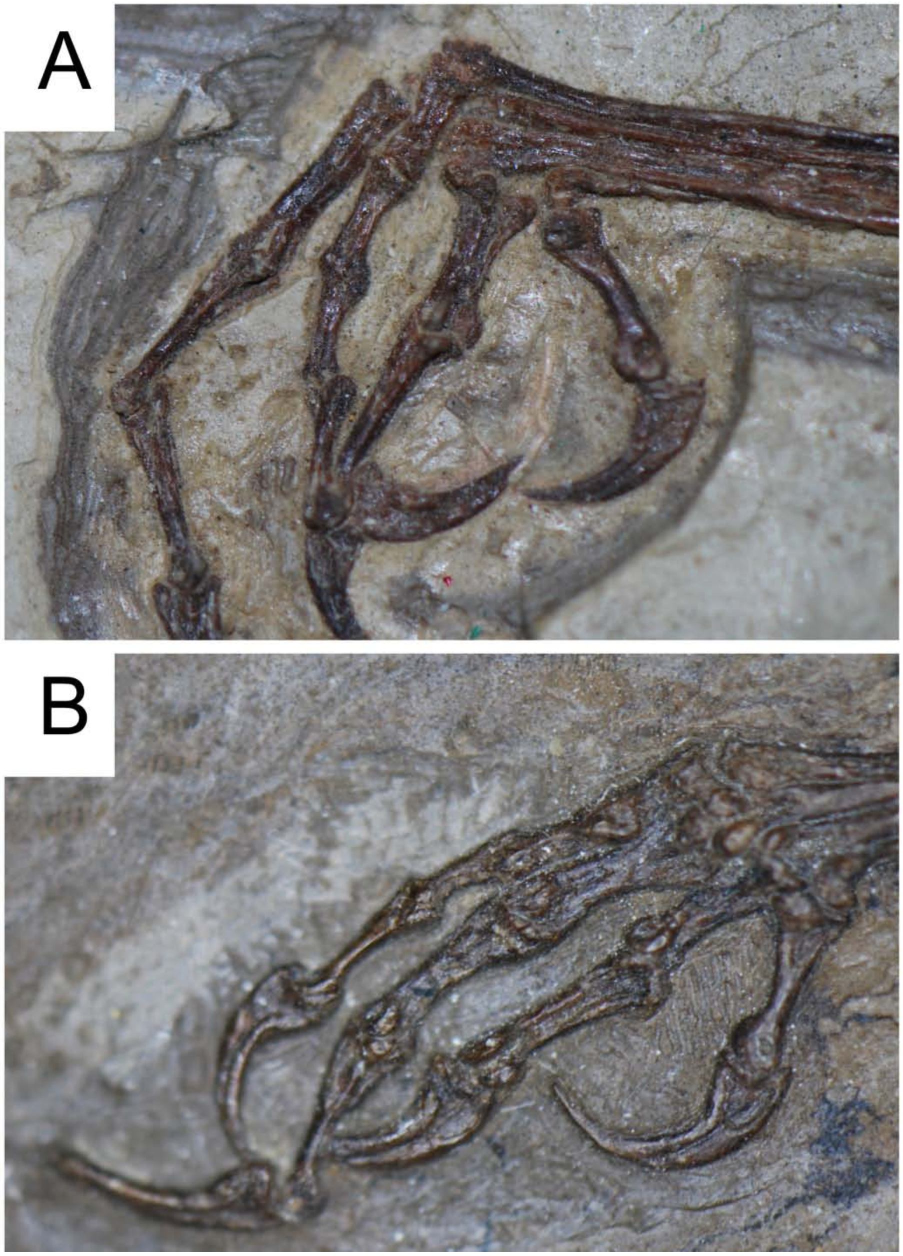

Fig. 18: Photos of some enantiornithine feet, showing slender toe IV. A.) PMOL AB00041B, an undescribed enantiornithine from the Yixian Formation, western Liaoning, China. B.) *Dapingfengornis*, PMOL AB00017.

In general, the loadings of the modern-only and modern+fossil hindlimb analyses do not vary greatly (Figs. 3, 5, 7, 9, 11, 13 and 14), suggesting that hindlimb proportions have remained relatively stable since the Early Cretaceous. The PC1-PC2 and PC2-PC3 scatterplots of the modern+fossil hindlimb analysis (Fig. 13A, B) show a significant isolation of primitive fossil birds (and microraptorines) from modern birds, primitive ornithurines (with a few exceptions), and enantiornithines. This may be a result of the different posture in early birds—early birds did not have an antitrochanter and, therefore, may have used more hip-driven locomotion than knee-driven locomotion (Hertel and Campbell, 2007). *Archaeopteryx* has been reconstructed with a fully upright posture, with the femur nearly vertical (Martin et al., 1998); the femur was clearly not bound to the body wall with muscle. Some primitive ornithurines, such as *Gansus* and *Hongshanornis*, plot well within modern ornithurines in the PC1-PC2 scatterplot (Fig. 11A), whereas *Yanornis* and *Yixianornis* plot with the more primitive birds. *Gansus* and *Hongshanornis* had a more advanced posture, whereas *Yixianornis* and *Yanornis* retained a more primitive posture with a femur that may have contributed more to locomotion than the femur of modern birds.

Although the PC1-PC2 and PC2-PC3 scatterplots of toe length and the hindlimb analyses are unique (Figs. 9, 11, respectively), when combined into a toe+hindlimb analysis the PC1-PC2 scatterplot is very similar to the PC1-PC2 scatterplot of the toe length analysis, except that the negative and positive values are flipped (Fig. 13). The loadings are also similar in that toe I has the strongest overall loading (Figs. 8A, 12A). This analysis suggests that the avian hindlimb is relatively stable in its proportions when compared to the foot. This is also reflected in the scatterplot of the hindlimb analyses (Figs. 5, 11), which generally shows greater overlap and less significant clustering than the toe length and toe+hindlimb analyses (Figs. 8, 12). This is also reflected in the NPMANOVA results (Table 2–6).

CONCLUSIONS

The foot and hindlimb of birds has been considered highly variable in morphology, and the birds of the Lower Cretaceous Jehol Group show a wide range of diversity. The use of PCA helps to illustrate variation between avian morphotypes. The results of the PCA confirm that primitive birds, enantiornithines, and microraptorines have a different hindlimb posture than primitive ornithurine and modern birds. Modern birds, primitive ornithurines, and some more advanced enantiornithines have an antitrochanter that is indicative of a femur bound to the body wall with muscle, which results in knee-driven locomotion. More primitive birds, early enantiornithines (e.g., those found in the Jehol Group), and dromaeosaurs lack an antitrochanter and, therefore, probably had a femur that was free to contribute to hip-driven locomotion. Enantiornithines show relatively restricted foot morphology, however, the hindlimb morphology is relatively variable.

One of the main tenants in ornithology is that the hindlimb is one of two relatively variable parts of a bird (the other being the bill), due to the constraints that flight places on a body form. The PCA results in this study, however, suggests that the foot itself is more evolutionarily plastic than the hindlimb. The hindlimb of birds is still variable, and the overall lengths of its three elements do vary with respect to each other, however, the variation is not as significant as the variation of the toe lengths.

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THE PLUMAGE AND SOFT TISSUES OF *CONFUCIUSORNIS*

ABSTRACT

Previous interpretations of the plumage of *Confuciusornis* suggested that the primary feather rachises were weak and could not support flight, and that the long primary feathers relative to the ulna indicated a narrow, long wing similar to that of swifts. Data presented herein suggest that the rachises of the primary feathers of *Confuciusornis* were robust and comparable to modern birds, and that its wing shape was much wider and broader. The 10th (outermost) primary feather is very short, less than half the length of the 9th primary. The 7th and 8th primaries are the longest. The secondaries are also comparatively long, contrary to that seen in modern fast-flying birds, and resulted in a broader wing. Use of laser fluorescence highlights soft tissue, including scales and skin and muscle complexes, allows for a complete soft-tissue reconstruction of *Confuciusornis*, and a complete and accurate description and interpretation of its enigmatic paired tail feathers. *Confuciusornis* had reticulate scales on the feet and large, expanded phalangeal pads, similar to the morphology in modern perching birds. The proximal tibiotarsal muscle complex (*m. gastrocnemius*) is relatively small, which is another indicator of arboreality. The propatagium of birds is the primary lift-generating feature between the wrist and body wall, and it is robust in *Confuciusornis*. The sternal keel may also extend further cranially than previously interpreted. These features suggest that *Confuciusornis* was a powered flyer. The paired tail feathers of *Confuciusornis* and other primitive birds were rachis dominated, and may represent a primitive type of tail feather.

INTRODUCTION

Confuciusornis sanctus was described originally by Hou et al. (1995) from a partial skeleton consisting of a complete crushed skull, elements of the axial skeleton, and a mix complete and partial limbs. The initial argument with regards to *Confuciusornis* was mainly over the preservation of the skull and whether it was preserved in a dorsal or lateral view, and in early specimens the skull was difficult to visualize (Martin et al., 1998). Evidence of feathers was also present on the slab (Chiappe et al., 1999). Initially described as Late Jurassic in age (Hou et al., 1995; Chiappe et al., 1999), recent studies indicate that *Confuciusornis* is Early Cretaceous (Barremian) (Chang et al., 2009). *Confuciusornis* remains, however, the most primitive beaked bird based on its morphology and phylogenetic placement (Marugán-Lobón et al., 2011 and references therein).

Confuciusornis has several unique osteological characteristics among both ancient and modern birds (Chiappe et al., 1999). It possesses an unusually large and robust deltopectoral crest, often with a clearly defined foramen. Toe II is large and robust, whereas toes III and IV are smaller and slimmer. The postorbital is large and robust and the skull is clearly diapsid (Hou et al., 1999). When the horny beak is preserved, it is upturned—a unique feature amongst Mesozoic birds (Hou et al., 1999).

Soft tissues, other than feathers and the keratinized sheath of the beak (Hou et al., 1999), have not been previously reported for *Confuciusornis*. The pattern of scaling on the foot (e.g., scutilate, scutilate-reticulate, etc.) is unknown. Similarly, the extent of the pre- and postpatagium is also unknown in *Confuciusornis*.

There are now thousands of *Confuciusornis* specimens in repositories around the world, mostly in China. Some of these specimens display exceptionally preserved plumages. To date, however, there has been no detailed description of that plumage. Many studies discuss the elongate tail plumes found on some specimens, their morphology, and whether or not they represent sexual dimorphism (e.g., Martin et al., 1998; Peters and Peters, 2009; O'Connor et al., 2012). Nudds and Dyke (2010) examined the primary feathers of *Confuciusornis* in a study on the rachises and the robustness of the feathers and flight ability. The primary feather lengths of *Confuciusornis* are exceptionally long, with a primary feather:total-arm-length ratio that compares favorably to modern fast-flapping birds (Wang et al., 2011). These studies, however, have focused solely on the primaries of *Confuicuisornis* and not the plumage as a whole. The preservational mode of the feathers of *Confuciusornis* is also poorly understood. The purpose of this study is to reconstruct the plumage and soft tissue of *Confuciusornis* from exceptionally preserved specimens housed in institutions in China.

Christiansen and Bonde (2004) examined in detail the body plumage of *Archaeopteryx* (Berlin specimen), which suggests that an extensive study of fossilized plumage is possible on any specimens with exceptional preservation. Longrich (2007) redescribed the hind limb plumage of *Archaeopteryx* from the counterslab of the Berlin specimen, and also performed a complete plumage reconstruction that included flight ability. The feathers of most *Archaeopteryx* specimens are preserved as impressions, left after the original soft tissue decayed (Christiansen and Bonde, 2004). The isolated feather attributed to *Archaeopteryx*, however, is not preserved as an impression, and this feather has been the recent focus of studies regarding the coloration of *Archaeopteryx* (Carney et al., 2012; Manning et al., 2013).

The feathers of a bird wing consist of three major and a varying number of minor types of feathers (Fig. 1). The three major types of feathers are the primaries, secondaries and, when present, the tertials. Also present on the wing are greater primary coverts and greater secondary coverts; lesser primary and secondary coverts may also be present. Many birds possess an alula, a bastard wing that aids in maneuvering (Proctor and Lynch, 1993).

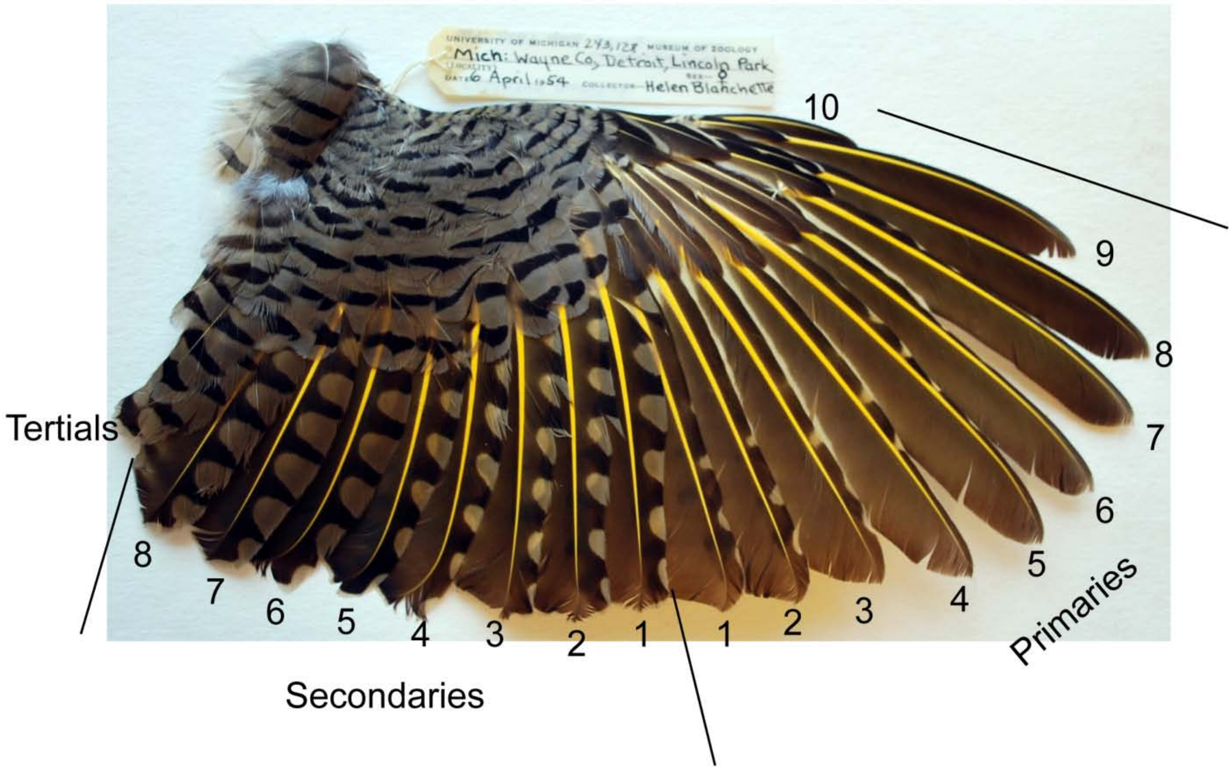

Fig. 1: Photograph depicting the different types of feathers on a bird wing. The feathers that insert on the hand are the primary feathers, the feathers that insert on the ulna are the secondary feathers. These feathers are covered by the greater primary and secondary covert feathers.

Many studies discuss the elongate tail retricies (or plumes) found only on some specimens of *Confuciusornis*. Specimens with and without elongate tail feathers have been found on the same rock slab. Hypotheses have been proposed for these plumes—the most common being sexual dimorphism (Martin et al., 1998; Hou et al., 1999; contra to Chiappe et al., 1999, 2008, 2010; Peters and Peters, 2009, 201), which are based on body size, not tail plumes. These studies, however, do not discuss the morphology of the tail feathers. Recent studies have attempted to discern the accurate morphology of the *Confuciusornis* tail feathers. Originally described as featureless and ribbonlike (Chiappe et al., 1999), more recent studies suggest that these types of feathers are either rachis dominated (Chuong et al., 2003), or undifferentiated flattened sheets of keratin flanking a rachis (O'Connor et al., 2012, and references therein).

Confuciusornis tail feathers consist of a long portion, previously described as relatively featureless, and only the distal portion possesses barbs identical to those found on modern feathers (Chiappe et al., 1999). This feather morphology is unique with respect to all feathers due to its combination of a so-called featureless portion, with some portion of the feather still containing barbs. Extant birds with featureless, ribbonlike feathers (i.e., some Birds of Paradise [Paradisaeidae]) do not possess barbs on any portion of the feather (Fig. 2A). Several groups of extant birds have feathers with barbs restricted to the distal portion of the feather. For example, some members of the Motmotidae (Mot-mots) and Caprimulgidae (Nighthawks and Nightjars) do not have an enlarged rachis and, when the feather originally develops, the barbs are present along the entire shaft. These barbs have special, weakened bases so that they break off when the bird preens, leaving barbs present only in the distal area of the feather (Fig. 2B). Birds with rachis-dominated feathers have barbs present along the entirety of the feather length (e.g., Indian peafowl *Pavo*, Fig. 2C).

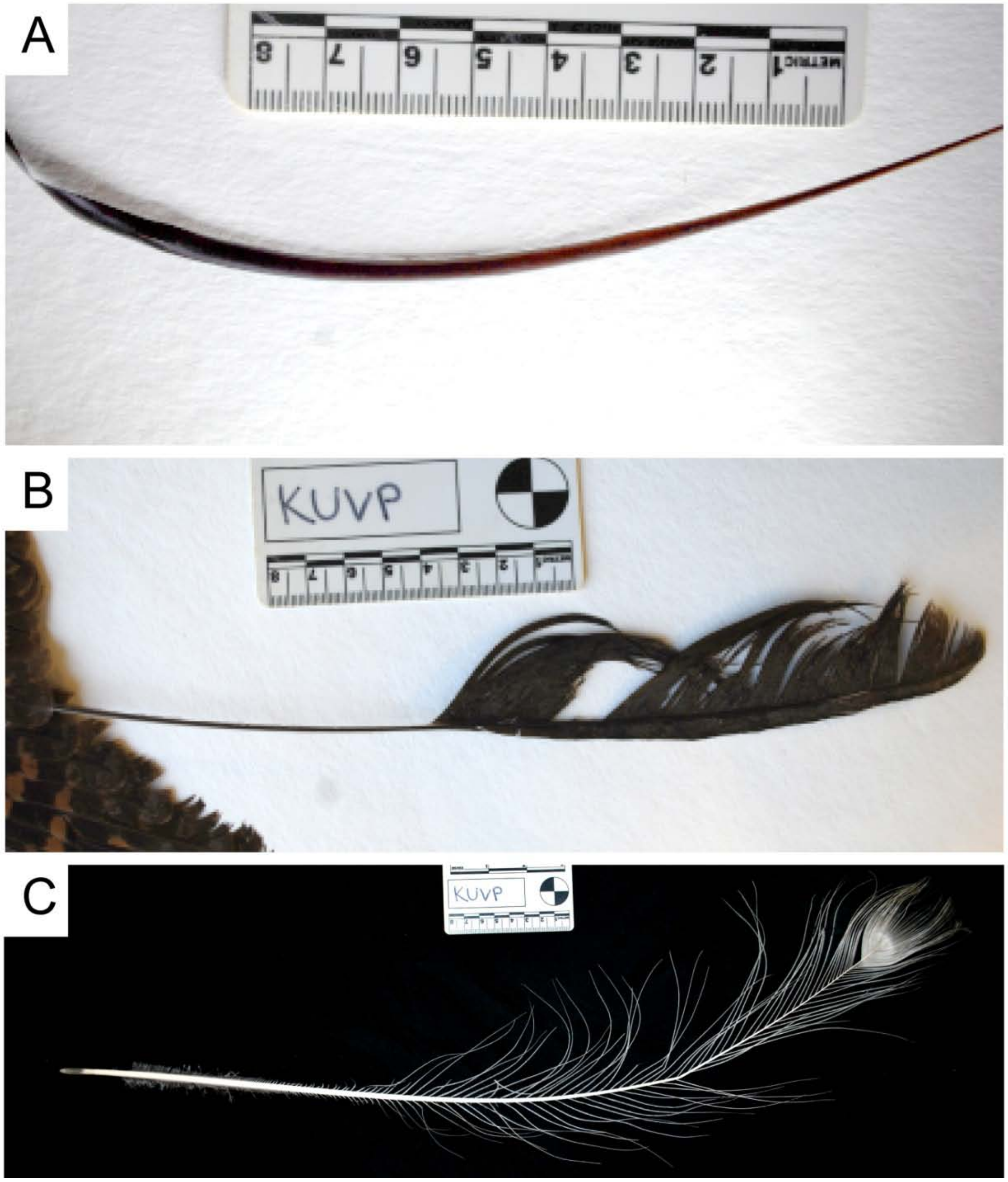

Fig. 2: Photographs of examples of modified feathers in modern birds. A.) Birds of paradise—note the flattened sheet of keratin without any barbs. B.) Standard-winged Nightjar. C.) Indian peafowl (white). Note the diminished barbs that are present on the proximal portion of the rachis.

The feather evolution model by Prum (1999) proposed that feathers began as simple, hollow, filamentous tubes. In this model, down is a primitive type of feather. Modern studies of feather regeneration, however, indicate it is a complex process (Lucas and Stettenheim, 1972; Maderson et al., 2009) and, therefore, the model of Prum (1999) may be oversimplified. Feathers comprise a central rachis, with branching barbs and barbules, which grow within a hollow tube called a feather sheath; this creates a tube-within-a-tube—not a simple hollow filament. As the feather grows, the barbs are curled inside the feather sheath. As the feather matures, the sheath splits and the barbs uncurl, resulting in a feather that appears featureless proximally due to the covering sheath, but with barbs uncurling at the distal end. Clues to feather evolution may be found in *Confuciusornis* tail feathers, depending on their structure and function.

GEOLOGIC SETTING AND TAPHONOMY

All specimens of *Confuciusornis* are from the Lower Cretaceous Jehol Group in Northeastern China (Fig. 3). The majority are found in the Yixian Formation, the lowermost formation in the Jehol Group, which is comprised primarily of volcanic breccia, tuffaceous sandstone and conglomerate, and shale (Jiang and Sha, 2006). The volcaniclastic sediments were deposited in a (or several) lake basin(s) that resulted from active tectonic processes in the area. Many of the volcaniclastic beds have been interpreted as debris and density flows or suspension loads and turbidity currents (Jiang et al., 2011). Unfortunately, provenience data is unknown for many specimens of *Confuciusornis*, including the ones used in this study.

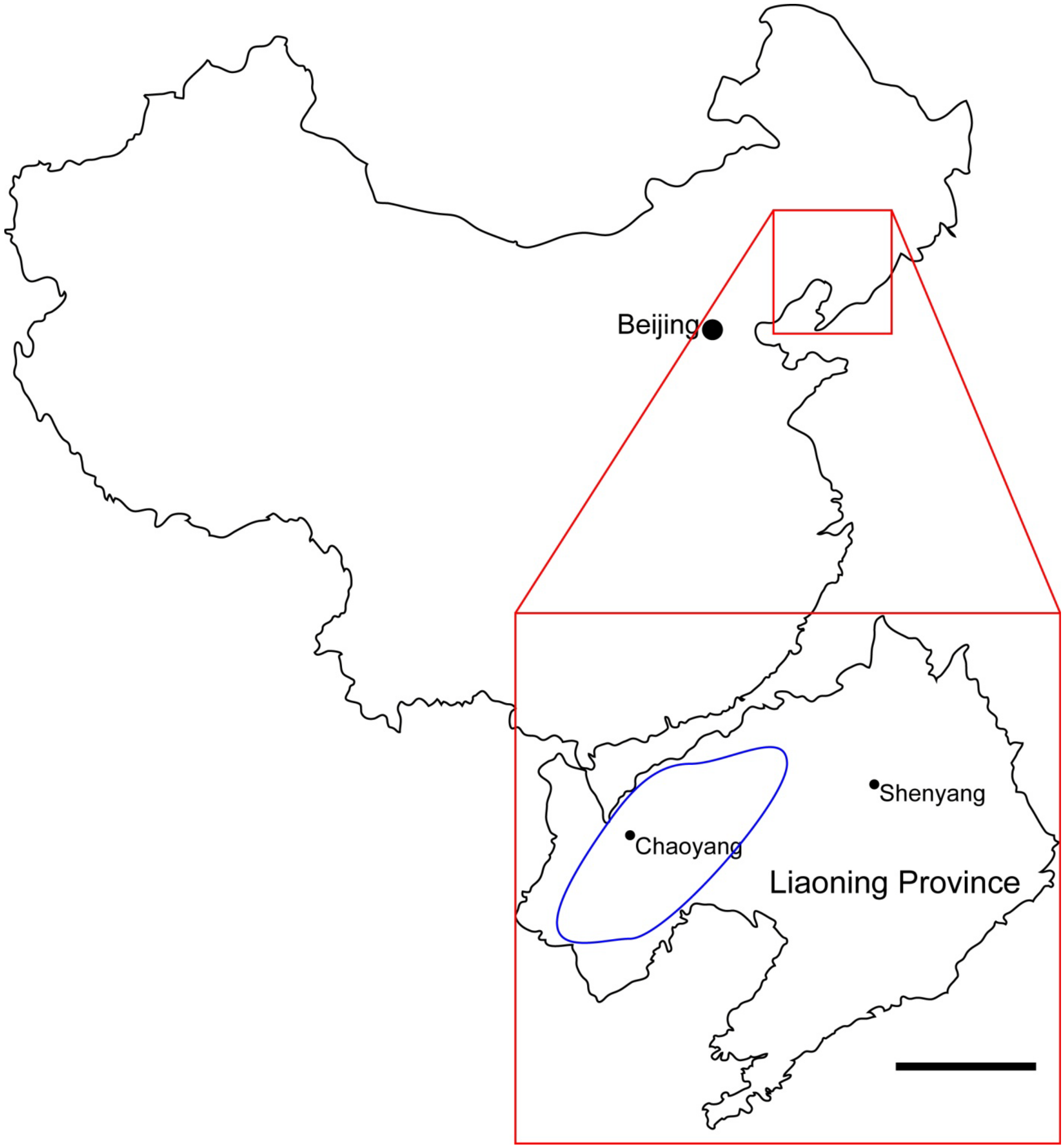

Figure 3: Map showing the general location of the Jehol Group in Northeastern China, western Liaoning province. Scale bar for Liaoning Province=155 km. Blue oval indicates the general area within which Jehol Group outcrops are located. For basin distribution and outcrop area see Jiang and Sha, 2006, Jiang et al., 2011, and Jiang et al., 2014.

The lacustrine beds of the Jehol Group are famous for their fossils, and multiple interpretations of the depositional environment have been made (Jiang et al., 2011 and references therein). The environment has been interpreted as warm and arid, warm and humid, or semi-arid, but was most likely a lush, gymnosperm-dominated environment with large, deep lakes (Burnham, 2008). There has been no firm consensus on the preservation style of the fossils, especially the soft tissues, however, a recent study has suggested that at least some portion of the soft tissues found in Jehol Group specimens are composed of carbon (Jiang et al., 2014). They state, however, that these tissues could not have undergone the carbonization method of fossilization, and instead suggested that these tissues were charred by pyroclastic flows. They also stated that there is no evidence for mineral replacement in the soft tissues. There are mass mortality events of *Confuciusornis* resulting in beds with more than a thousand individuals in a single layer, and the most parsimonious explanation for this is a sudden, rapid, and catastrophic eruption event. Early Cretaceous volcanism, therefore, played a crucial role in the preservation of the Jehol Biota (Jiang et al., 2014).

INSTITUTIONAL ABBREVIATIONS

IVPP = Institute of Vertebrate Paleontology and Paleoanthropology, Beijing, China. STM = Shandong Tianyu Museum, Pingyi, Shandong, China. PMOL = Paleontological Museum of Liaoning, Shenyang Normal University, Shenyang, Liaoning, China.

MATERIALS AND METHODS

Fossil material was examined mainly at the Institute for Vertebrate Paleontology and Paleoanthropology in Beijing, China. Other specimens at the Tianyu Museum in Pingyi, China, and the Paleontological Museum of Liaoning in Shenyang, China, were also used. Specimens used are IVPP V13156, IVPP V 13168, PMOL AB00150, STM13-33, STM13-39, STM13-124, and STM13-45. IVPP V 13156 and STM13-45 were primarily used for plumage reconstruction.

The specimens were photographed using a laser fluorescence methodology being developed by Tom Kay from the Burke Museum of History and Culture in Seattle, Washington, USA. A 447nm 300mw blue laser or a 447nm 400mW blue laser pointer, in conjunction with a 50^{o} diffraction diffuser, was used to illuminate the specimens (Fig. 4). When used in conjunction with either a yellow longpass filter (LP-470, Midwest Optical) or an orange longpass filter (YA2, Promaster), the fossil will fluoresce. The surrounding matrix will also glow, especially with the use of the orange longpass filter, which can backlight carbonized structures, such as feathers (Fig. 5). This type of laser fluorescence must be accomplished in a darkroom with little or no natural light input—a complete lack of natural light is preferred. The specimens were also photographed with UV light and a UV camera lens filter (Hoya NXT HMC UV) to compare the two types of fluorescence. Specimens were photographed using a Nikon D60 with an 18-55 mm standard lens and an 85 mm macro lens.

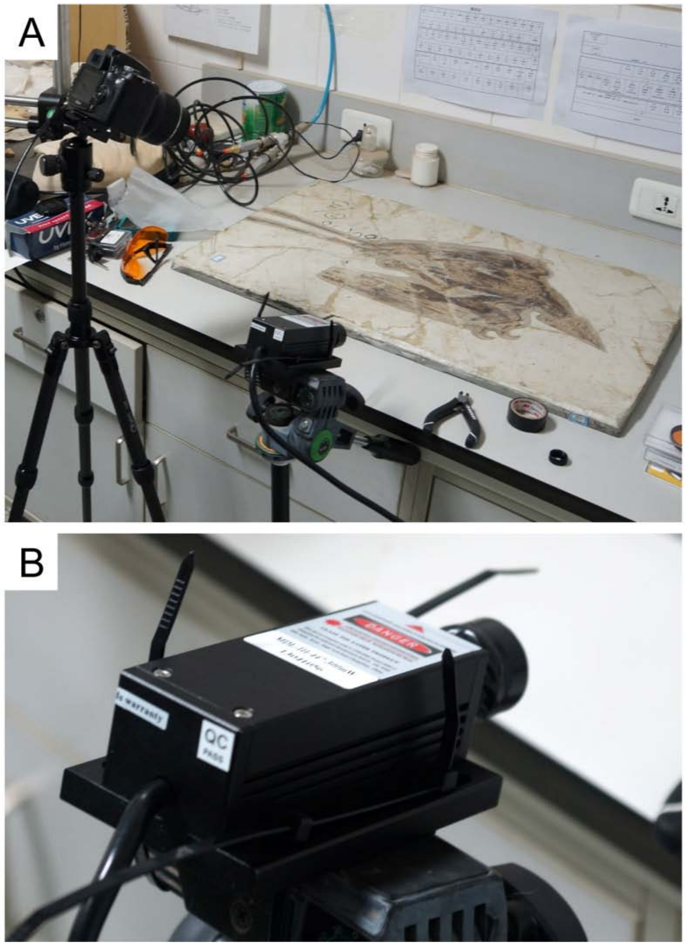

Fig. 4: Photograph of the laser photography setup. Note that this uses the lab laser—the laser pointer is a handheld unit where only the camera is affixed to a tripod. Photographs courtesy of Zhang Shaoguang. A.) Photograph of setup including camera and 447nm 300 mW lab laser. B.) Close up of 447nm 300 mW lab laser.

The primaries and folded secondaries on the wing of IVPP V13156 were measured to reconstruct the wing shape. This reconstruction was then compared to full spread-wing specimens of modern birds to elucidate the flight ability of *Confuciusornis*. Specimens at the Tianyu Museum were also examined and photographed to record the number of secondaries present, however, these specimens were not measured. Specimens from the Tianyu Museum and the Paleontological Museum of Liaoning were also used to reconstruct the insertion of primary and secondary feathers on the hand and ulna. Primaries are numbered from the inside (proximal) to the outside (distal), following standard ornithological practices (Proctor and Lynch, 1993). Only specimens from the IVPP were photographed using laser fluorescence due to the lack of dark room availability at other locations.

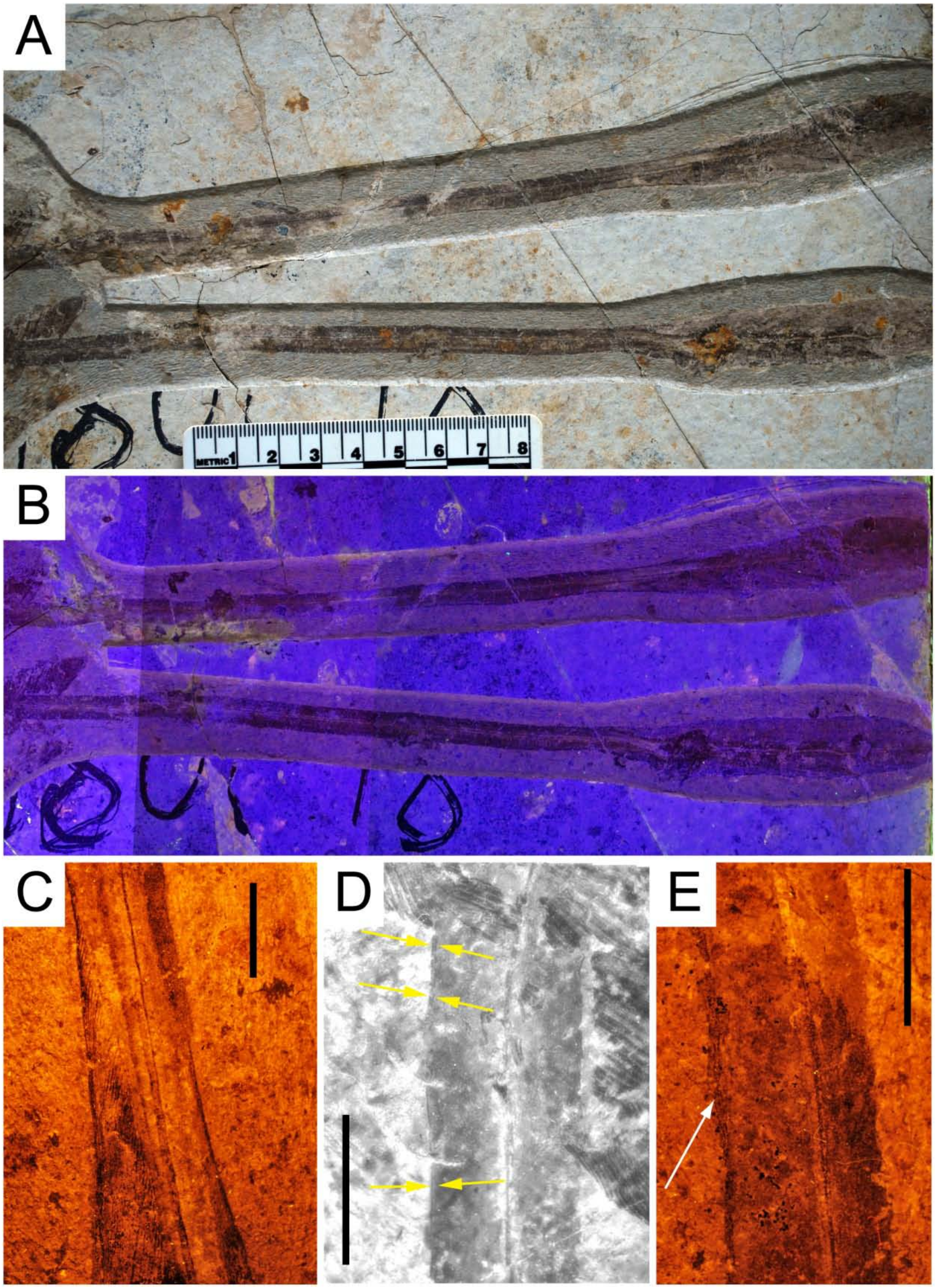

Fig. 5: (Opposite page) Photographs of the long, paired tail feathers. A.) Feather under white light. B.) Feather under laser light. C.) Close up of distal portion under laser fluorescence. Scale bar 6 mm. D.) Close up of feather shaft wall (courtesy of T. Kaye). Yellow arrows indicate shaft wall. Scale bar 6 mm. E.) Frayed section of feather wall, indicated by arrow. Scale bar 6 mm.

Photos were processed using ThumbsPlus ® to increase contrast and add additional filtering to further highlight structures. An approximate cross section of the tail feathers was also performed by translating line density using astronomy software (ImageLab, Aragon Systems, Sweden). The image of the tail feather was rotated until the shaft was vertical, then the image was compressed to 200 pixels. This was done in order to average all of the pixels along the vertical axis. A blur filter was added to remove noise, and the image was inverted to aid in clarity of further processing. Using the astronomy software, a small box was drawn to highlight the area for cross sectioning; this box averaged the vertical pixel rows and generated an intensity plot that represents the cross section through the feather. Note that this is not a true cross-section. Cross sections were taken in the barbless region of the tail feather and in the proximal barbed region of the tail feather, where the barbs first begin to appear (Fig. 6).

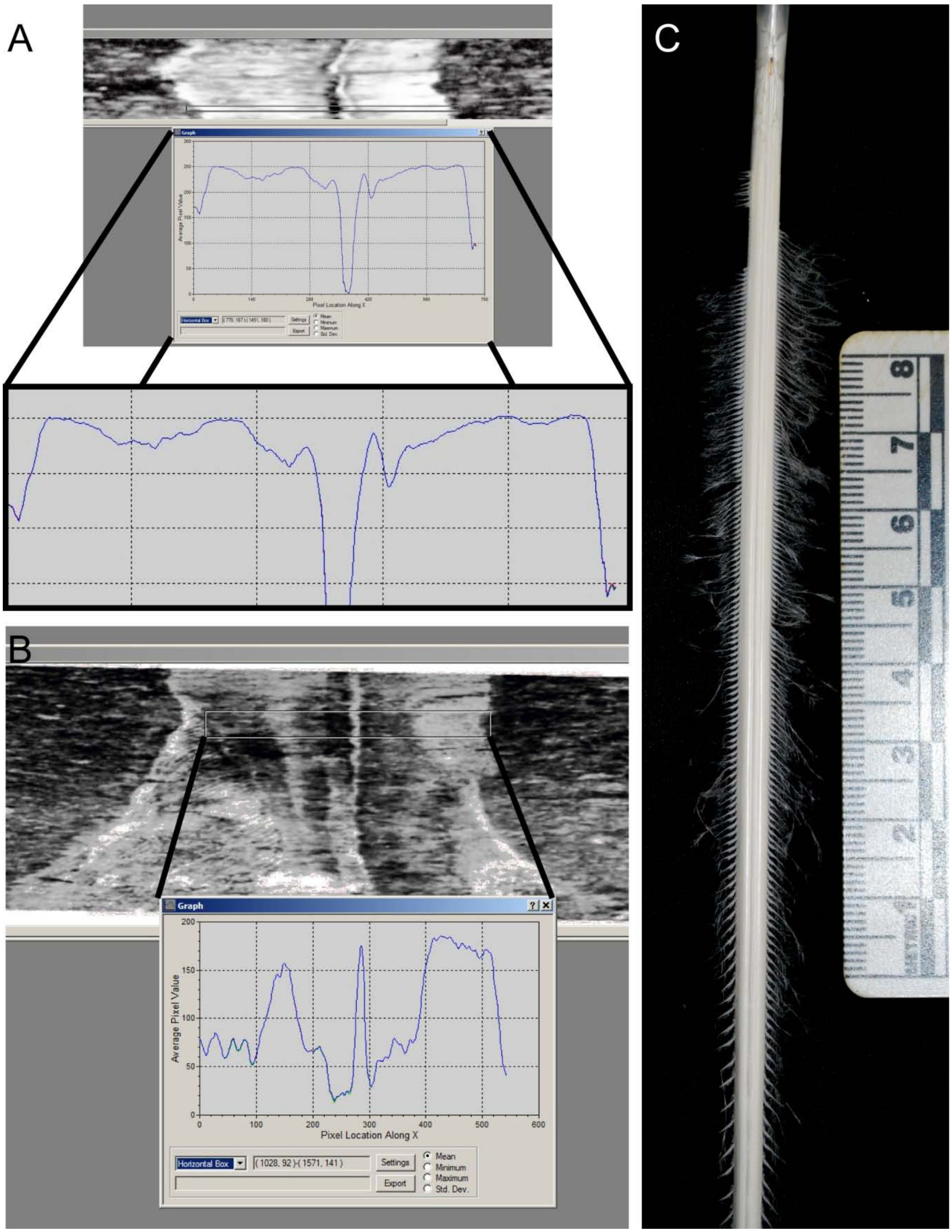

Fig. 6: Best-guess cross-sections of tail feathers created using astronomy software. Note that this cross-section is "upside down" and cannot be rotated due to the readout presented by the software. A.) Distal proximal portion of

feather. B.) Distal portion of feather containing barbs. C.) Rachis of a tail feather from male peafowl (*Pavo*) for comparison. Note the groove at the midline of the rachis. This is the same feather from Fig. 5.

RESULTS

The soft tissue preservation of specimen IVPP V 13156 is especially excellent. The specimen is preserved dorsal-side up, with the right wing partially outstretched and the left wing folded closer to the body (Fig. 7). On the right wing, 10 primaries are preserved (Table 1) (Fig. 7). Primary coverts are also preserved, evidenced by the overlapping rachises and barbs present on the proximal portion of the wing. The 10th and outermost primary is significantly shorter (97.61 mm) than the 9th (186.7 mm). The rachises of the primary feathers are strong and robust, varying from 0.9 mm to 1.9 mm (Table 2). The lower values are due to the covering of the proximal rachis by barbs or other feathers, therefore, a more distal portion of the rachis was measured (Fig. 7B). PMOL AB00150 illustrates the primary feather rachises inserting on the hand, as does STM13-39 (Fig. 8). Secondary feathers are also present on IVPP 13156, although they are folded and overlapping the proximal first primaries (1–5). There is strong evidence for greater secondary coverts based on the presence of overlapping barbs and rachises. There is no evidence of tertial feathers. *Confuciusornis* has at least 10 secondaries based on feather count (STM13-33, STM13-39, STM13-124), however, there are ulnar quill knobs on STM13-39, which dictate how many secondary feathers are present. Ulnar quill knobs are a phenomenon previously not reported in *Confuciusornis* (Fig. 8C). STM13-39 possesses only 8–9 ulnar quill knobs (Fig. 8C), as one quill knob proximal to the ulna is missing, and the distal ulna has been heavily weathered. STM13-39 shows the insertion of secondaries on the ulna within the postpatagium, unfortunately the proximal ~1–1.5 cm has been prepared away (Fig. 8B). The insertion of the feathers into the postpatagium does seem to match the general location of the ulnar quill knobs. There may be another 2–3 secondaries that insert on the distal ulna (Fig. 8C). STM13-124 has the highest number of secondaries, however, several overlap and several appear much shorter than the others (~half the length), which may indicate these are either secondary coverts or growing feathers. The exact topography of the wing of *Confuciusornis* is difficult to determine, as the exact direction of overlap may be impossible to distinguish based on the fossils. The dorsal and ventral coverts are approximately the same length based on IVPP V 13156, which is preserved dorsal-side up, and STM-13-45, which is preserved ventral-side up (Fig. 9).

Specimen #	IVPP V13156
10th primary	97.61
9th primary	186.7
8th primary	202.37
7th primary	265.62
6th primary	258.5
5th primary	249.26
4th primary	217.05
3rd primary	167.79
2nd primary	171.04
1st primary	153.64

Table 1: Primary feather lengths of IVPP V 13156. Measurements in mm.

Specimen #	IVPP V13156	Notes:
10th primary	N/A	
9th primary	1.18	~107 mm from the metacarpus
8th primary	1.64	~107 mm from the metacarpus
7th primary	1.9	~107 mm from the metacarpus
6th primary	1.84	Taken more proximally
5th primary	1.33	Much more distal due to overlap
4th primary	0.9	Much more distal due to overlap
3rd primary	<0.5	
2nd primary	<0.5	
1st primary	<0.5	

Table 2: Primary feather rachis widths of IVPP V 13156. Measurements in mm.

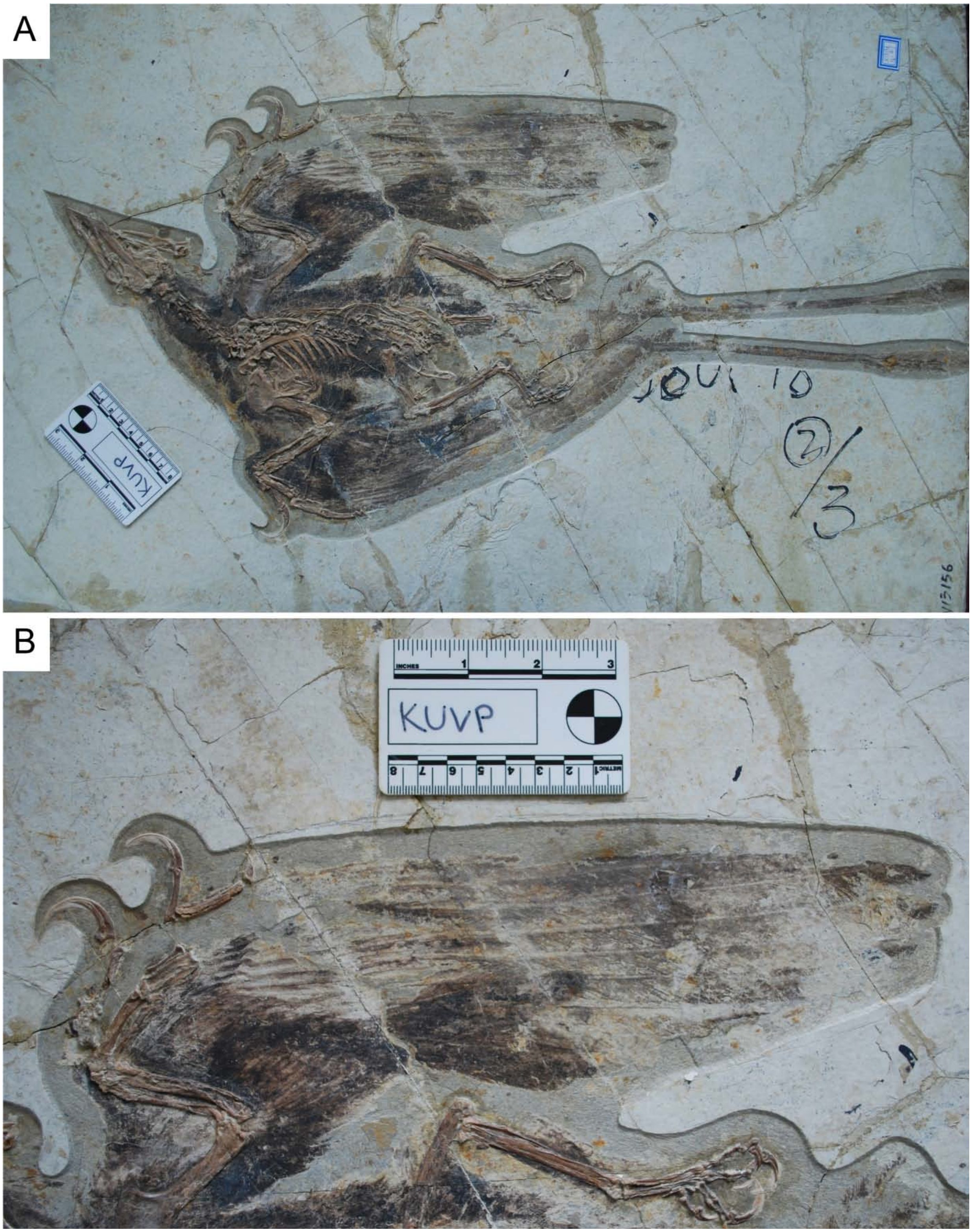

Fig. 7: Photograph of IVPP V 13156. A.) Full specimen B.) Close up of right wing.

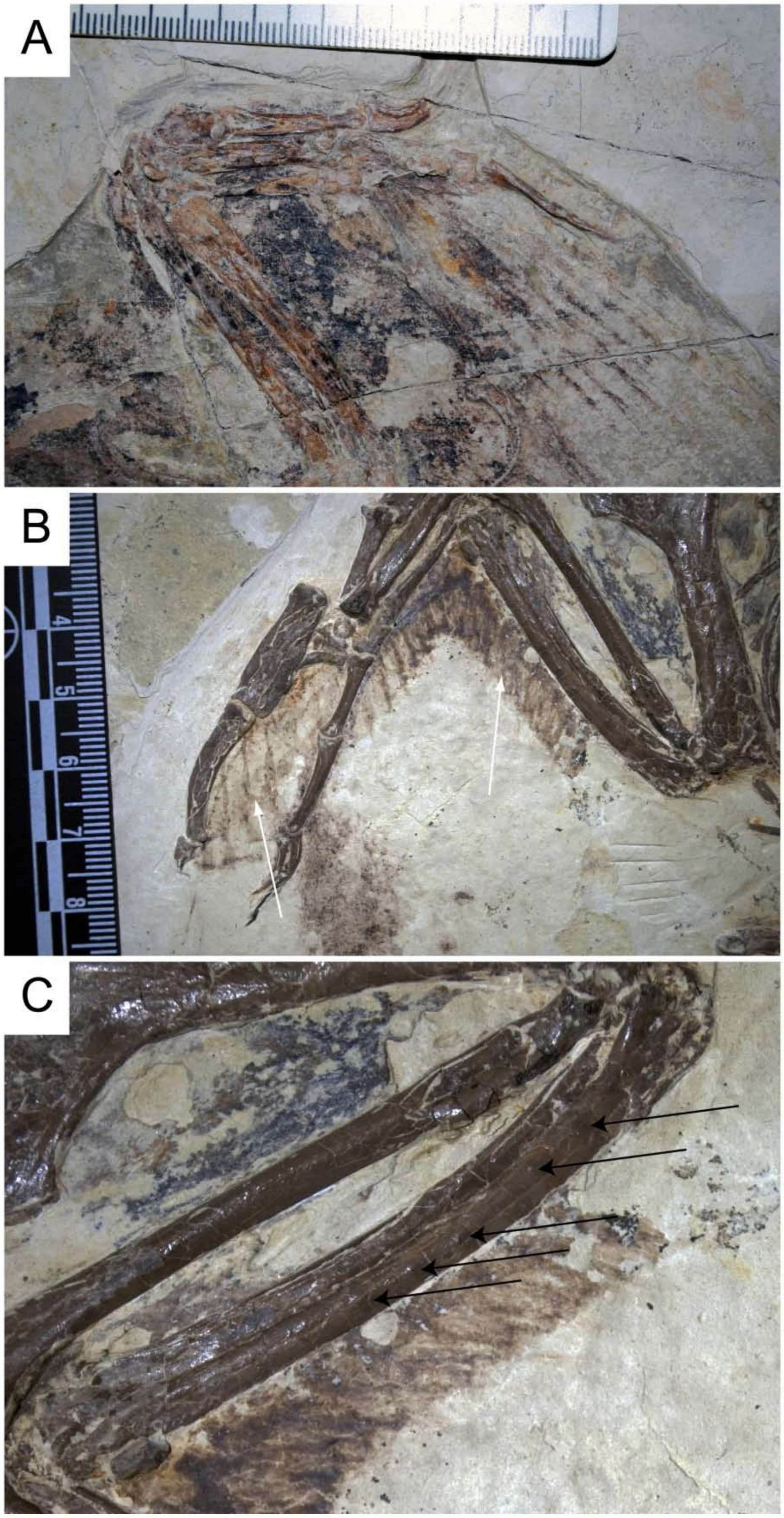

Fig. 8: Photographs showing primary calami inserting on the hand and secondary calami inserting on the ulna as well as quill knobs of *Concfuciusornis*. A.) PMOL AB00150 B.) STM13-39. Arrows indicate primary and secondary calami within the postpatagium. C.) Ulna of STM13-39 showing quill knobs, indicated by arrows.

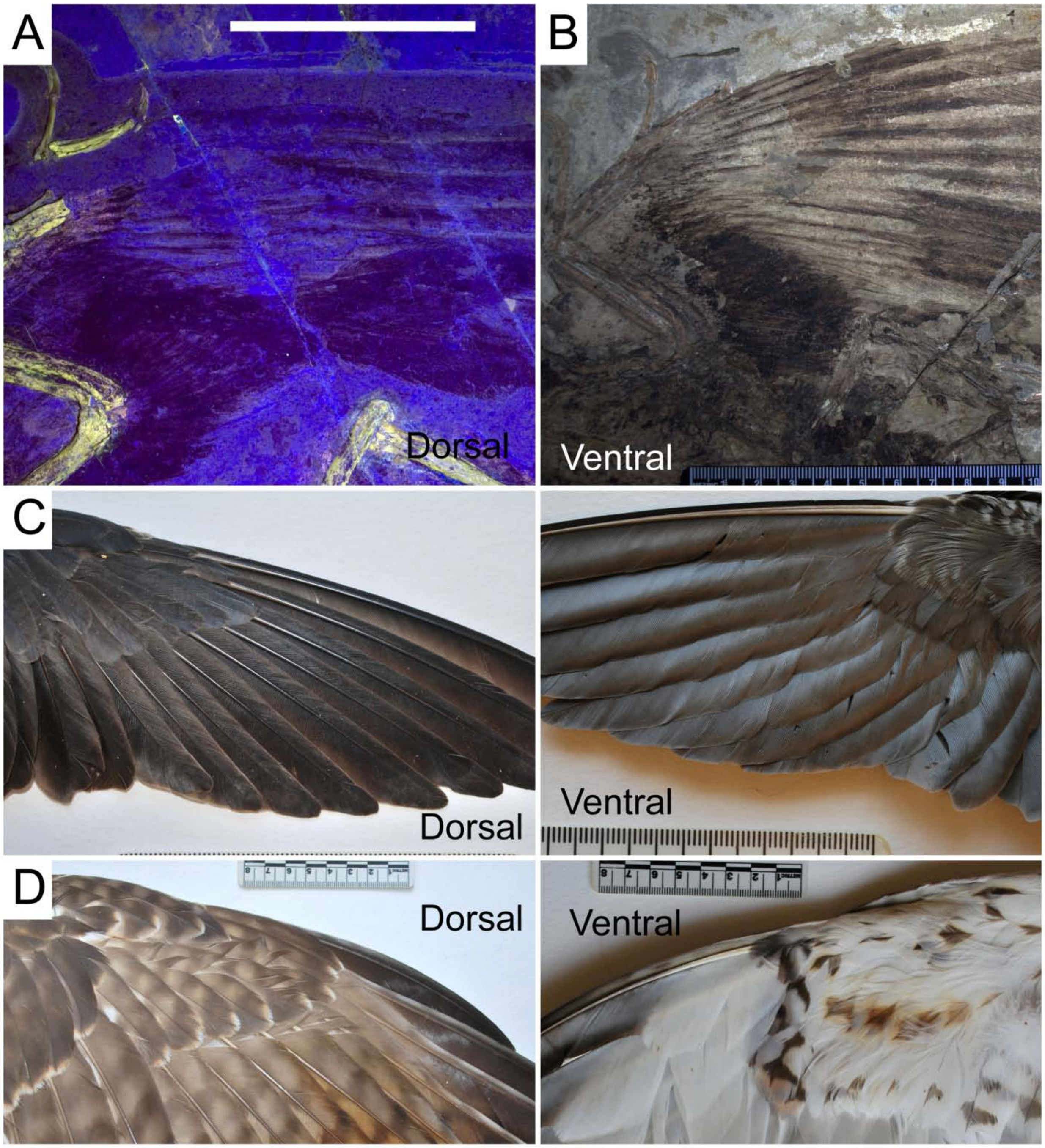

Fig. 9: Photographs showing dorsal and ventral primary and secondary coverts in *Confuciusornis* and select modern examples. A.) IVPP V 13156, under laser fluoresence. Scale bar=7 cm B.) STM13-45. C.) Purple martin from University of Michigan Natural History Museum. D.) Red-tailed hawk from University of Michigan Natural History Museum.

IVPP V 13156 also has paired elongate tail plumes found in many other *Confuciusornis* specimens in this study. Unlike most other *Confuciusornis* specimens, the tail feathers of IVPP V 13156 possess clear anatomical detail (Fig. 5). The total length of the tail feather is ~253 mm. The barbless portion of the tail is ~188 mm long, and the portion of the tail feather that possesses barbs is ~65 mm long. Using laser fluorescence, fine detail can be observed (Fig. 5B).

The tail feathers of *Confuciusornis* have two distinct vertical components and at least four distinct horizontal components in the barbless region (Fig. 5C). The innermost is a dark line at the very center of the shaft, which is surrounded by a white or pale area. Outside the white area is broader dark area that may or may not be subdivided into smaller components (Fig. 5C). The final horizontal component is the shaft wall (Fig. 5D, E). These components are not always visible, even on the same feather. There are other small details that are preserved on the tail feathers of IVPP V 13156 that are not common on less well-preserved specimens. The barbs on the tail are asymmetrical (Fig. 5A, B). There appears to be an outer wall on the barbless region of the feather (Fig. 5D) that is ~1 mm thick. This outer wall is not always visible. One portion of the more proximal tail feather shaft appears frayed or contains multiple branching parts (Fig. 5E). This is the only area of the proximal, barbless area of the tail feather where this morphology is found.

Two cross sections of the tail feathers created with astronomy software highlight a few key morphologic structures. The first is a deep central groove (Fig. 6). On either side of the groove there are slight elevations, analogous to natural levees on meandering rivers. Moving away from the center, the feather seems to plateau, however, there are some changes in relative density that may correlate to a wavy surface (Fig. 6). The distal cross section shows more complexity than the proximal cross section (Fig. 6). The central groove—represented here as a peak—is still present but there is more topography than in the proximal cross section.

Several key morphologic landmarks are also visible on the tail retricies. There is a clearly defined outer wall and inner groove, which appears as a dark line in the center of the shaft (Fig. 6). Surrounding the inner groove are two paler lines, which may represents raised areas surrounding the ventral groove (Fig. 6). Moving out from the center, there are alternating vertical stripes of light and dark, representing areas where the rachis is filled with spongy material. These vertical stripes are more visible distally, especially where the rachis tapers sharply and the barbs appear. This pattern of alternating light-and-dark vertical stripes with a dark groove in the center is identical to the rachis-dominated tail feathers found in male peafowl (commonly: peacock, genus *Pavo*) (Fig. 6C).

The body (i.e., contour) feathers of *Confuciusornis* are rarely well preserved. Most often, the body feathers are preserved as little more than a carbon film, with no morphologic detail present, and only the positioning on the body allows for their interpretation as body or contour feathers. In some specimens, however, there is evidence for a thick layer of feathers, at least in the cervical region (STM13-51, STM13-7) (Fig. 10). Some specimens, especially those that also possess the long, paired tail feathers, also have elongated feathers on the head, indicating a crest (Fig. 11), which may indicate sexual dimorphism in terms of plumage as originally suggested by Martin et al (1998). STM13-7 (Fig. 8B) does not have evidence of elongated feathers, however, the matrix around the skull appears to have been prepared away, which would have obliterated any evidence of crest feathers. STM13-51, another specimen with well-preserved cervical plumage, does not have evidence of a crest, and also lacks the paired tail feathers (Fig. 10A).

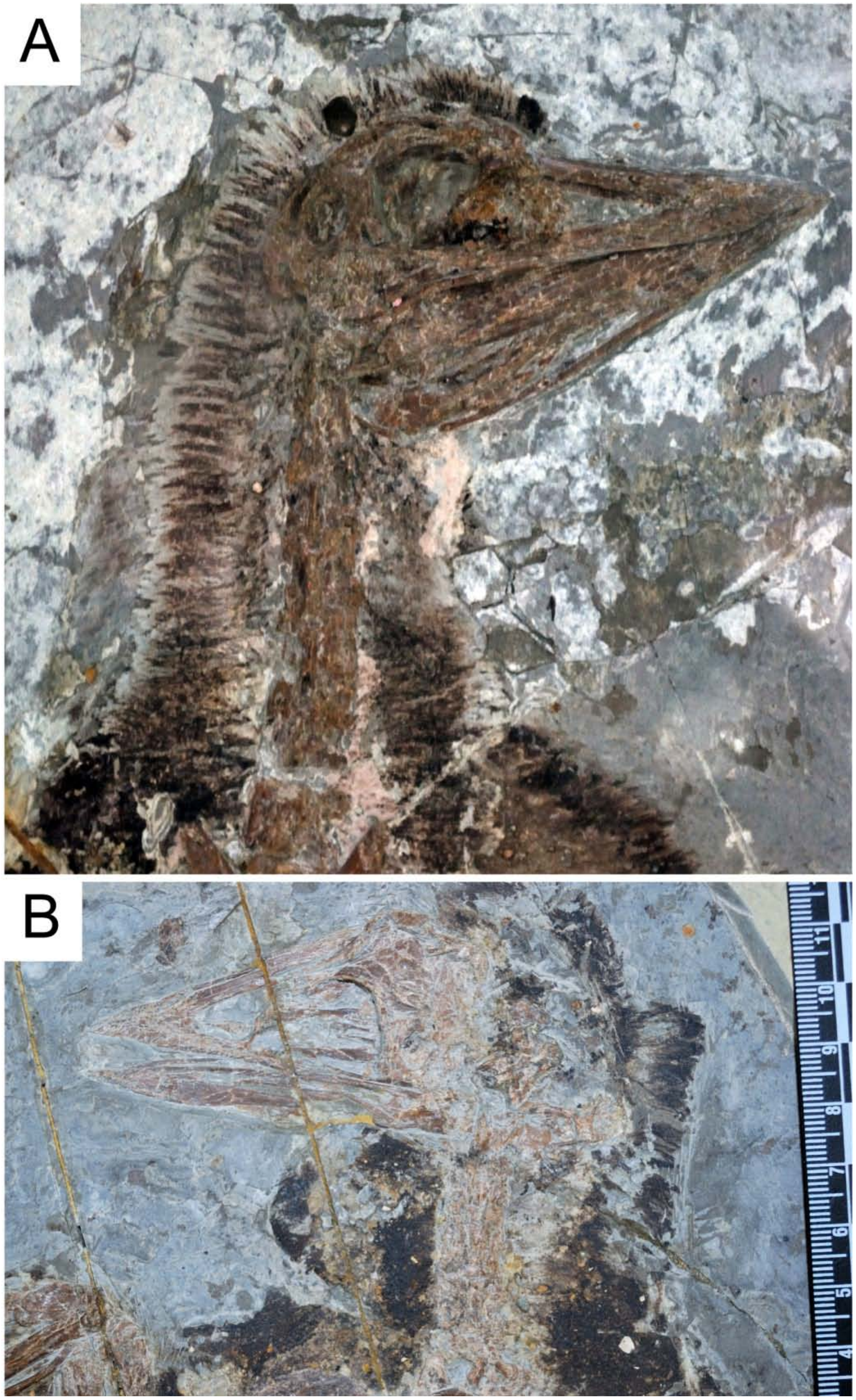

Fig. 10: Specimens of *Confuciusornis* with thick neck feathers. A.) STM13-51. B.) STM13-7.

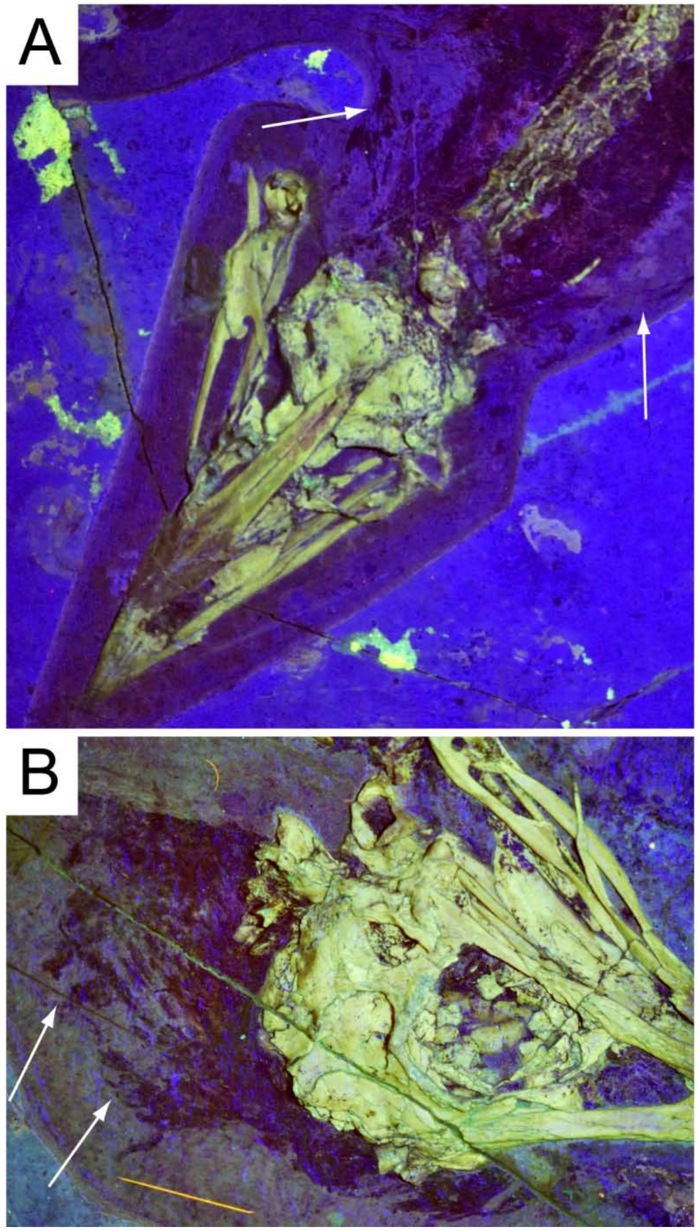

Fig. 11: Specimens of *Confuciusornis* with evidence of a crest. A.) IVPP V 13186. B.) IVPP V 13156.

Further caudally, *Confuciusornis* lacks the typical tail fan seen in modern birds, primitive ornithurines, and potentially one enantiornithine (O'Connor et al., 2009). On well-preserved specimens of *Confuciusornis*, however, there is some evidence for tail feathers other than the elongate, paired plumes (Fig. 12). These other types of feathers, identical in morphology to contour features and possessing clear barbs and central rachises, form a structure termed herein as a tail puff. This tail puff is morphologically different than the upper tail coverts and undertail coverts seen in modern birds, mainly by their increased length, and are also located not only at the base of the tail (i.e., the pelvis and free caudals) but also appear to be located along the pygostyle. STM13-33 has the best-preserved evidence of a tail puff. The feathers of the puff range in length from 2 cm to 4 cm long near the elongate tail plumes. STM13-45, which lacks the paired tail plumes, does have some evidence of a tail puff, with the centermost feathers up to 4 cm long (Fig. 12B). The tail puff of STM13-45, however, is generally smaller than that of STM13-33.

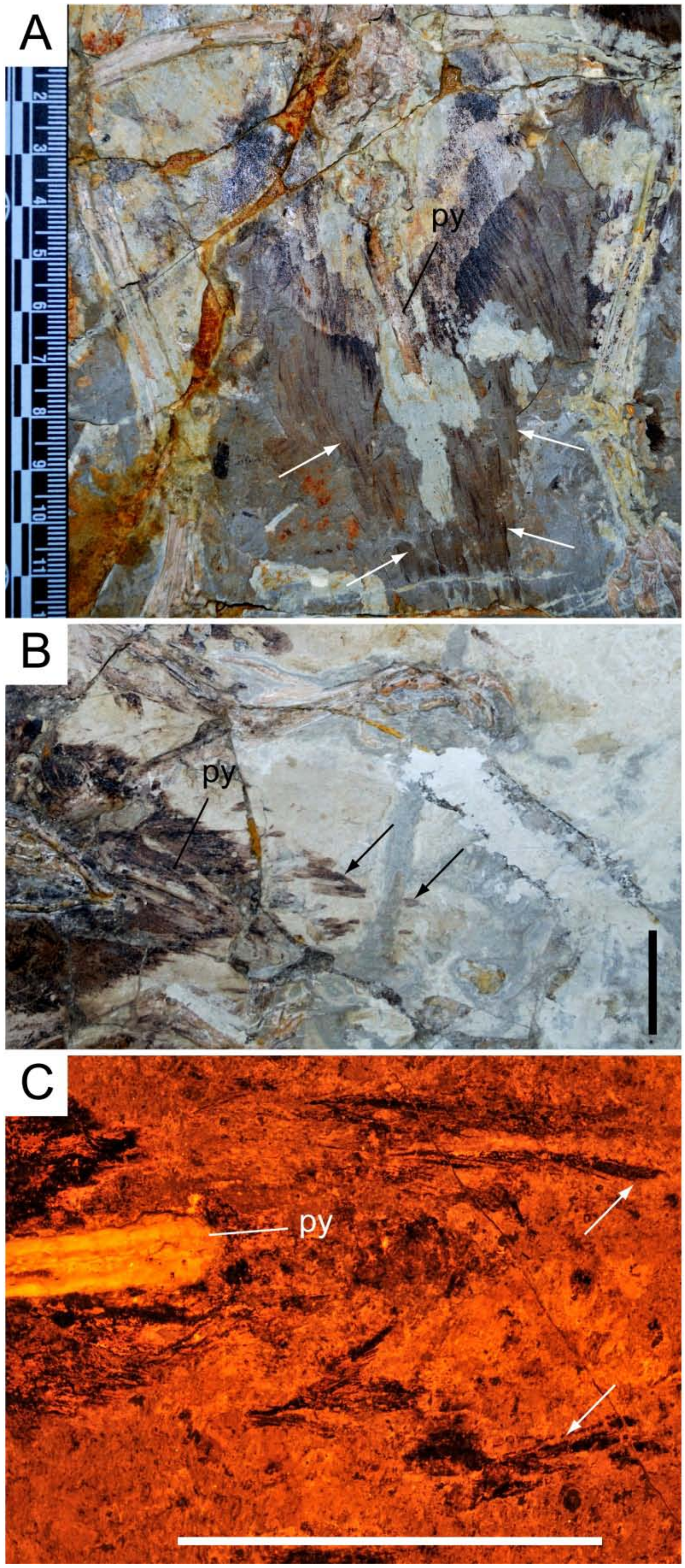

Fig. 12: The tail puff of *Confuciusornis;* py=pygostyle. Arrows indicate tail puff feathers. A.) STM13-33. B.) STM13-45. Scale bar approximately 4 cm. C.) IVPP V 13156. Scale bar approximately 3 cm.

The exact coloration of *Confuciusornis* is still unknown, although Wogelius et al (2011) reported using trace metal analyses to determine color patterns in *Confuciusornis*. In rare cases, avian fossils can preserve color patterns, however, the exact color is not preserved. One specimen of *Confuciusornis* (STM13-33) preserves the coloration pattern in the dorsal secondary coverts (Fig. 13). The primaries and secondaries appear to be monochromatic, however, only portions of the flight feathers are preserved. The covert feathers appear lighter towards the base of the feather and gradually become darker distally, and each covert feather is tipped in dark color, perhaps black (Fig. 13).

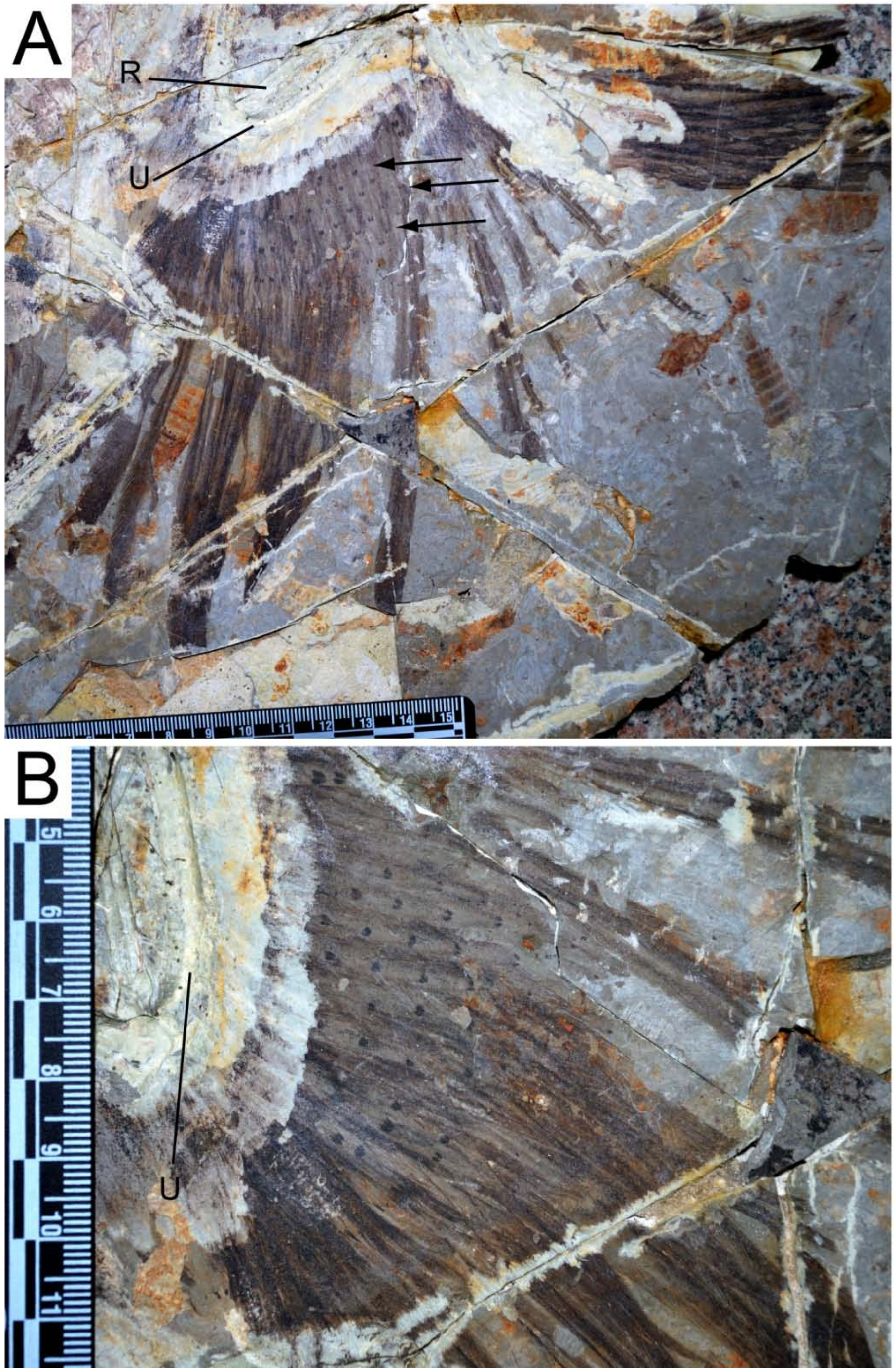

Fig. 13: Color pattern in the wing of *Confuciusornis* (STM13-33). Arrows point to coloration patterns on the secondary covert feathers. R=radius, U=ulna. A.) Photograph of the wing of STM13-33. B.) Close up of secondary coverts.

IVPP V 13156 also contains different kinds of preserved soft tissue. Scales, patagium (skin), and muscle are all revealed under laser fluorescence on IVPP V 13156. These soft tissues are normally invisible under natural light (Fig. 14). Laser fluorescence reveals pinkish halos surrounding areas on the right and left tibiotarsi, which also appear under UV light as tan halos (Fig. 14B). Skin and muscle tissue appears as a pinkish halo, whereas scales are yellow, violet, and blue (Fig. 14C). All of these colors are visible only with the yellow longpass filter. Scales and soft tissues are also visible using the orange longpass filter (Fig. 14D), however, as brighter areas of fluorescence in the matrix, not variations in color.

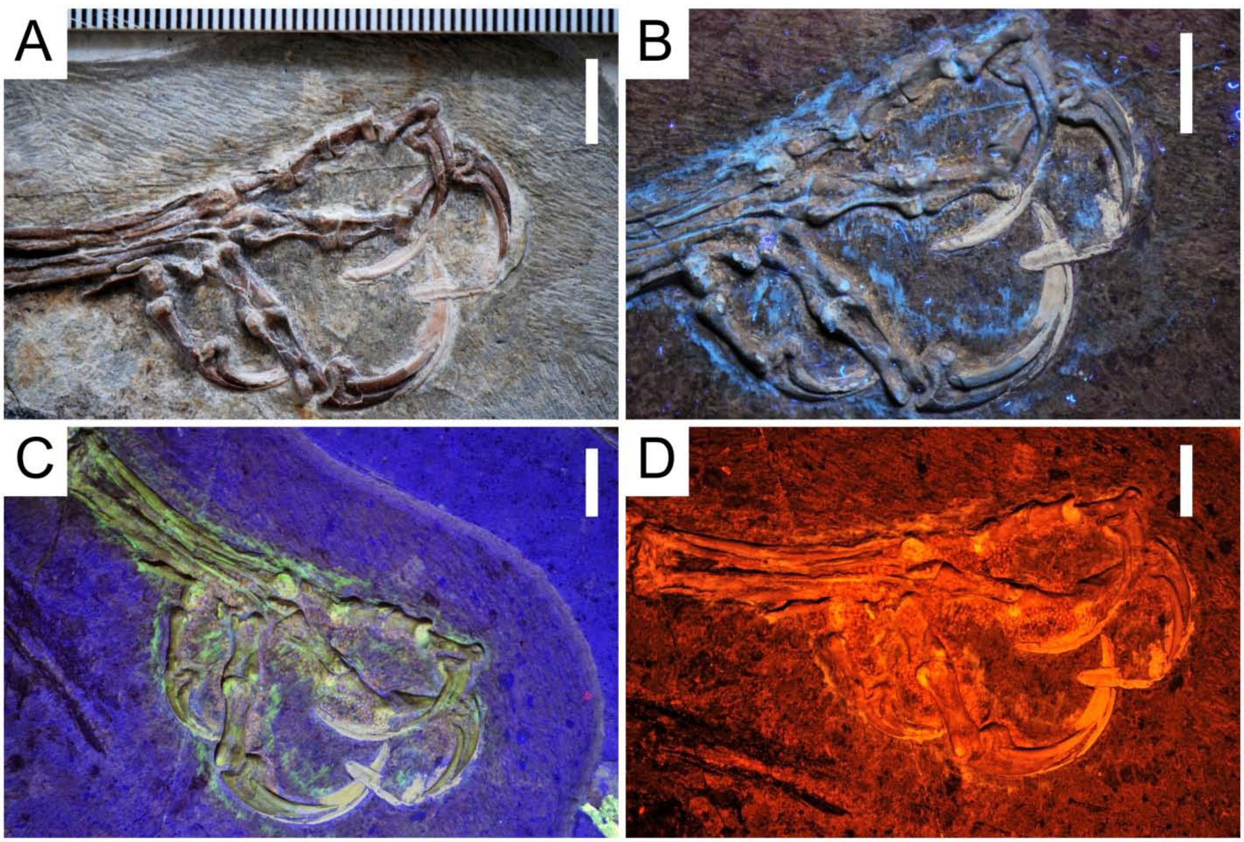

Fig. 14: Comparison of feet of IVPP V 13156 under white light, UV light, and laser fluorescence. All scale bars 8 mm. A.) White light. B.) UV light. C.) Yellow longpass. D.) Orange longpass.

There are scales and pads preserved on the feet (Fig. 15), which are preserved ventral-side up. Scales are preserved both on the matrix, and on the bone of the phalanxes and the tarsometatarsus. The scales of *Confuciusornis* appear to be entirely reticulate. The feet, however, are preserved ventral-side up, which may obscure any scutate scales as they are usually found on the dorsal side of the toes and tarsometatarsus. The scales are relatively spread out away from the phalanxes on the right foot of IVPP V 13156, however, on the left foot the scales are preserved mostly *in situ*. Pads can be distinguished on both left and right feet (Fig. 15), and this evidence suggests that *Confuciusornis* had large phalangeal pads and small interphalangeal pads (Fig. 15C). Many of the pads are compressed and spread out from the foot. Although the pads on the left foot are compressed laterally, they also appear to align roughly with the phalanxes (Fig. 15C). There is no sign of interphalangeal pads. There is also evidence of a large, fleshy metatarsal pad (Fig. 15D). The pad on the left foot is preserved *in situ* and directly on the phalanx (Fig. 15D).

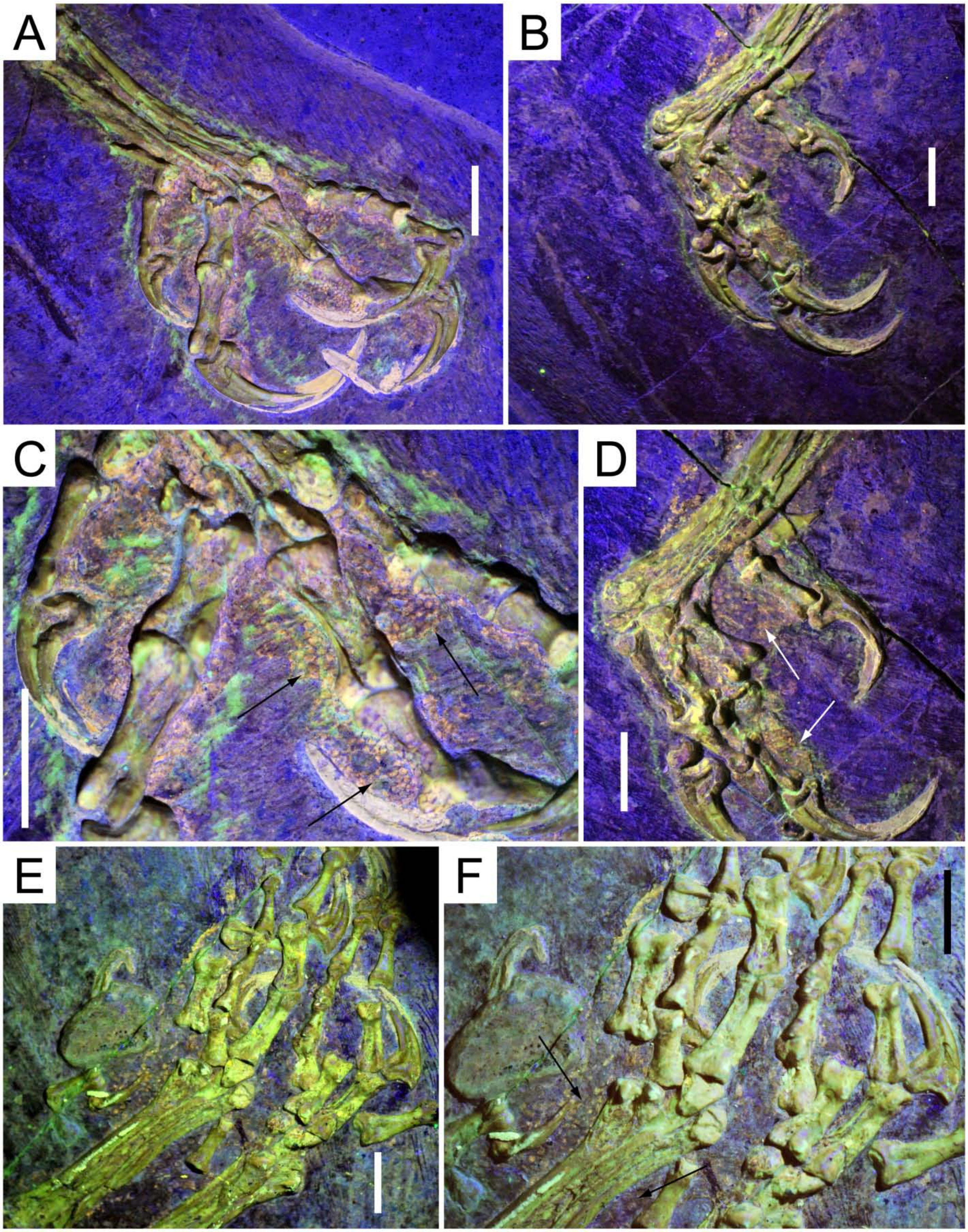

Fig. 15: Photographs of the feet of IVPP V 13156 and IVPP V 13168. A.) Right foot, yellow longpass. Scale bar 7 mm B.) Left foot, yellow longpass. Scale bar 7 mm C.) Close up of right foot, yellow longpass. Scale bar 7 mm.

Arrows indicates areas of soft tissue preservation. D.) Close up of left foot, yellow longpass. Scale bar 7 mm. Arrows indicates metatarsal pad and phalangeal pad preserved *in situ*. E.) IVPP V 13168, yellow longpass. Scale bar 5 mm F.) Close up of IVPP V 13168, yellow longpass. Scale bar 5 mm. Arrows indicate areas of disarticulated reticulate scales.

Under laser fluorescence, there are several areas of soft tissue preserved that are not visible under natural light on IVPP V 13156. These areas appear as pinkish halos in unprocessed laser fluorescence photos (Fig. 16). There is a significant pinkish halo around the tibiotarsus (Fig. 16A). The halo is widened proximally and thins distally down to the joint. The pinkish halo has been prepared away from the tibiotarsus proximally. The halo is wider laterally than medially on the right tibiotarsus, and subequal on the left (Fig. 16A). There is a similar pinkish halo around the distal end of the long, bladelike pygostyle (Fig. 16B). A similarly shaped dark area is also present (under white light) around the distal portion of the pygostyle of STM13-39 (Fig. 17). Another pinkish halo is present on the wings, especially visible on the hand (Fig. 16C), and where the propatagium would be expected (Fig. 16D). The postpatagium of STM13-39 is ~7 mm deep on the ulna and at least 15mm deep on the fingers (Fig. 8). The postpatagium on the ulna of IVPP V13156 is more difficult to measure, however, the postpatagium on the hand is ~13 mm deep.

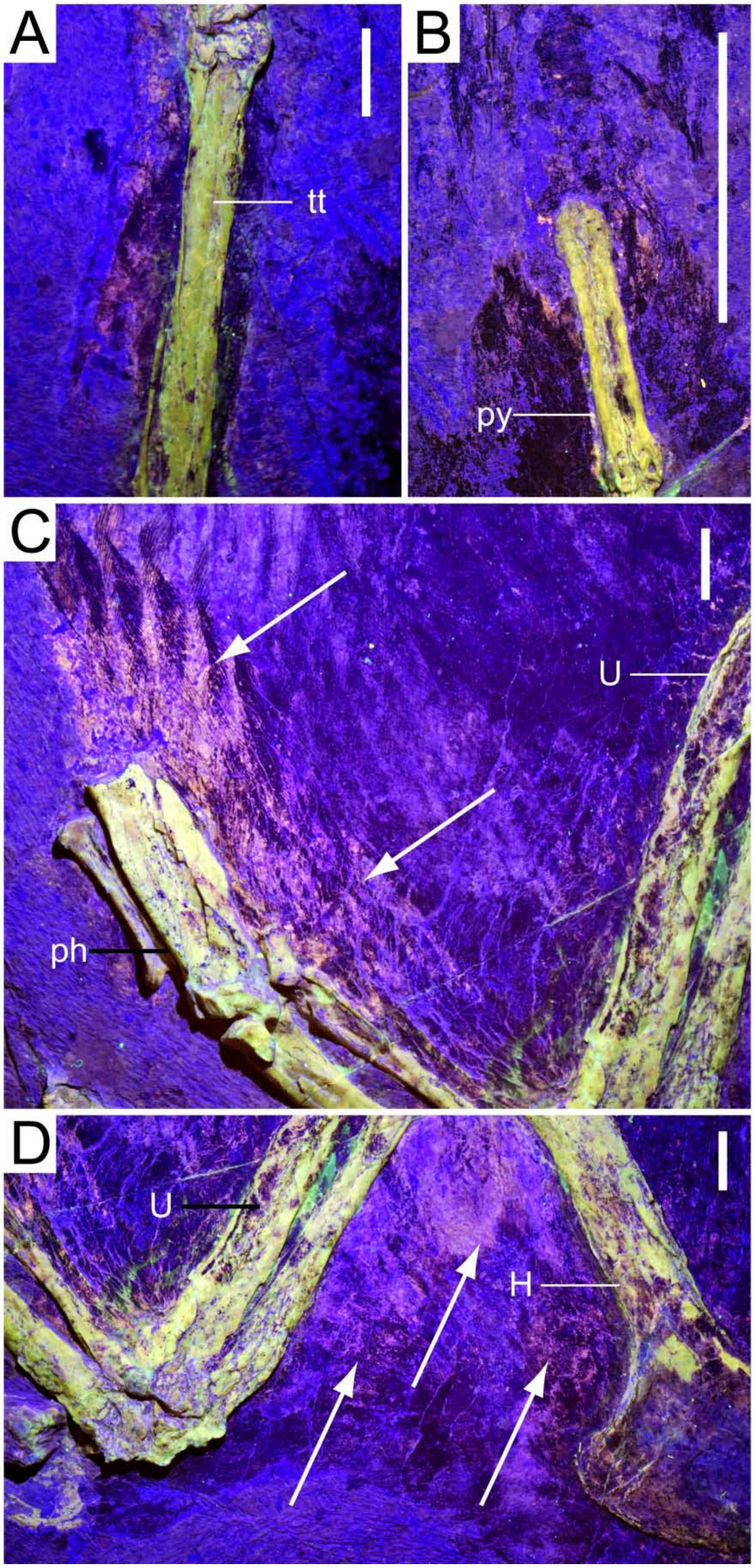

Fig. 16: Photographs of soft tissue under laser fluorescence from IVPP V13156; tt=tibiotarsus, py=pygostyle; U=ulna; ph=phalanx; H=humerus. A.) Tibiotarsus. Note the dark carbonized preservation and the pinkish halo,

representing the *m. gastrocnemius*. Scale bar 8 mm. B.) Pygostyle. Scale bar 3 cm. C.) Wing showing postpatagium. Arrows indicate areas of preserved soft tissue. D.) Wing showing propatagium. Scale bar 5 mm. Arrows indicate areas of preserved soft tissue.

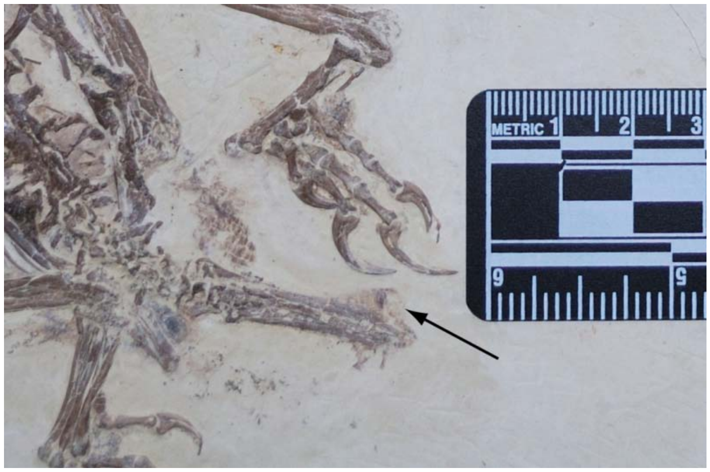

Fig. 17: Photograph of soft tissue around the pygostyle of STM13-39 that may represent the uropygial gland or muscle mass.

DISCUSSION

The results provide evidence for the reconstruction of *Confuciusornis* soft tissue with correct plumage morphology and coloration (Fig. 18). *Confuciusornis*, like all birds, has both primary and secondary coverts, and like all birds appears to have both dorsal and ventral coverts (see Fig. 9). The relative lengths of the dorsal and ventral coverts are unusual—in most birds, the ventral coverts are either shorter than the dorsal coverts (e.g., woodpeckers, passeriform birds, quail), or much longer (e.g., seabirds, waterbirds). Swallows (Passeriformes) have dorsal and ventral secondary coverts that are approximately the same length, however, the morphology of the primary and secondary coverts is different (Fig. 9C), whereas in *Confuciusornis* the primary and secondary coverts appear approximately the same. Red-tailed hawks (*Buteo jamaicensis*) are the only species examined here that have dorsal and ventral coverts of approximately the same length, and they are shorter relative to the primaries than the coverts of *Confuciusornis* (Fig. 9D). Although previous studies have suggested that the rachises of *Confuciusornis* primaries are thin (Nudds and Dyke, 2010), IVPP V 13156 has proximal primary rachis widths of 1.9 mm to 0.9 mm—the smaller measurements were actually taken 1–2 cm lower on the feather because of overlapping barbs. The rachises of *Confuciusornis* are clearly more robust than previously reported, suggesting that the interpretation that *Confuciusornis* was a weak flyer because of the width of its primaries is likely incorrect (contra Nudds and Dyke, 2010).

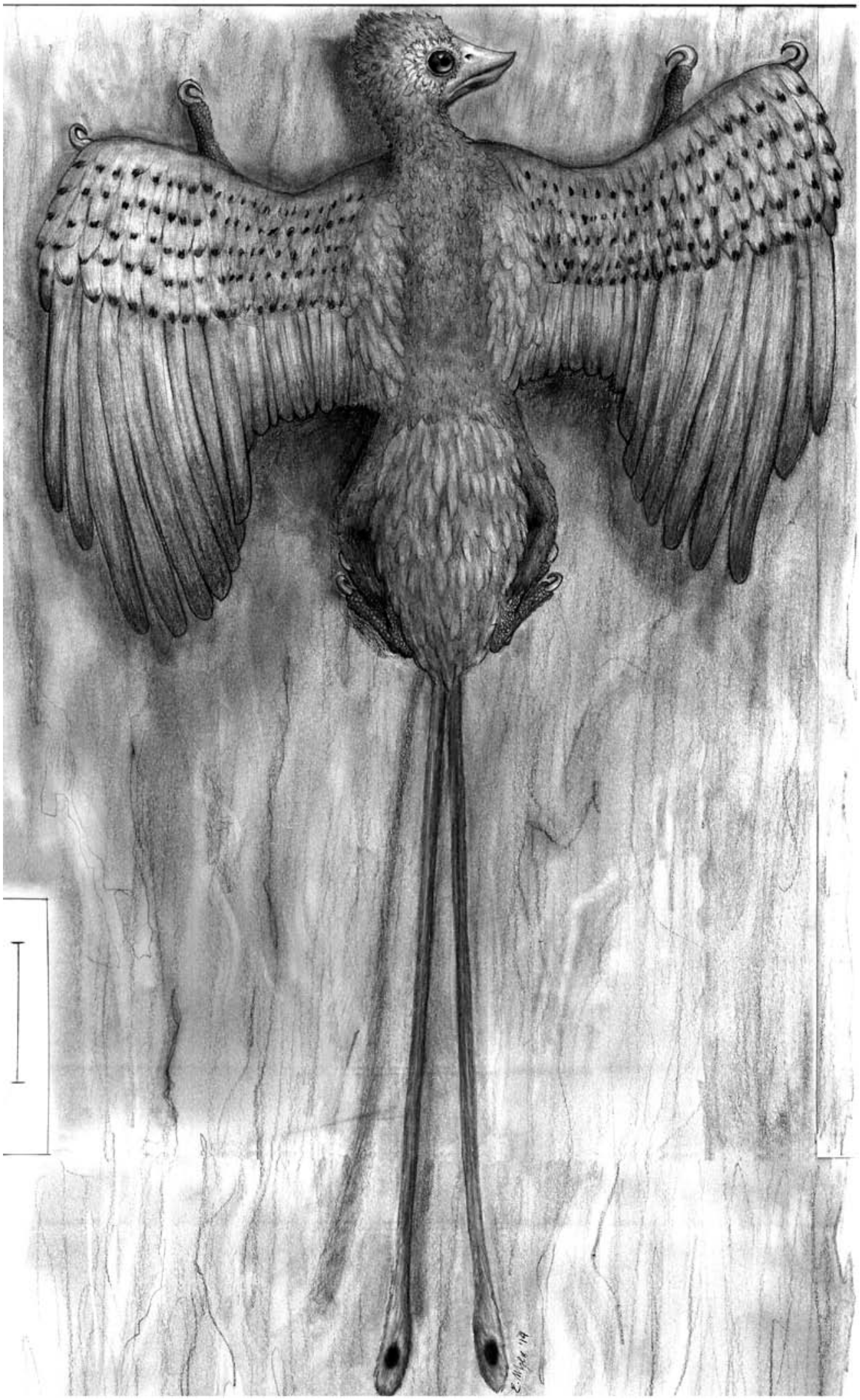

Fig. 18: New reconstruction of *Confuciusornis*, drawing courtesy of Elizabeth Myers. Scale bar 6 cm.

Flight feather analysis and comparison with modern birds

Birds can be classified into different flight styles based on the shape of the wing as formed by the primaries and secondaries. Such birds as woodpeckers have a strongly (sometimes very strongly) shortened 10th primary, and utilize phugoid gliding, in which a bird snaps its wings out, flaps, and draws the wings back into the body. Birds with rounded, cuplike wings with strongly curved primaries (e.g., quail) are short-burst fliers, which have a strong take off from the ground and then glide some distance. Birds with rounded, shorter wings can maneuver through tight foliage (e.g., many passeriforms and accipiters). Birds with slender, sharply pointed wings are fast-flying birds with poor maneuverability. Birds with long, narrow wings with a high aspect ratio are dynamic soarers (e.g., albatross), which fly mainly by soaring. Similarly, birds with shorter wings, in which the primary feathers splay out with gaps between them (i.e., slots), also rely on soaring (e.g., high-lift wings of buteo hawks) (Brown, 1963).

The primaries of *Confuciusornis* are very long in comparison to total arm length (Wang et al., 2011). This is similar to such fast-flying birds as falcons, swifts, and swallows (Fig. 9C). *Confuciusornis*, however, does not have the same overall wing morphology as modern fast-flying birds. In falcons and especially swallows and swifts, the 10th (outermost) primary is extremely long, and in swifts it is the longest primary present (Fig. 9C). In *Confuciusornis*, however, the 10th primary is approximately half the length of the 9th (Fig. 19, Table 1). The 10th primary appears to be approximately the same length as some of the dorsal greater primary coverts, although the exact length of some of the greater primary coverts is hard to distinguish. This is similar to the condition seen in some woodpeckers (e.g., Northern Flicker, *Colaptes auratus*) and some corvids (e.g., Black-billed magpie, *Pica pica*) (Fig. 20).

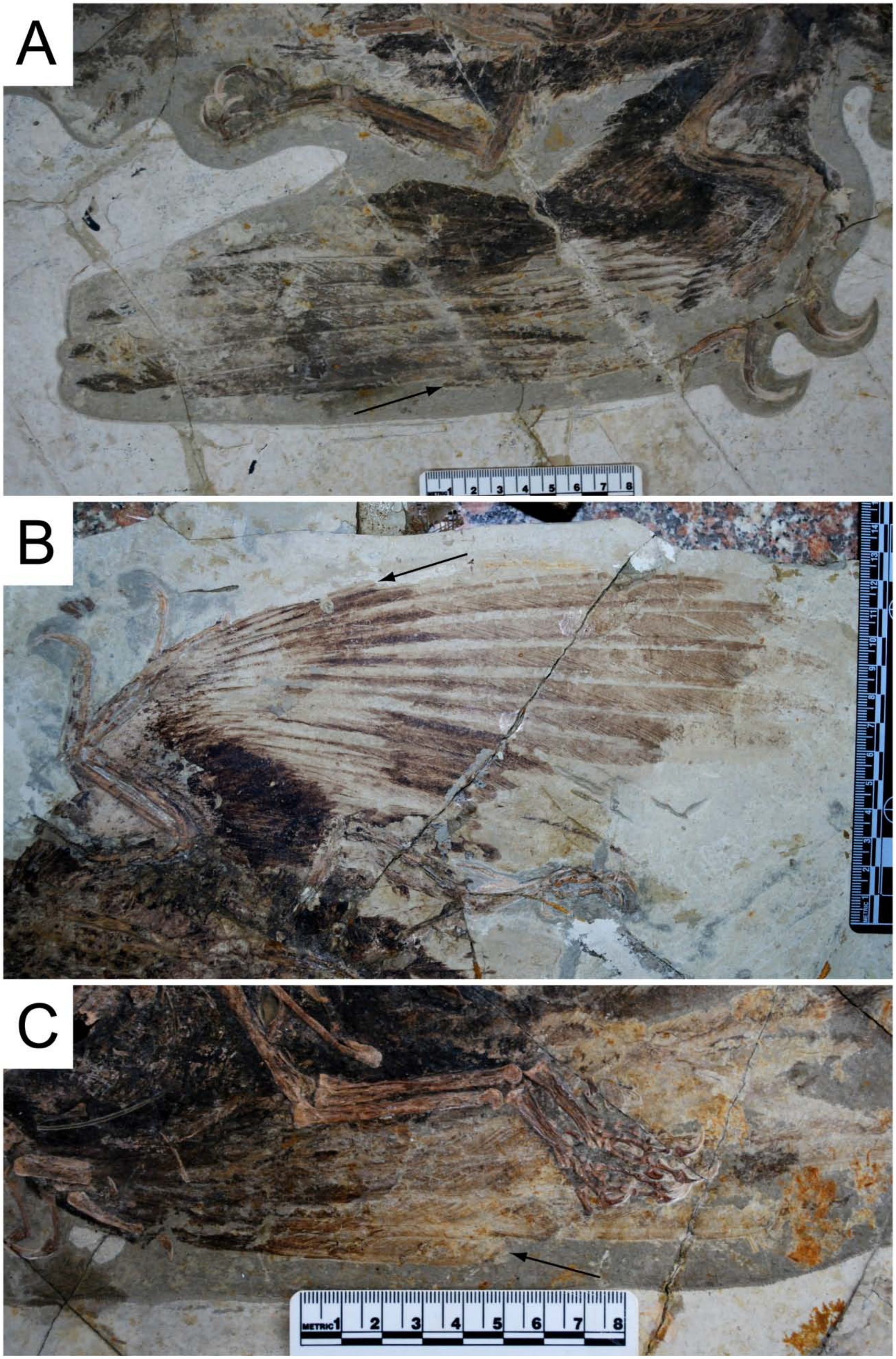
A
B
C

Fig. 19: (Opposite page) Photographs of the wing of *Confuciusornis* with arrows indicating the shortened 10th primary. A.) IVPP V 13156. B.) STM13-45. C.) IVPP V 13168.

A direct comparison of ratios between primary lengths of several different modern birds and *Confuciusornis* is shown in Table 3. All 10 primaries, as well as the lengths of the 1st (outermost) secondary of *Confuciusornis* are compared to modern birds, in order to better understand the potential flight methods and ability of *Confuciusornis*. Although the secondaries do not directly contribute to lift as do the primaries, they still serve an aerodynamic function. Each *Confuciusornis* primary was compared directly to its modern counterpart—to average the primaries together would result in a loss of data (e.g., Wang et al., 2011).

Name	*Colaptes auratus*	*Colinus virginianus*	*Progne subis*	*Falco sparevis*	*Cardinalis cardinali*	*Pica pica*	*Confuciusornis*
Specimen	243,128	235,266	237,246	233,618	236,461	235,421	IVPP V13156
10th primary	38.1	65.08	114.22	120.5	60.73	63.93	97.61
9th primary	99.2	72.24	108.79	138.64	67.98	117.52	186.7
8th primary	121.81	78.4	103.24	138.65	70.76	152.27	202.37
7th primary	127.74	80.3	100.1	128.59	70.66	164.53	265.62
6th primary	127.27	80.75	90.07	119.43	74.86	170.46	258.5
5th primary	126.48	78.77	85.42	111.42	72.57	167.24	249.26
4th primary	124.02	77.15	74.97	98.78	71.35	153.85	217.05
3rd primary	111.98	72.73	70.19	91.38	68.24	148.04	167.79
2nd primary	109.49	68.59	59.89	83.53	67.07	142.78	171.04
1st primary	106.28	67.77	50.86	75.55	65.39	130.49	153.64
1st secondary	98.67	67.77	N/A	70.45	69.88	137.28	130.24
10th:9th	0.384072581	0.900885936	1.049912676	0.86915753	0.893350986	0.543992512	0.522817354
9th:8th	0.814383056	0.921428571	1.053758233	0.999927876	0.960712267	0.771786957	0.922567574
8th:7th	0.953577579	0.97633873	1.031368631	1.078233144	1.001415228	0.925484714	0.761877871
7th:6th	1.003692936	0.994427245	1.111357833	1.076697647	0.943895271	0.96521178	1.02754352
6th:5th	1.006246047	1.025136473	1.0544369	1.071890145	1.031555739	1.019253767	1.037069726
5th:4th	1.01983551	1.020998056	1.139389089	1.127961126	1.017098809	1.087032824	1.148398986
4th:3rd	1.1075192	1.060772721	1.068100869	1.080980521	1.045574443	1.03924615	1.293581262
3rd:2nd	1.022741803	1.060358653	1.171981967	1.093978211	1.017444461	1.036839894	0.980998597
2nd:1st	1.030203237	1.012099749	1.177546205	1.105625414	1.025692002	1.094183462	1.113251757
1st prim:1st sec	1.077125773	1	N/A	1.072391767	0.935746995	0.950539044	1.179668305

Table 3: Comparison of relative primary feather lengths between modern birds and *Confuciusornis*. The top portion of this table are the direct measurements (in mm), whereas the bottom portion of the table represents the ratio between different feather lengths.

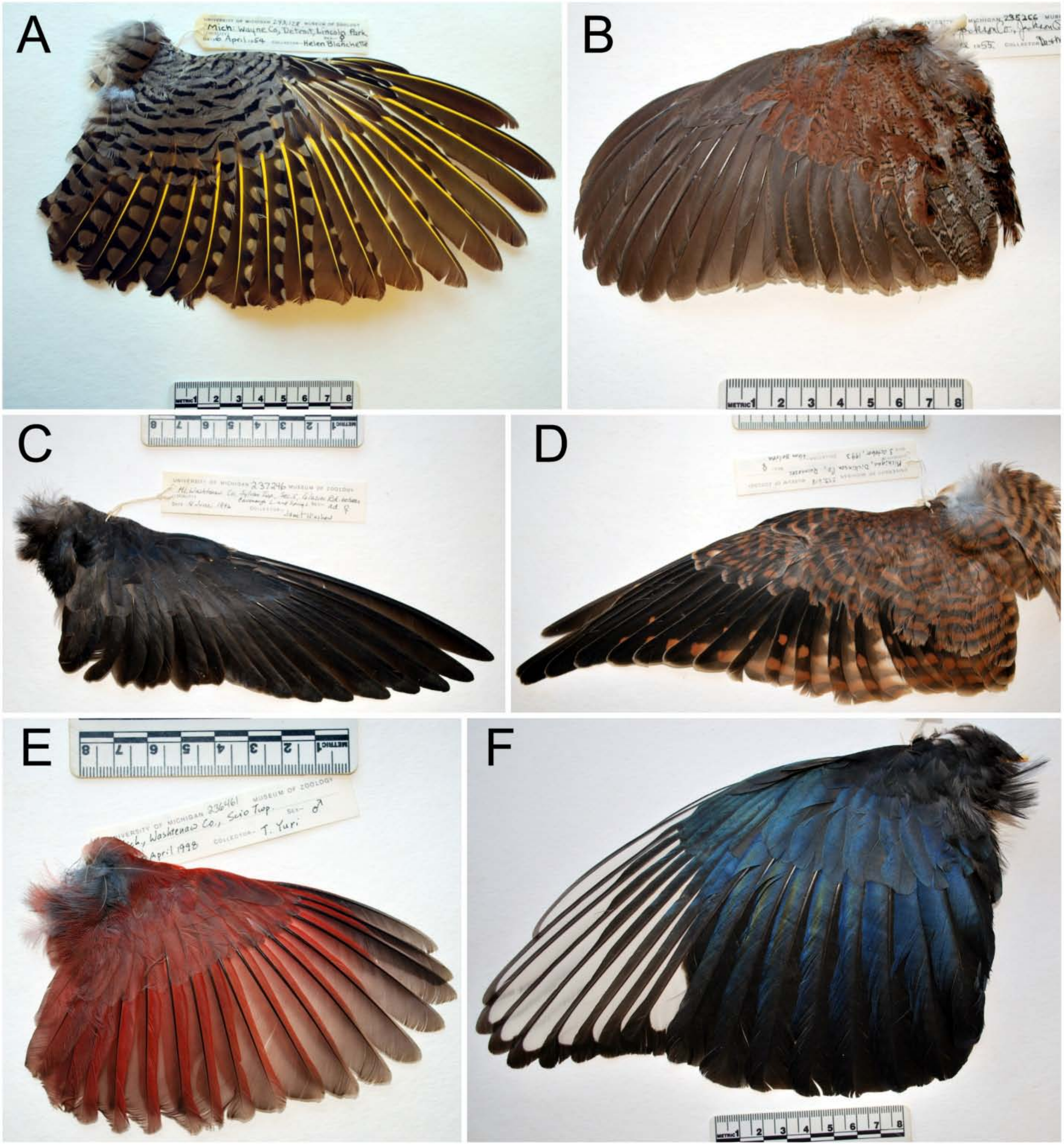

Fig. 20: Photographs of spread wings of modern birds. All specimens are seen in dorsal view. A.) Northern Flicker (*Coalptes auritus*), University of Michigan Museum of Zoology Ornithology Collections (UMMZ) 243,128. B.) Northern Bobwhite (*Colinus virginianus*), UMMZ 235266. C.) Purple Martin (*Progne subis*), UMMZ 237246. D.) American Kestrel (*Falco sparevis*), UMMZ 233,618. E.) Northern Cardinal (*Cardinalis cardinalis*), UMMZ 236461. F.) Black-billed Magpie (*Pica pica*), UMMZ 235421.

The 10th:9th primary ratio for *Confuciusornis* is 0.52, which is closest to the Black-Billed Magpie (*Pica pica*) (Table 3). The wing shape of *Confuciusornis* equates well with *P. pica*, however, there are also some similarities with the Northern Cardinal (*Cardinalis cardinalis*) and woodpeckers in the first primaries. Although *Confuciusornis* has exceptionally long primaries in comparison to the bones of the arm, the primaries in relation to each other are not comparable to those of swallows, falcons, and other fast-flying birds (Table 3).

The length of the primaries and their lengths relative to each other, as well as total primary length, is important for determining flight ability. Previous studies on *Confuciusornis* flight ability (Wang et al., 2011 and references therein) have overlooked the shortened 10th primary—only three specimens examined in this study (IVPP V13156, IVPP V13168, and STM13-45) have a visible shortened 10th primary. Many *Confuciusornis* specimens are preserved with semifolded wings—this results in the apparent disappearance of the short 10th primary, perhaps overlooked as a greater primary covert, or simply preserved under the longer 9th primary (Fig. 21), and the wing looks very narrow and pointed.

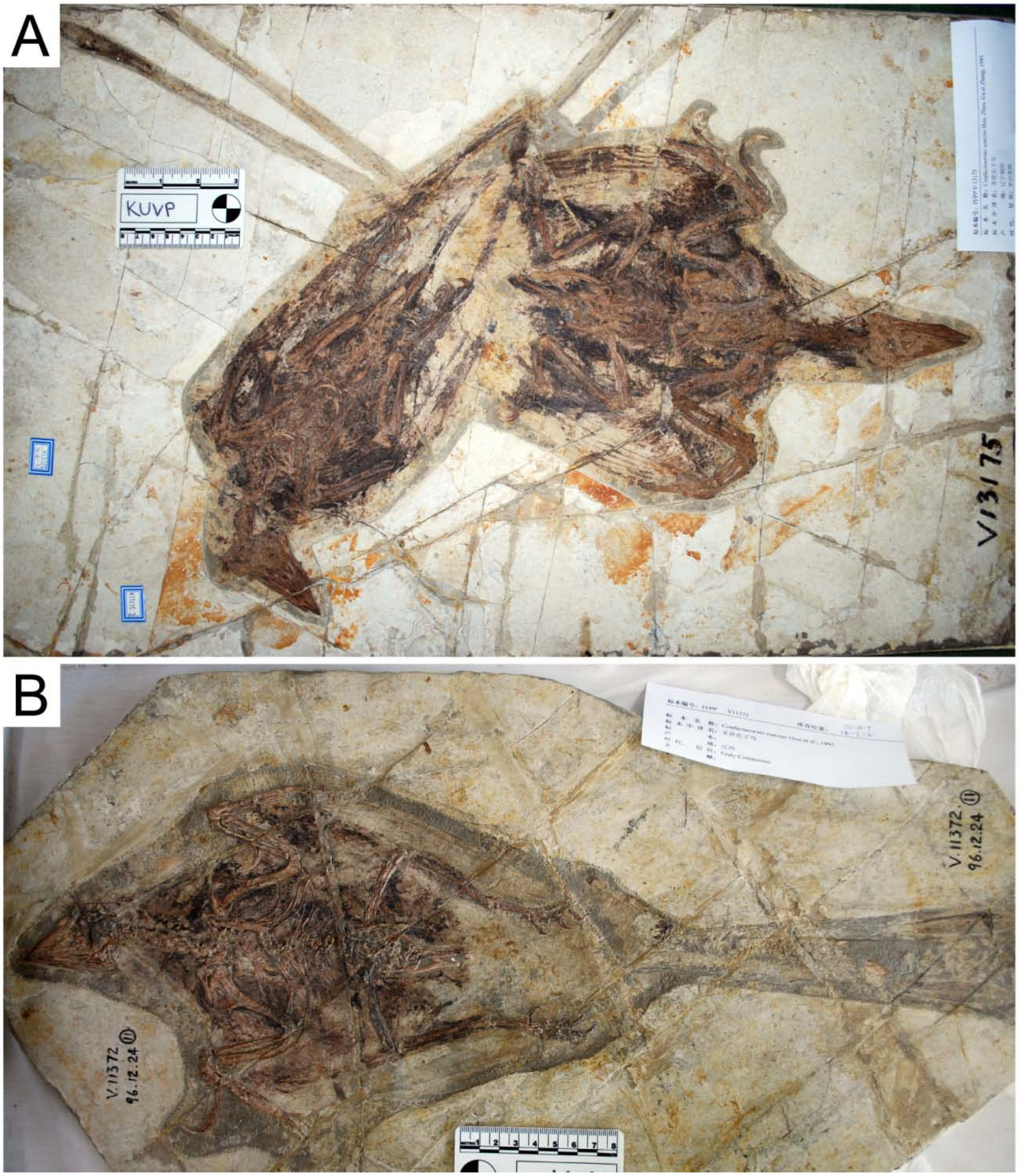

Fig. 21: Examples of *Confuciusornis* with folded wings, obscuring the 10th primary.

The reconstruction of the wing of *Confuciusornis*, with the short 10th primary included, shows a rounder wingshape than was previously suggested (Fig. 22). A rounder wingshape is found in modern bird groups that are primarily forest dwelling and allows for greater maneuverability within close spaces within tree crowns and underbrush (Perez-Tris and Telleria, 2001). *Confuciusornis* does have, however, extremely long 9th–6th primaries in comparison to total arm length, which would make maneuverability significantly more difficult. When compared to the surrounding feathers, the ratios are comparable to modern birds (Table 3), however, the secondaries are much shorter than the primaries in relation to modern birds with rounded wingtips (Fig. 22). This results in a wingshape that is not seen in modern birds today, with extremely long, but rounded primaries and relatively short secondaries. The exact aerodynamic function of this wing has yet to be determined, however, the aspect ratio (AR) is calculated as 7.22 (excluding any potential tertial feathers) or 6.7 (including potential tertial feathers).

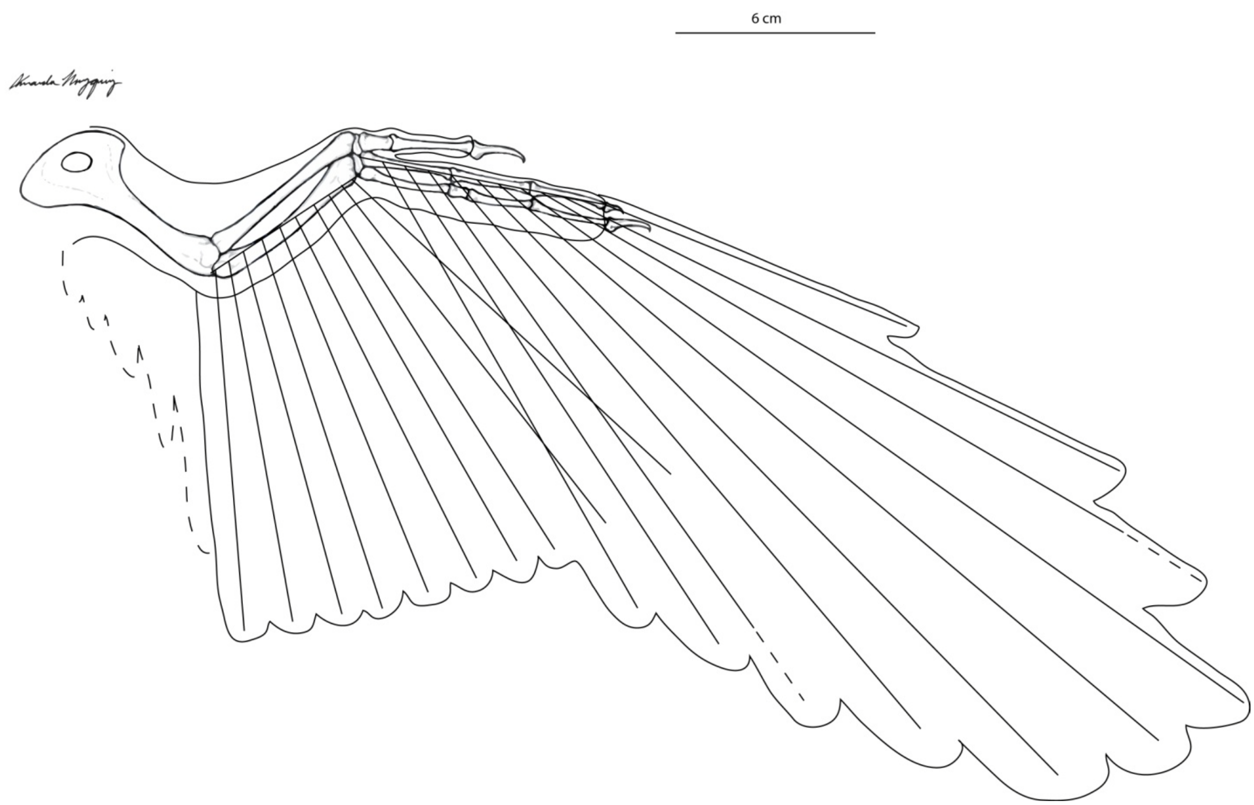

Fig. 22: Reconstruction of the wing of *Confuciusornis*. Lines represent the lengths of the primary feathers. Outstretched arm reconstruction courtesy of Amanda Muzquiz.

IVPP V 13156 has three primaries that are not complete and cannot be easily reconstructed—9, 8, and 3. Proximally, the 8th and 9th primaries have been weathered or prepared away, making the determination of exact length difficult. The 8th primary is likely between 250 and 275 mm long, based on specimens, such as STM13-45, which indicates that the 6th, 7th, and 8th primaries are approximately the same length (Fig. 19B). The 9th primary is significantly shorter, likely between 200 and 225 mm long. The 3rd primary, which has lost a significant distal portion, was likely between 175 and 200 mm long (Fig. 14A–B).

The exact function of the shortened 10th primary is unknown. In modern birds, the alula, or bastard wing, is comprised of short, asymmetrical feathers that attach to the vestigial thumb of the bird. The alula itself sits slightly above the airfoil formed by the wing and is separately mobile from the primary airfoil, which would be impossible for a shortened 10th primary (Meseguer et al., 2005). *Confuciusornis* lacks an alula, however, the shortened 10th primary did not likely serve the same function as an alula.

Tail feathers of Confuciusornis

Confuciusornis tail feathers maintain a relatively constant width until the appearance of barbs, after which the central shaft tapers very rapidly down to the width of a normal rachis (see Fig. 5C). The central shaft in this area of rapid tapering also has more structure and complexity than the more proximal areas (Fig. 5). In contrast, modern bird tail feathers—even those that are modified—have a rachis that tapers gradually towards the distal end. Even in highly modified tail feathers, such as those of motmots or peafowl, the barbless region tapers at a fairly constant rate (see Fig. 2B, C).

The pygostyle of STM13-33 is not well preserved, however, the feathers surrounding it are exceptionally well preserved. Although there is no evidence for a true tail fan, there are long feathers that clearly insert along the pygostyle and the free caudals (Fig. 12). Some of these feathers, especially the most distal tail puff feathers, may be as long as 4 cm. These tail puff feathers overlap the long, paired retricies in STM13-33 (Fig. 12A). Other specimens, including IVPP V13156 and STM13-45, show evidence of longer tail puff feathers with or without paired elongate tail feathers (Fig. 12B, C). This tail puff likely served an aerodynamic purpose, although there is only a small likelihood that these feathers were used in the same manner as a tail fan.

The enigmatic, elongate tail feathers of *Confuciusornis* are long, rachis-dominated tail feathers. The pseudo-cross section is similar to that of a rachis-dominated tail feather from a modern bird (Fig. 6). When compared to a plumbaceous feather with barbs, however, the feather lacks real topography and complexity (Fig. 6). The internal morphology of the tail feathers of *Confuciusornis* is comparable to the internal structure of the rachis-dominated *Pavo* tail feathers. *Pavo* tail feathers, however, have many small, residual barbs that line the proximal edge of the large rachis, and possess large barbs for most of the rest of the feather length. *Confuciusornis* does not appear to have barbs until the distal-most 4–6 cm (Fig. 23). The frayed edge of a proximal portion of one tail feather of IVPP V 13156 may represent residual barbs, however, this type of structure is not seen elsewhere on the feather, nor has it been found in any other *Confuciusornis* specimens examined in this study. The more likely explanation is that part of the outer wall of the rachis was damaged, and the keratin frayed naturally.

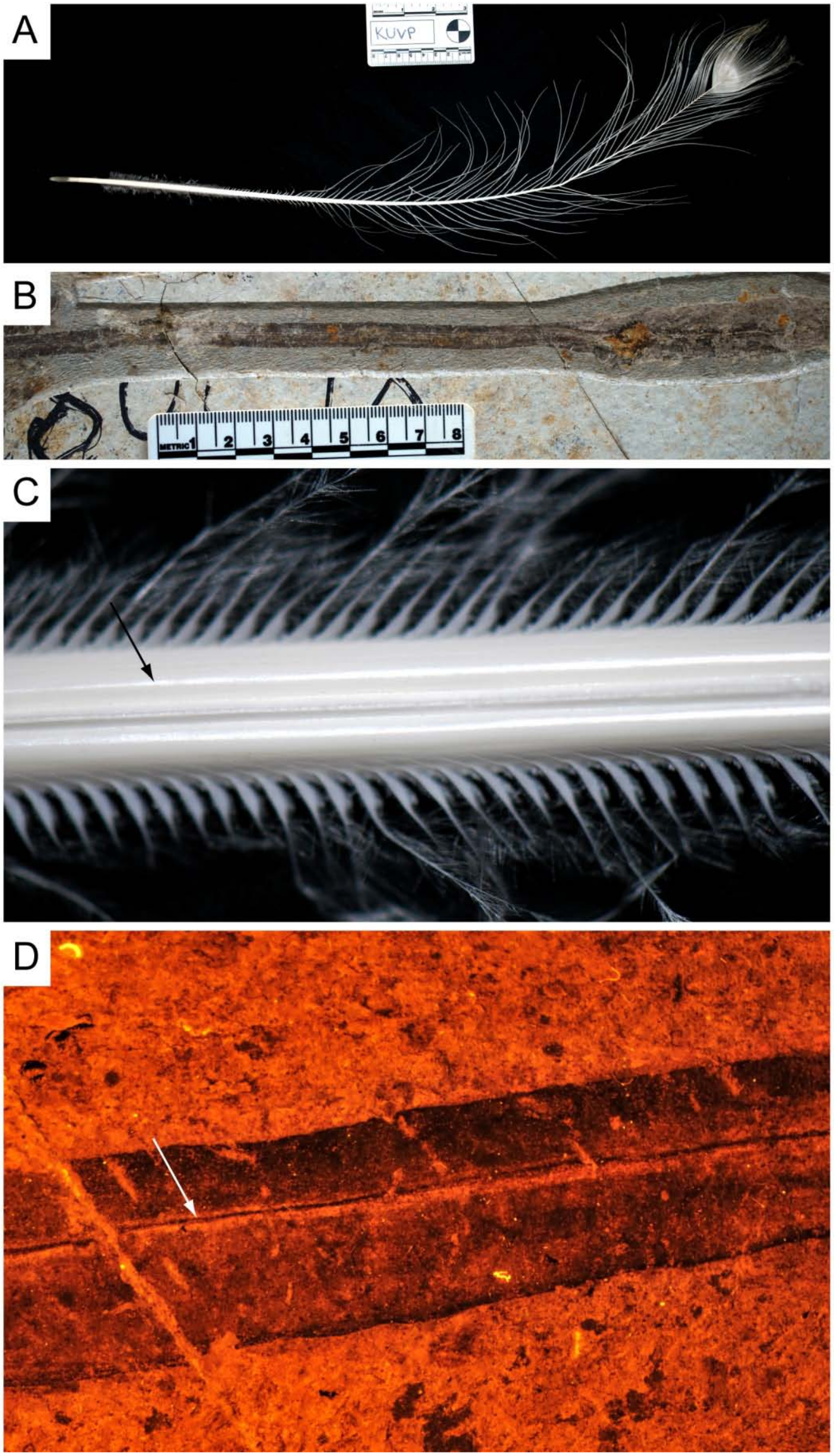

Fig. 23: Photographs directly comparing *Confuciusornis* and peacock tail feathers. A.) Complete peacock tail feather. B.) Complete *Confuciusornis* tail feather. C.) Close up of the rachis in A. Note large medial groove indicated by

arrow. D.) Close up of the proximal portion of the rachis of a *Confuciusornis* tail feather (IVPP V13156). Note the medial groove indicated with an arrow and its similarity to C.

The type of rachis-dominated feathers of *Confuciusornis* is surprisingly common in Mesozoic birds, including *Liaoningornis* and *Cathayornis* (Zheng, 2009). Some enantiornithines (e.g., *Dapingfangornis*, *Paraprotopteryx*) have tail retricies very similar in morphology to those found in *Confuciusornis* (Li et al., 2006; Zheng et al., 2007). They are also found in some maniraptorans (e.g., *Epidexipteryx*) (Zhang et al., 2008). *Liaoningornis* is unusual in that it is an ornithurine bird (Hou, 1997). There is a distinct possibility that this rachis-dominated morphology with the barbs restricted to the distal end, and a rapid taper of the large rachis down to what would be considered a normal-sized rachis, may be primitive, as this morphology is seen only in *Confuciusornis*, *Paraprotopteryx*, and *Dapingfangornis*, all of which are relatively primitive birds. *Liaoningornis* is more advanced than these other birds, and the barbs extend relatively further up the large rachis, and the taper is much more gradual than that seen in *Confuciusornis* (Fig. 24).

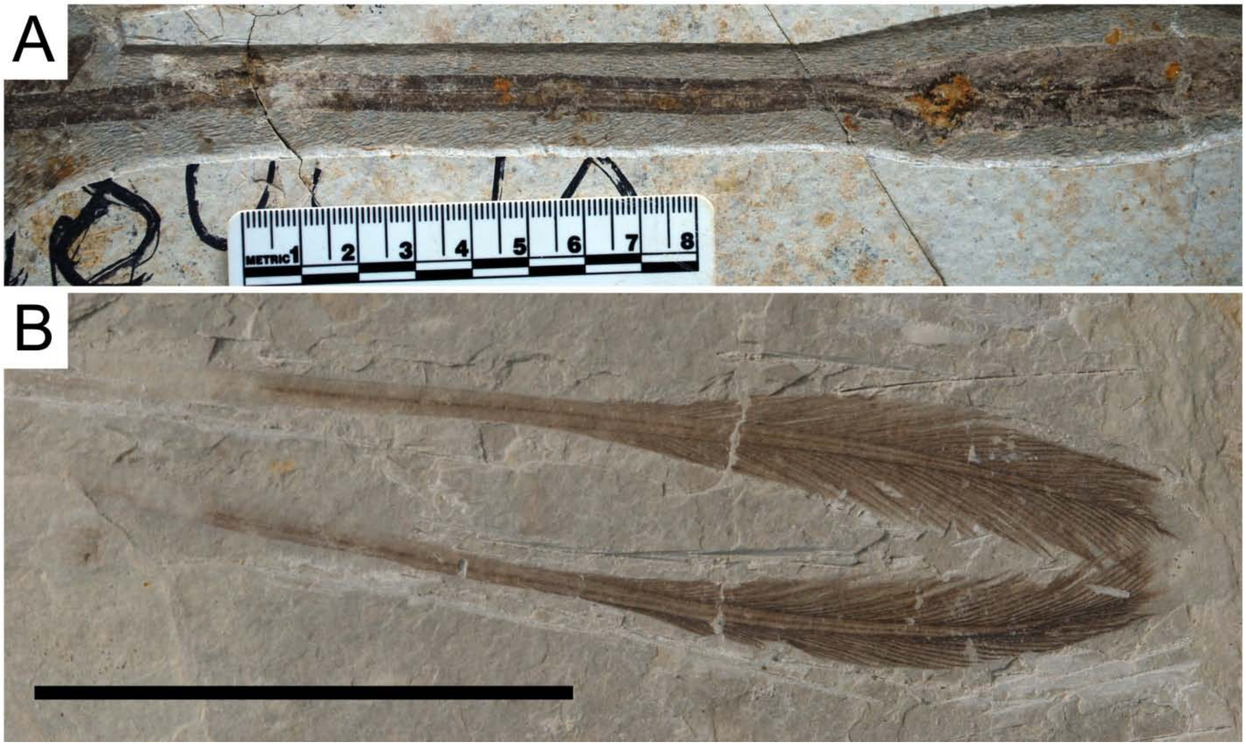

Fig. 24: Photographs of tail feathers of *Confuciusornis* and *Liaoningornis*. A.) *Confuciusornis*, IVPP V13156. B.) *Liaoningornis*, STM 34-7. Scale bar approximately 2 cm.

Comparison with previous interpretations of Confuciusornis *plumage and taphonomy*

There have been multiple studies that have discussed the presence of melanosomes in Mesozoic Chinese fossils (e.g., Li et al., 2010), and some have discussed melanosomes in *Confuciusornis* (e.g., Zhang et al., 2010). A recent study on the plumage coloration of *Confuciusornis* by Wogelius et al. (2011) used a trace metals-based interpretation on plumage coloration. A specimen of *Confuciusornis* was taken to a synchrotron rapid-scanning x-ray fluorescence facility and scanned, and a trace elemental map was produced of the specimen. Based on their methods, they interpreted areas of dense copper concentration as darker pigmented. This resulted in plumage reconstruction in which the distal primary feathers were pale, and there was a gradational shift towards darker colors proximally. They also suggested a strongly melanized (dark) body, and in the secondaries, however, primary coverts, secondary coverts, and portions of the proximal secondaries were pale, as were the distal primaries.

The plumage coloration seen in STM 13-33 strongly contradicts the plumage interpretation suggested by Wogelius et al (2011). STM13-33 preserves coloration patterns, especially in the secondary coverts (Fig. 13). There is no evidence of gradational change in the secondaries from light to dark. The primaries are monochromatic, and appear to be similar in color to the secondaries, which suggests that the interpretation of a color shift between primaries and secondaries is incorrect. Furthermore, within the contour feathers of STM 13-33 there are multiple colors within each feather, which indicates that testing for plumage coloration using a single data point source (or even multiple points) within a single feather may not represent the entirety of the feather itself (see Manning et al., 2013 for this method). The tail puff feathers of STM 13-33 are darker on the edges and paler in the middle (see Fig. 12A), and the greater secondary coverts show a similar pattern. The secondary coverts also show a pattern where the distal ends of the feathers are extremely dark. This is in direct contrast to the reconstruction suggested by Wogelius et al (2011), in which no mention of this type of spotted pattern is made.

McNamara (2013) discussed the possibility of taphonomic alteration of color-preserving molecules in feathers. She points out that dark visual tones in feathers do not always correspond to a high abundance of melanosomes, and do not necessarily correlate with the mode of melanosome preservation—furthermore, the chemical structure of the chromatophore and how it responds to taphonomic changes are unknown in feathers. She also states that fossil melanosomes vary in their mode of preservation, and, therefore, that those melanosomes that can only be identified by their shape and appearance are subject to modification by temperature and pressure during lithification. McNamara (2013) also discussed the chemical identification of plumage coloration, and suggested that distribution of trace elements in fossils may result from taphonomic modification of any original coloration. She also suggests that these trace elements may have been derived from sources other than melanin, including external sources such as sedimentary particles.

Jiang et al. (2014) reported that the soft tissues of *Confuciusornis* specimens were preserved as charred carbon remains of feathers, and that these specimens were likely caught in a pyroclastic flow and deposited in the lakes during a volcanic eruption. Some specimens of *Confuciusornis*, especially those with relatively poorly preserved plumage, may be preserved in this manner, however, this method of preservation would burn away much of the soft tissue and fine details (e.g., plumage color, scale patterns). Specimens such as IVPP V 13156, STM 13-33 and STM 13-45, which preserve excellent plumage with barbules and/or color patterns, as well as extensive soft tissues including scales and muscle, are unlikely to have been caught in a pyroclastic flow. More than one type of preservation style contributed to the excellent preservation seen in Jehol Group specimens.

Soft-tissue reconstruction

Large phalangeal pads and small interphalangeal pads in arboreal birds facilitate grasping (Chapter 2). The presence of large, fleshy phalangeal pads is a strong indication that *Confuciusornis* was indeed an arboreal bird. *Confuciusornis* likely did not possess the same type of scale pattern seen in many modern aboreal birds, including passeriform birds which possess both scutate and reticulate scales on the tarsus and toes, and instead possessed a reticulate-only scale pattern on the foot (Proctor and Lynch, 1993).

This pinkish halo is interpreted to be skin and/or muscle. Avian skin has a network of dermal smooth muscles (*musculi nonstriati dermatis*) (Clark, 1993) and, therefore, the pinkish halos surrounding the tibiotarsi may represent surficial muscle or deep tissue mass. The tibiotarsal halo likely represents the remains of the *m. gastrocnemius*, the main muscle of the lower leg, and associated tendons. The *m. gastrocnemius* of *Confuciusornis* does not appear to be particularly robust—extrapolation of the outer edge of the muscle through the prepared area suggests the maximum thickness of the halo was only slightly thicker than that of the tibostarsus itself (Fig. 16A), or slightly >5.82 mm. The *m. gastrocnemius* of ground birds is more robust than that of perching birds (Earls, 2000), further providing evidence that *Confuciusornis* was an arboreal bird.

The muscles of the femur were either not preserved or have been prepared away. The femur was a freely moving limb element and was not bound to the body wall with muscle as in modern birds, based on hindlimb proportion (see Chapter 3) and the lack of an antitrochanter on the pelvis (Fig. 25). This is consistent with other primitive birds, including *Sapeornis* and some primitive ornithurines.

Fig. 25: Pelvis of *Confuciusornis* (IVPP V 13168) under laser fluorescence, showing lack of antitrochanter. Arrow indicates where trochanter should be found.

Ulnar quill knobs are small projections of bones formed on the ulna that serve as attachment points for secondary feathers, and are formed by increased strain on the ligamentous connection between the secondaries and the ulna (Edington and Miller, 1942). Ulnar quill knob prominence may be related to the development of the muscles within the postpatagium. *Confuciusornis*, like almost all modern birds, has 10 primaries. The exception to this rule is the 9-primary oscine birds, which have reduced the outermost primary, and some have lost it entirely (Suzanna and Hall, 2005). When distal feathers are well preserved and do not overlap (e.g. IVPP V 13156 and STM13-45) a feather count for both primaries and secondary feathers is easy;

however, when the feathers overlap, counting feathers based on proximal rachises can be difficult. A feather count based on the calami within the postpatagium may be possible in some cases, however, there are also difficulties associated with this method. Secondaries are relatively easy to count based on calami within a patagium, as the smaller rachis of the secondary covert directly overlies the rachis of the secondary feather itself (Fig. 26). The greater primary covert rachis, however, is approximately the same size as the primary feather rachis, and inserts directly next to it, not above it, making a true feather count nearly impossible.

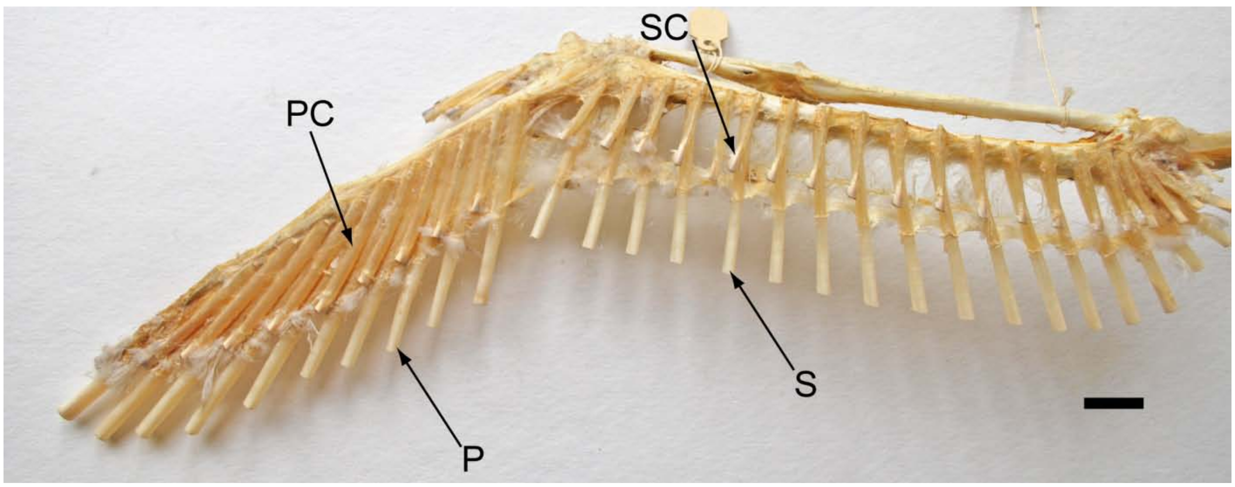

Fig. 26: Photograph of a modern avian wing showing placement of primary and secondary cover calami. P=Primary, S=Secondary, PC=Primary coverts, SC=Secondary coverts.

Birds posses both a propatagium and a postpatagium (Clark, 1993)—flaps of skin on both the front and the back of the wing. Specimens STM13-39 and IVPP V 13156 both preserve postpatagium (Fig. 8, 16C). IVPP V 13156 also preserves the propatagium of the wing, visible under laser fluorescence (Fig. 16D). The propatagium is the important lift-producing structure in the proximal portion of the avian wing (Brown and Cogley, 1996). The function of the postpatagium in birds is less well understood, but is the site of insertion of the primaries and secondaries—the main flight feathers. Deep insertion of flight feathers is necessary, so that the forces associated with powered flight do not cause the feathers to twist and distort the pattern of airflow. The depth of the postpatagium is likely as a result of the aerodynamic forces that act upon the primary feathers (Fig. 26).

The pinkish halo around the distal portion of the pyogstyle (Fig. 16B) as well as the dark area around the distal portion of the pygostyle of STM13-39 (Fig. 17) is similar to soft-tissue structures associated with the pygostyle in modern birds. The first is the knot of muscle, the *M. bulbi retricium*, into which the tail fan inserts (e.g., Vanden Berge and Zweers, 1993). The paired tail feathers of *Confuciusornis* (which does not possess a tail fan) would require a deep and muscular insertion similar to the *m. bulbi retricium* in modern birds. The longer tail puff feathers of *Confuciusornis* may insert alongside the elongate tail feathers (Fig. 12), although many of the puff feathers appear to insert cranial to the pinkish halo. A second possible explanation is that the pinkish halo does not represent muscle tissue but rather a gland. In general, bird skin lacks glandular tissue, however, birds do posses a large oil gland—the uropygial gland—on the uropygidum (the fleshy tail mass) with which they keep their feathers waterproof (Clark, 1993). This pinkish halo may represent a uropygial oil gland, with which *Confuciusornis* kept its feathers waterproof.

Confuciusornis life habit, flight ability, and evolutionary implications

The feet and hindlimbs of *Confuciusornis* are informative about its life habit. The foot morphology of *Confuciusornis* —including large, highly recurved pedal claws, a fairly robust, reflexed hallux, large phalangeal pads, and reduced interphalangeal pads—reflects that of typical extant arboreal birds. *Confuciusornis*, furthermore, has a relatively small tibiotarsal muscle complex (specifically *m. gastrocnemius*), which is more typical of arboreal birds (Earls, 2000) that have enlarged the digit flexors, not the gastrocnemius.

The presence of only reticulate scales on the feet and tarsometatarsus is difficult to interpret, as only the underside of the foot is preserved. The dorsal side of the foot may have had scutate scales, however, it is still embedded in the matrix. The feet of IVPP V 13168 also have scales and (Fig. 15E, F) appear to be reticulate as well, although they disarticulated. Many modern birds have scutate or scutate-reticulate scaled feet, however, many modern birds also possess reticulate-only scaled feet (Homberger and Brush, 1986; Proctor and Lynch, 1993, p. 74). The function of the reticulate-only scaled feet of *Confuciusornis* is not understood at this time, however, an area covered with reticulate scales is more flexible than an area covered with scutate scales (Brush, 1985). Although there is some evidence that reticulate scales on the feet of birds have evolved multiple times (Brush, 1985), a reticulate-only scale pattern may represent the primitive condition.

Previous interpretations of *Confuciusornis* flight ability have been based on two assumptions: 1) The primaries are extremely long relative to the arm and that the outermost primary is the longest; and 2) The rachises of the primary feathers are thin and weak. Others have rebutted the weakness of the primary rachises (Paul, 2010; Zheng et al., 2010), and our data support the refutation of the original interpretation of weak primaries. The primaries of *Confuciusornis* were strongly robust, with rachis widths comparable to modern birds. Furthermore, the wing shape of *Confuciusornis* was not the highly swept back, pointed wing of a fast-flying bird; rather, the wing was much broader and rounded. The secondaries of *Confuciusornis* were long, unlike the secondaries of modern fast-flying birds, which are relatively short compared to the outermost primaries (Fig. 7, 20, 22). The secondaries of

Confuciusornis, however, are still much shorter than the primaries. The keel of *Confuciusornis* has been reconstructed as small and restricted to the caudal half of the sternum (Zhou and Farlow, 2001). The keel of *Confuciusornis* is certainly small and is not deep, however, the caudal margin of the sternum may be more sharply angled than previously interpreted, and the keel may be more expanded cranially (Fig. 27).

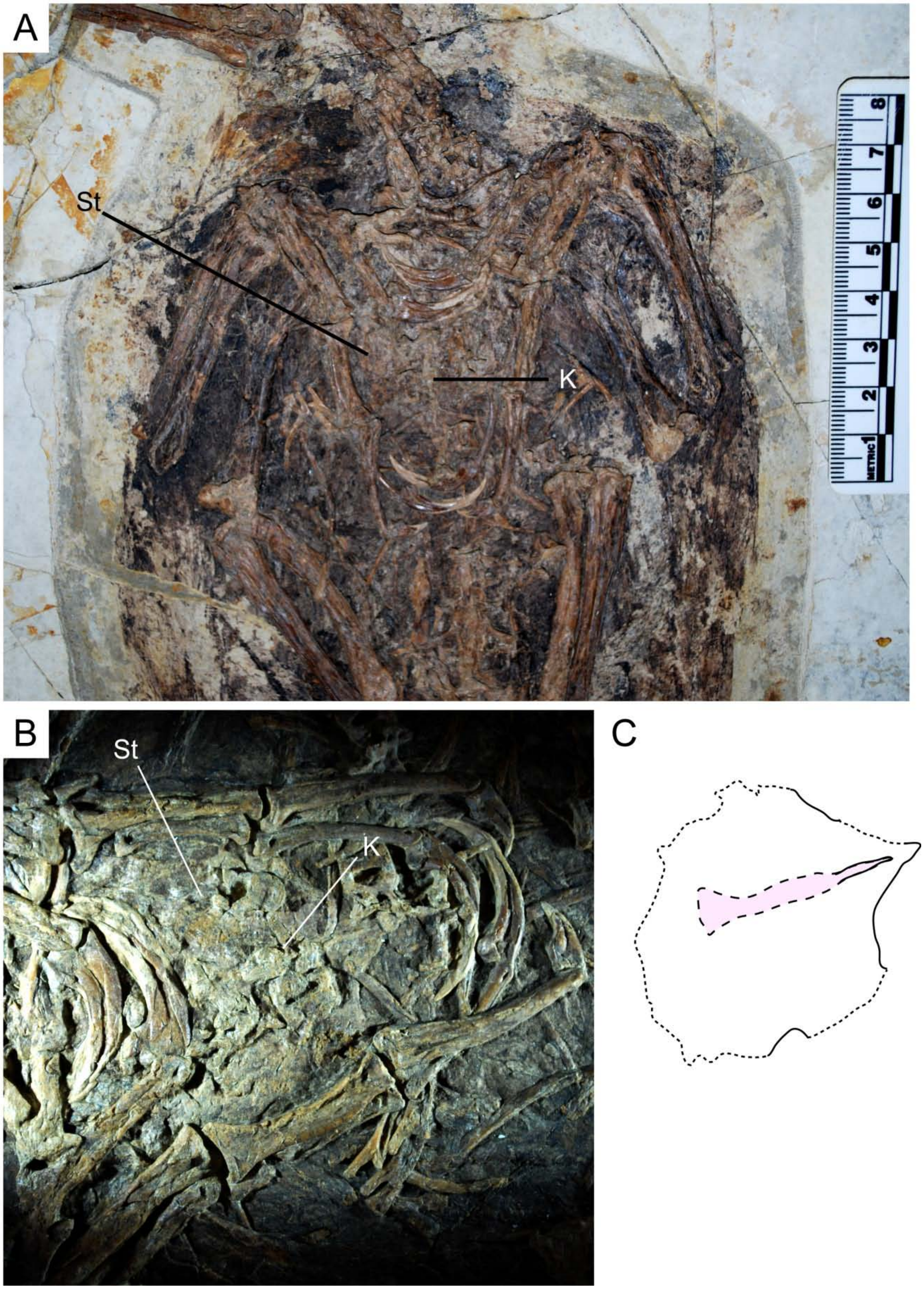

Fig. 27: Photograph and line drawing of the keel of IVPP V 13175 (1). St=sternum; K=keel. A.) Abdomen of the specimen; note the forelimbs are crossed over the chest obscuring portions of the sternum. B.) Sternum under LED

cross-lighting. Note the ridge of bone that is continuous from the caudal margin of the sternum to beneath the bones of the hand. C.) Line drawing of the sternum in B.

The presence of unlar quill knobs suggests that there was a significant amount of force being placed on the flight feathers. The combination of a robust propatagium, deep postpatagium, and long primaries and secondaries that form a relatively round, broad wing shape suggest that *Confuciusornis* had little difficulty with powered flight. Despite the fact that *Confuciusornis* lacked an acromion process (on the scapulacoracoid), it certainly had the ability for powered flight based on the presence of an ossified keel (Zhou and Farlow, 2001); however it did not possess the same upstroke as found in modern birds. The interpretation of the environment surrounding the lacustrine deposits of the Lower Cretaceous Jehol Group (e.g. Zhou, 2006) suggests that the area was densely forested; however, although the wing of *Confuciusornis* is significantly rounder than previously interpreted, it is still extremely long relative to the body. The calculated aspect ratio of the wing of *Confuciusornis* is between 6.7 and 7.2—the aspect ratio of Passeriform birds varies between 6 and 9 (Greenewalt, 1975), and many other birds have an aspect ratio between 6 and 7.5, with the notable exceptions of seabirds (e.g., Albatross, gulls, terns), shorebirds, and long-duration fast-flying birds (e.g., swifts) (Savile, 1957). Whether *Confuciusornis* was highly maneuverable or capable of soaring cannot be identified from the aspect ratio calculated here—however, *Confuciusornis* was not a long-duration fast flyer, and did not have a flight style similar to that of swifts. The exact flight style and method that *Confuciusornis* used is still unclear, and only an in-depth analysis of the shoulder girdle, forelimb morphology, wingshape, and aerodynamic modeling will begin to clarify this mystery.

CONCLUSIONS

Use of a 447nm blue laser and a combination of yellow and orange longpass filters in a new method of laser fluorescence has highlighted previously unknown soft-tissue structures in *Confuciusornis sanctus*. These structures include scales, areas of skin and/or muscle, and internal feather anatomy. The tail feathers of *Confuciusornis* consist of (1) a tail puff, composed of slightly elongated contour feathers, and (2) paired rachis-dominated feathers with barbs restricted to the distal portion. Similar rachis-dominated tail feathers are seen in some maniraptorans and enantiornithines. In enantiornithines, some birds possess a rachis-only portion smaller than that of *Confuciusornis* and the area containing barbs is relatively longer. Some enantiornithines (e.g., *Dapingfangornis*, *Paraprotopteryx*), however, have tail retricies very similar in morphology to those found in *Confuciusornis*.

The hindlimb soft tissue consists of scales and skin and/or muscle outlines present in specimen IVPP V 13156 and IVPP V 13168. The scales of *Confuciusornis* are reticulate, with no evidence of scutate scales. *Confuciusornis* also possesses enlarged phalangeal pads, whereas the interphalangeal pads are reduced. This morphology is typical of arboreal birds (also see Chapter 2). The outline of the hindlimb musculature is also mostly preserved, mainly the tibiotarsal musculature (specifically the *m. gastrocnemius*). This musculature is not robust, further supporting the interpretation of *Confuciusornis* as arboreal. *Confuciusornis* had a hand completely encased in postpatagium, identical to modern birds. The propatagium is also well developed, indicating a strong aerodynamic surface from the tip of the primaries all the way to the body wall.

For the first time, an accurate count and reconstruction of the flight feathers on the forelimb of *Confuciusornis* is produced. *Confuciusornis* has 10 primaries and between 10–12 secondaries. Ulnar quill knobs are present, which have not been previously reported; however, weathering has obscured or destroyed some of the quill knobs. Feather calami are also visible within preserved postpatagium in specimen STM13-39, aiding in the feather number count. The 10th (outermost) primary of *Confuciusornis* is less than half the size of the 9th primary. The 8th and 7th primaries are the longest. This results in a rounder wing shape than had been previously interpreted. The primary feather rachises are thick and robust. The secondaries are also long, resulting a broad wing, typical of forest dwelling and/or soaring birds; previous interpretations reconstructed a narrow, tapered wing, like those of modern fast-flying birds. Furthermore, *Confuciusornis* was not as strong a flier as modern birds, had no acromion process, no triosseal canal, and did not have as deep a keel, however previous reports suggesting that *Confuciusornis* could not fly based on feather morphology were incorrect. Furthermore, an accurate color pattern of the feathers—although not the exact colors—is reconstructed as monochromatic flight feathers and primary and secondary coverts with very dark tips with lighter barbs proximally, contrary to previous reports of plumage coloration in *Confuciusornis*.

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A NEW METHODOLOGY FOR STUDYING AVIAN NEOICHNOLOGY AND THE EFFECTS OF GRAIN SIZE AND MOISTURE CONTENT ON DOMESTIC CHICKEN (*GALLUS GALLUS*) TRACKS

ABSTRACT

A new experimental setup using a collapsible wooden tray, monopod, and digital video camera is used to observe and collect modern bird tracks produced by domestic chickens *(Gallus gallus*). This setup is unique because it simultaneously captures tracemaker behavior, trace morphology, and media consistency (i.e., grain size and moisture content) all at once, and can be used in the laboratory and in natural environments. Using this setup we determined that bird track morphology varies in a predictable manner with respect to sediment grain size and the percent of water present. The finer the sediment grain size, the more detail is likely to be preserved. If the sediment is completely dry, no track details will be preserved—digit impressions will be broad and will not taper at the tips, digit impression length will be longer than the actual toe lengths. If the sediment is wet (8.8%–6.7%), the digit impressions will taper to points, will not be as wide as in dry sediment, and will not preserve pad impressions. If the sediment is variably moist (5.3%–3.2%), the detail of pad or scale impressions, depending on the grain size, may be present. This study also quantifies the trackway parameters of behaviors, including start-stop walking, walking, running, takeoff, and landing. We propose a sinuosity index to that allows for quantification of sinuous avian trackways. Both takeoff and landing traces are significantly deeper than the proceeding or following walking and running traces. Start-stop walking does not always result in side-by-side paired tracks, and often the bird will pause in midstride. Linking behavior and morphology of tracks can be used to better interpret ancient behavior and the depositional environment that ancient tracks were produced in.

INTRODUCTION

The study of modern bird tracks is an area largely unexplored in ornithology today. Professional trackers mainly dominate the study of bird tracks (e.g.,, Brown et al., 2003; Elbroch and Marks, 2001), and ichnologists rarely perform neoichnological studies in an attempt to use modern trackways to interpret ancient trackways and the behavior that produced them (e.g., Farlow, 1989; Genise et al., 2009). The purpose of this paper is to present a new experimental setup for studying avian traces, media consistency, behaviors, and tracemakers simultaneously that objectively links tracemaker, behavior(s), and the trace(s) produced. This paper also explores the effect of media grain size and moisture content on track and trackway morphology. The objective of this research is to initiate the first steps in filling the gap that currently exists between ornithology and avian neoichnology to improve our understanding ancient avian behavior as record by tracks.

The Dutch Wadden Sea has been the source of multiple avian neoichnological studies. Swennen and Van Der Baan (1959) performed an early study on modern bird tracks and traces in which multiple types of feeding traces were observed. Multiple types of probe marks were reported, along with scythinglike traces from Shelducks, trampled hollows from gulls, and traces of Turnstones rolling over rocks to find prey. There were also purported swimming traces of a Shelduck (Swennen and Van Der Baan, 1959, fig. 7a). Cadhee (1990) also reported trampling by gulls in the Dutch Wadden Sea, but also discusses Shelduck trampling. His research focused more on sediment reworking and bioturbation than the previous study, and there was no mention of other Shelduck feeding behaviors (e.g., scything), or other avian feeding behaviors (e.g., probing or pecking).

Farlow (1989) produced the earliest modern neoichnological study on bird tracks in comparison to dinosaur tracks. He attempted to compare ostrich (*Struthio camelus*) track and trackway morphology and production to theropod dinosaur tracks and trackways. This study examined depth of the tracks, stride length, footprint length, step (i.e., pace) angle, and pace length. Farlow (1989) candidly admitted, however, that he "made no systematic effort to investigate ostrich footprint morphology as a function of gait or substrate conditions." He did make key observations about the acceleration of the ostrich, impression of the footprints (specifically depth), and direction of travel. This was first attempt to apply morphometric analyses to modern bird trackways that are commonly used for studying fossil trackways.

Genise et al. (2009) attempted to erect clear and concise categories of traces produced by shorebirds and the behaviors that resulted in them, and compare them to Eocene–Oligocene tracks from the Santo Domingo Formation of Argentina (Melchor et al., 2013). Such behaviors included walking, standing, lateral running, and different methods of landing and takeoff (Genise et al., 2009, fig 7, pg. 150–151). There are, however, no photographs provided of the traces produced by these behavior, only line drawings. No morphometric quantification of these behaviors in the form of single track (e.g., toe length, foot length, foot width, angle of divarication, Fig. 1) or trackway measurements (e.g., stride length, pace length, pace width, see Fig. 1) was provided on the modern tracks. These types of measurements are often performed on fossil tracks and trackways (e.g., Kim et al., 2006; Lockley et al, 2009; Falk et al., 2010). Some of these measurements, however, were provided for the fossil tracks used by Genise et al. (2009) in de Valais and Melchor (2008, table 1, pg. 148).

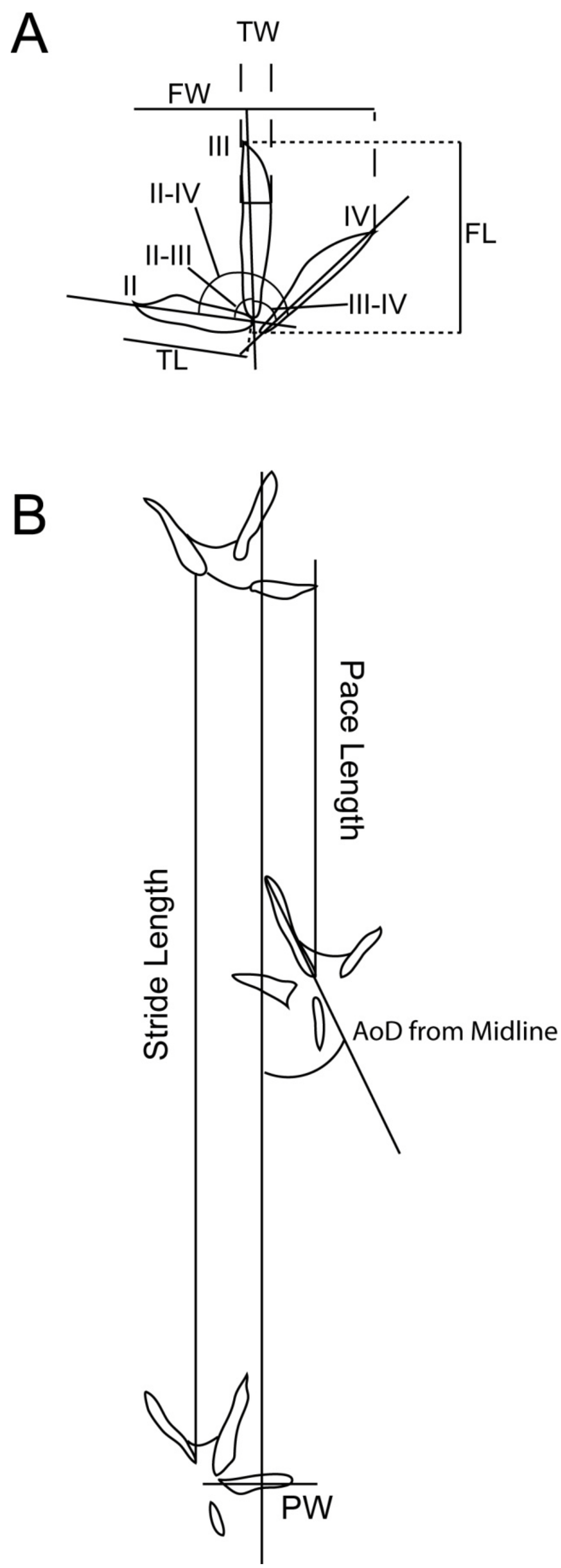

Fig. 1: All measurements taken on bird tracks collected. AoD=Angle of divarication. II=Toe II, III=Toe III, IV=Toe IV, II-III= AoD between toes II and III, III-IV=AoD between toes III and IV, II-IV=AoD between toes II and IV,

TL=Toe length, TW=Toe width, FL=Foot length, FW=Foot width. A.) Single-track measurements taken on all tracks. B.) Trackway measurements used in this study. Note AoD from Midline was not taken on sinuous trackways.

Melchor et al. (2012) applied a similar approach to Miocene bird tracks from Argentina. These tracks were webbed and attributed to a flamingolike bird. They observed modern flamingos feeding in a shallow pond and measured angle of gate, length of the tarsometatarsus (from the photographs), and pace length (Melchor et al., 2012). Other unique measurements used in this study include medial width (between toe II and toe III) and lateral width (between toe III and toe IV). They also used oblique pace instead of the standard pace length (see Melchor et al., 2010, fig. 2). They then measured pace length of the walking and feeding birds from video footage, and measured pace length relative to tarsometatarsal length.

Some ichnological studies (e.g., Currie, 1981; Frey and Pemberton, 1987) did not primarily focus on avian neoichnology, but did provide some information on the subject. Currie (1981) briefly discussed the variation in the angle of divarication between different types of birds; however, the focus of the paper was a new ichnogenus of Cretaceous bird track from North America (*Aquatilavipes*). Frey and Pemberton (1987) examined a present day *Psilonichnus* ichnocoenosis, a suite of invertebrate traces used to identify certain depositional environments. Included in this study were photographs of peck marks of shorebirds (Frey and Pemberton, 1987, fig. 13).

Detailed neoichnological experiments have been carried out in the laboratory, although this is generally performed with invertebrates (e.g., Elders, 1975; Smith and Hasiotis, 2008; Counts and Hasiotis, 2009; Halfen and Hasiotis, 2011). Detailed neoichnological laboratory experiments with vertebrates are more rare. These experiments, however, are usually done with small lower vertebrates (e.g., amphibians, reptiles) (e.g., Brand, 1996; Hembree and Hasiotis, 2007). Experiments using bats have recently been performed (Jones and Hasiotis, 2012), however, very few studies use controlled conditions with larger vertebrates. Milan and Bromley (2007) performed controlled experiments with a severed emu foot using cement containing different amounts of water. They then sectioned each track to examine the track and undertrack morphology.

With few exceptions (e.g., Melchor et al., 2012), the majority of avian neoichnological studies lack quantitative analysis. This is contrary to the methodology performed on fossil bird tracks, in which a series of measurements are performed (e.g., Lockley et al., 1992, 2006). The experimental setup presented here links the simultaneous recording and collecting of modern bird tracemaking behavior to specific media conditions, which allows observation of how track morphology and behavior changes with media consistency and grain size. Using this data, quantification of traces and behaviors produced by modern birds is now possible, which can then be applied to fossil bird tracks and trackways for more accurate descriptions and interpretations of behavior and paleoenvironment.

MATERIALS AND METHODS

The majority of the research was performed with domestic chickens (*Gallus gallus*) on a farm north of Lawrence, Kansas. Several different individual chickens of differing size and breed—mostly cross-breeds and bantams, specifically Silver Sebrights—were used in this experiment. A brief run was also performed at a bird feeder on private property in Milan, Michigan, U.S.A., using Mourning Doves (*Zenaida macrocura*); however, no plaster casts were made and no data was analyzed. The setup was placed inside a chicken pen, sediment and (when necessary) water were added to the tray, and the camera turned on. The door was opened until at least one chicken entered the pen, then the door was shut and the setup abandoned. During the experiment using chickens, the researcher stood several yards away, out of the birds' direct line of sight, to avoid influencing the behavior of the birds. During the experiment conducted in Michigan, the observer waited in a nearby house so as to not disturb or influence the birds.

The experimental set up is composed of several pieces (Fig. 2). A foldable wooden tray 123 cm long by 72 cm wide and 4 cm deep, built in two equidimensional sections, and hinged together at the midpoint, so that it can be easily folded, carried, and transported by car. The tray was painted with a water-resistant, latex paint. On one side of the tray, two holes are drilled for a monopod attachment using threaded bolts, washers, and wingnuts (Fig. 2B). The monopod has two components, vertical (106 cm) and horizontal (35.5 cm) (Fig. 2B), with a tripod head bolted onto the end of the horizontal component (Fig. 2C). A Sony Handycam© digital camcorder was mounted onto the tripod head, however, any camera including small, high-definition sports cameras, can be used. The digital camcorder was adjusted to face the tray at a 90º angle. The entire experimental setup takes <15 minutes to assemble and can be used in a laboratory setting, a controlled outdoor setting (e.g., aviary or coop), or a natural environment (e.g., lake shore, pointbar, sand bar, etc.). The monopod can be used separately from the tray by inserting it into the ground directly, for use in natural environments where the researcher does not want to potentially change the properties of the media (e.g., pointbars, beach).

Fig. 2: Photographs of the tray during setup and completed use. A.) The tray, unfolded. B.) The tray, folded. C.) The monopod separated from the tray, showing separate components. D.) The tripod head and its positioning on the monopod. E.) The tray and its plastic dropcloth covering.

After the tray and monopod were assembled, a sheet of plastic drop cloth was laid over the tray and folded under each edge (Fig. 2D). The plastic lining is intended to prevent any water leakage from the hinge joint in the bottom of the tray. Sediment was then added to the tray. When necessary, water was added to the sediment. The media was then smoothed out with a piece of wood, a plastic door sweep, or a squeegee to create an even surface for track production.

In this study, five sediment grain sizes were used: coarse sand (phi=35), medium sand (phi=60), fine sand (phi=120), mixed coarse and fine sand (phi=35-120), and mud collected from either the Kansas River, Clinton Lake outside of Lawrence, Kansas, USA, or purchased at a hardware store that sold sand for construction purposes. Four runs with different moisture regimes were conducted for most sediment types. For the mud runs, dry mud could not be used, so only three runs were produced. The sediment was kept in buckets between uses and allowed to dry naturally with one to two weeks (sometimes longer) between runs.

The same chicken was used multiple times in some cases (e.g., three coarse sand runs, two mixed sand runs), however, the chicken used depended on its willingness to leave the coop and explore the experimental setup. After traces were produced, the door to the pen was opened and the chickens left the pen, or the birds left the immediate area (e.g., the feeder). A sediment sample for moisture content analysis was taken using a Fisher Scientific glass vial immediately after the birds left. The vial and sediment were weighed, recorded, then baked for at least 24 hours to evaporate all moisture, then weighed and recorded again to obtain the percent moisture content by weight. In the mixed-sand runs, the vial caps were not properly sealed, resulting in no moisture content data for that series. Instead the moisture regimes are referred to as dry, moist, and wet. All tracks and trackways were photographed. Tracks were also cast in plaster

(DentStone®), with a few exceptions (see Results). No casts were produced for the runs using Mourning Doves.

A series of measurements were performed on the tracks and trackways on each plaster cast (see Fig. 1) using digital calipers or measuring tape for longer distances such as stride length. From these measurements the foot length:foot width (FL:FW) ratio was calculated. If no plaster cast was available, the photographs themselves were measured using the open source program GeoGebra©. GeoGebra© was also used to measure the angle of divarication (AoD) between the toes. Measurements were taken following the standard procedures for fossil tracks and trackways (see Lockley et al., 2006, 2009). In some cases, approximate track depth, usually of the distal portion of toe III, was also measured to determine if depth varies between walking, running, takeoff, and landing. Not included were several measurements used by de Valais and Melchor (2008, fig. 3; e.g., the angle of divarication (AoD) between toes I and III) and Melchor et al. (2012; e.g., oblique pace length), as they are not directly related to behavior or are not typical measurements used in avian ichnology.

RESULTS

Video of trace production is placed in supplemental data and can also be found online at (http://ichnology.ku.edu/). Media grain size and moisture content is found in Table 1. A list of all measurements taken is found in Tables 2–6

Sediment	Wet	Dry	Wet-Dry	% moisture
Coarse Sand 1	14.5	13.25	1.25	8.6
Coarse Sand 2	13.3	12.8	0.5	3.8
Coarse Sand 3	12.4	12	0.4	3.2
Medium Sand 1	15.9	14.5	1.4	8.8
Medium Sand 2	13.3	12.7	0.6	4.5
Medium Sand 3	13.7	13.2	0.5	3.6
Fine Sand 1	11.9	11.1	0.8	6.7
Fine Sand 2	13.1	12.4	0.7	5.3
Fine Sand 3	11.9	11.5	0.4	3.4
Mixed Sand	N/A	N/A	N/A	N/A
Mud 1	12	10.7	1.3	10.8
Mud 2	14.7	12.4	2.3	15.6
Mud 3	16.15	13.9	2.25	13.9

Table 1: Grain sizes and moisture contents used.

Coarse sand

Four runs using two different chickens were performed, beginning with a dry run. No plaster cast was taken from the dry run tracks. Three tracks were produced, comprising a single trackway (Table 2). The average toe III length was 57.6 mm, the average toe III width was 32.9 mm, and the average foot length:foot width (FL:FW) ratio was 0.79. The second run was wet sand (8.6% moisture); although many tracks were produced, only 7 were cast, 5 of which constituted a single trackway. The latter tracks in this trackway became slightly deformed by the plaster pour (Fig. 3), however, this only affected the toe width. The average toe III length was 56.9 mm, the average toe III width was 17.6 mm (13.8 mm without tracks 6 and 7), and the average FL:FW ratio was 0.79.

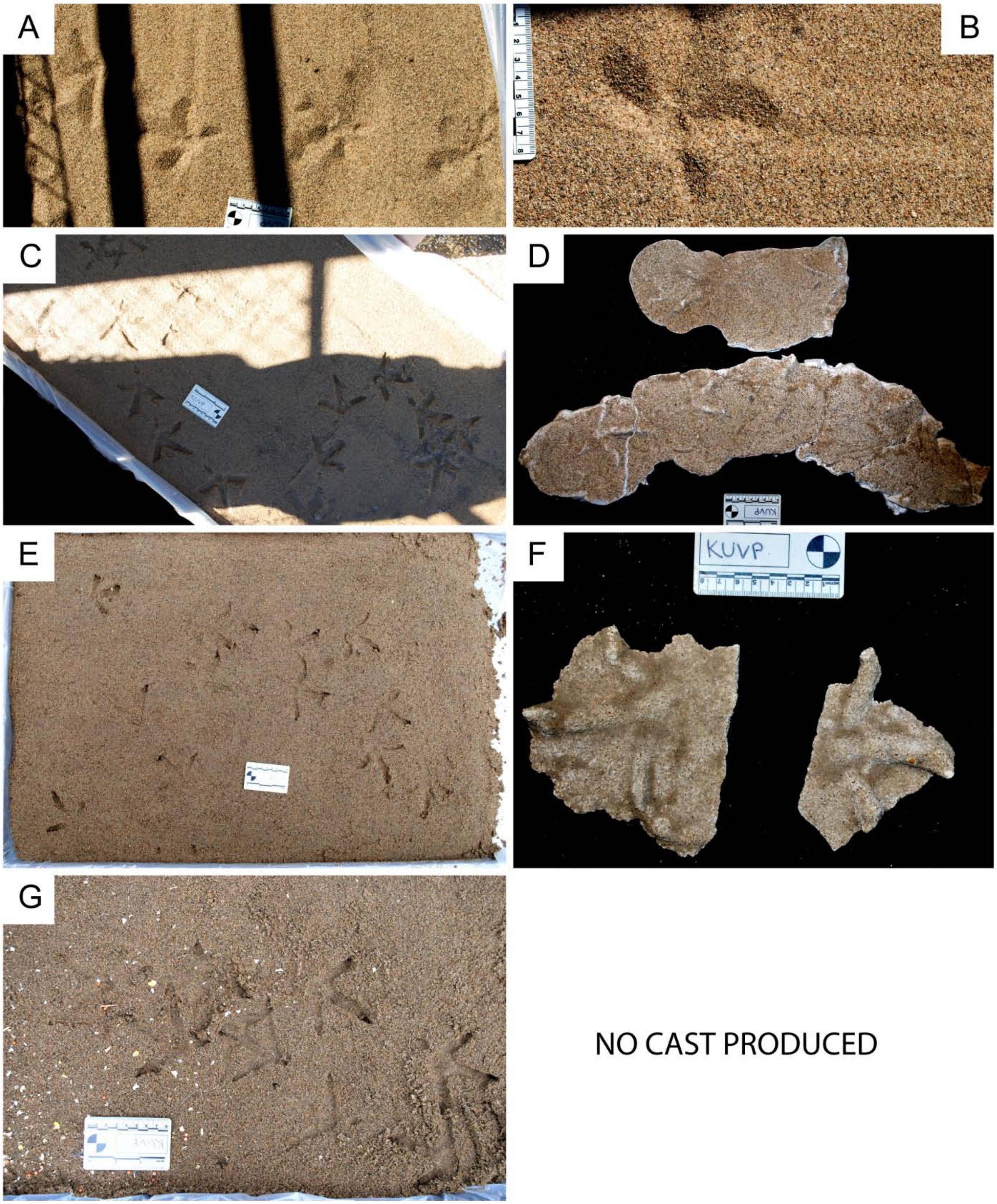

Fig. 3: Coarse sand runs, and plaster casts produced. A.) Coarse sand run, dry. B.) Close up of tracks produced in the coarse sand run. C.) Coarse sand run, wet. D.) Plaster cast produced of the wet coarse sand run. E.) First moist coarse sand run. F.) Plaster cast produced of the first moist coarse sand run. G.) Second moist coarse sand run.

The third and fourth runs were with moist sand (moisture content 3.8% and 3.2%, respectively), and the fourth run used a different chicken than the first three. This second chicken was slightly smaller than the first used. The third coarse sand run had only two tracks, with an average toe III length of 55.7 mm, an average toe III width of 16.3 mm, and an average FL:FW ratio of 0.725. The fourth run produced 6 tracks in two different trackways, and had an average toe III length of 47.7 mm, an average toe III width of 11.6, and an average FL:FW ratio of 0.84.

Coarse sand dry (Run 1)							
Track 1:	L	Toe I:	26				
		Toe II:	38.8		Pace length:	1-2:	199.4
		Toe III:	62.8			2-3:	139.1
		Toe IV:	47.1		Pace width:	1-2:	56
	W	Toe II:	29.4			2-3:	83.1
		Toe III:	32.8		Stride length:	1-3:	336.3
		Toe IV:	26.3		AoD from Mid:	1-	33.48
	AoD	II-III:	51.85			2-	12.12
		III-IV:	66.97			3-	39.77
		II-IV:	118.82				
	FL:	86.3					
	FW:	90.3					
Track 2:	L	Toe I:	30.8				
		Toe II:	42.3				
		Toe III:	51.3				
		Toe IV:	34.9				
	W	Toe II:	25.7				
		Toe III:	35.1				
		Toe IV:	28				
	AoD	II-III:	82.07				
		III-IV:	66.8				
		II-IV:	148.87				
	FL:	74.9					
	FW:	101.1					
Track 3:	L	Toe I:	N/A				
		Toe II:	61.1				
		Toe III:	58.6				
		Toe IV:	46.6				
	W	Toe II:	24.9				
		Toe III:	30.8				
		Toe IV:	29.1				
	AoD	II-III:	39.91				
		III-IV:	114.1				
		II-IV:	153.29				
	FL:	92.9					
	FW:	131.7					

Coarse sand wet (Run 2)							
Track 1:	L	Toe I:	15.78		Pace Length:	1-2:	193.57
		Toe II:	44.19			3-4:	177.04
		Toe III:	63.72			4-5:	155.72
		Toe IV:	50.38			5-6:	112.82
	W	Toe II:	11.54			6-7:	145.17
		Toe III:	15.01		Pace Width:	1-2:	35.11
		Toe IV:	13.16			3-4:	7.61
	AoD	II-III:	57.5			4-5:	8.56
		III-IV:	59.2			5-6:	19.6
		II-IV:	116.7			6-7:	46.2
	FL:	88.33			Stride Length:	3-5:	309.64
	FW:	109.94				4-6:	263.45
Track 2:	L	Toe I:	N/A			5-7:	251.12
		Toe II:	35.52				
		Toe III:	60.06				
		Toe IV:	48.59				
	W	Toe II:	14.91				
		Toe III:	11.51				
		Toe IV:	10.43				
	AoD	II-III:	52.8				
		III-IV:	82.8				
		II-IV:	135.6				
	FL:	69.96					
	FW:	99.95					
Track 3:	L	Toe I:	19.59				
		Toe II:	38.5				
		Toe III:	60.96				
		Toe IV:	42.58				
	W	Toe II:	10.32				
		Toe III:	15.59				
		Toe IV:	9.79				
	AoD	II-III:	57				
		III-IV:	79.4				
		II-IV:	136.4				
	FL:	73.48					
	FW:	103.84					
Track 4:	L	Toe I:	24.16				
		Toe II:	39.49				
		Toe III:	61.53				
		Toe IV:	41.29				
	W	Toe II:	18.61				
		Toe III:	15.77				
		Toe IV:	10.07				

	AoD	II-III:	60				
		III-IV:	59.2				
		II-IV:	119.2				
	FL:	87.56					
	FW:	94.52					
Track 5:	L	Toe I:	21.51				
		Toe II:	33.5				
		Toe III:	44.67				
		Toe IV:	41.02				
	W	Toe II:	9.81				
		Toe III:	11.36				
		Toe IV:	13.62				
	AoD	II-III:	57.6				
		III-IV:	67.2				
		II-IV:	124.8				
	FL:	61.56					
	FW:	92.69					
Track 6:	L	Toe I:	14.26				
		Toe II:	37.79				
		Toe III:	52.88				
		Toe IV:	42.36				
	W	Toe II:	20.65				
		Toe III:	28.38				
		Toe IV:	20.51				
	AoD	II-III:	64.2				
		III-IV:	41				
		II-IV:	65.2				
	FL:	88.3					
	FW:	98.03					
Track 7:	L	Toe I:	20.04				
		Toe II:	38.74				
		Toe III:	54.16				
		Toe IV:	43.57				
	W	Toe II:	20.58				
		Toe III:	25.56				
		Toe IV:	23.95				
	AoD	II-III:	64.2				
		III-IV:	71.4				
		II-IV:	135.6				
	FL:	86.13					
	FW:	104.04					

Coarse sand moist 1 (Run 3)							
Track 1:	L	Toe I:	N/A				
		Toe II:	35.3				
		Toe III:	59.62				
		Toe IV:	48.94				
	W	Toe II:	13.74				
		Toe III:	16.18				
		Toe IV:	11.29				
	AoD	II-III:	50.7				
		III-IV:	71.8				
		II-IV:	122.5				
	FL:	80.84					
	FW:	105.91					
Track 2:	L	Toe I:	N/A				
		Toe II:	34.51				
		Toe III:	51.87				
		Toe IV:	45.21				
	W	Toe II:	14.65				
		Toe III:	16.39				
		Toe IV:	10.7				
	AoD	II-III:	59.6				
		III-IV:	73.1				
		II-IV:	132.7				
	FL:	70.96					
	FW:	103.37					

Coarse sand moist 2 (Run 4)							
Track 1:	L	Toe I:	10.2		Pace length:	1-2:	140.8
		Toe II:	31.6			3-4:	122
		Toe III:	48.4			4-5:	81.6
		Toe IV:	37.2			5-6:	83.4
	W	Toe II:	12		Pace width:	1-2:	12.6
		Toe III:	13.2			3-4:	13.4
		Toe IV:	10.8			4-5:	35.4
	AoD	II-III:	50.47			5-6:	28
		III-IV:	70.62		Stride length:	3-5:	201
		II-IV:	121.09			4-6:	164.4
	FL:	73.4			AoD from Mid:	1-	15.11
	FW:	81.4				2-	<5
Track 2:	L	Toe I:	10.6			3-	9.27
		Toe II:	32.4			4-	8.44
		Toe III:	46.6			5-	5.89
		Toe IV:	38.6			6-	8.38
	W	Toe II:	11				
		Toe III:	12				
		Toe IV:	12.8				
	AoD	II-III:	50.36				
		III-IV:	71.32				
		II-IV:	121.68				
	FL:	72.2					
	FW:	86.4					
Track 3:	L	Toe I:	12.4				
		Toe II:	27				
		Toe III:	48.2				
		Toe IV:	31.8				
	W	Toe II:	8				
		Toe III:	10.2				
		Toe IV:	10.4				
	AoD	II-III:	51.5				
		III-IV:	64.78				
		II-IV:	116.28				
	FL:	74					
	FW:	74.8					

Track 4:	L	Toe I:	15				
		Toe II:	32				
		Toe III:	50				
		Toe IV:	40.6				
	W	Toe II:	10.8				
		Toe III:	10.2				
		Toe IV:	11				
	AoD	II-III:	58.89				
		III-IV:	57.89				
		II-IV:	116.58				
	FL:	71.8					
	FW:	85.4					
Track 5:	L	Toe I:	14.4				
		Toe II:	35.6				
		Toe III:	44.4				
		Toe IV:	48				
	W	Toe II:	9				
		Toe III:	12.6				
		Toe IV:	10.8				
	AoD	II-III:	55.66				
		III-IV:	55.22				
		II-IV:	110.88				
	FL:	67					
	FW:	87.2					
Track 6:	L	Toe I:	17.2				
		Toe II:	30.6				
		Toe III:	48.4				
		Toe IV:	41.8				
	W	Toe II:	11.2				
		Toe III:	11.6				
		Toe IV:	14.6				
	AoD	II-III:	42.63				
		III-IV:	74.42				
		II-IV:	117.05				
	FL:	66.4					
	FW:	87.6					

Table 2: Measurements of coarse sand runs. All measurements are in mm, unless the measurement is an angle, which are in measured in degrees. AoD from Mid is not taken on sinuous trackways. . L=Length of the toe.

W=Width of the toe. AoD=Angle of Divarication between the toes. II=Toe 2. III=Toe 3. IV=Toe 4. FL=Foot length. FW=Foot width. AoD from Mid=Angle of Divarication from Midline.

Medium sand

The same chicken was used for the dry and wet sand runs. A different chicken was used for the two moist sand runs. A third, smaller chicken joined the second chicken for the fourth run (Fig. 4).

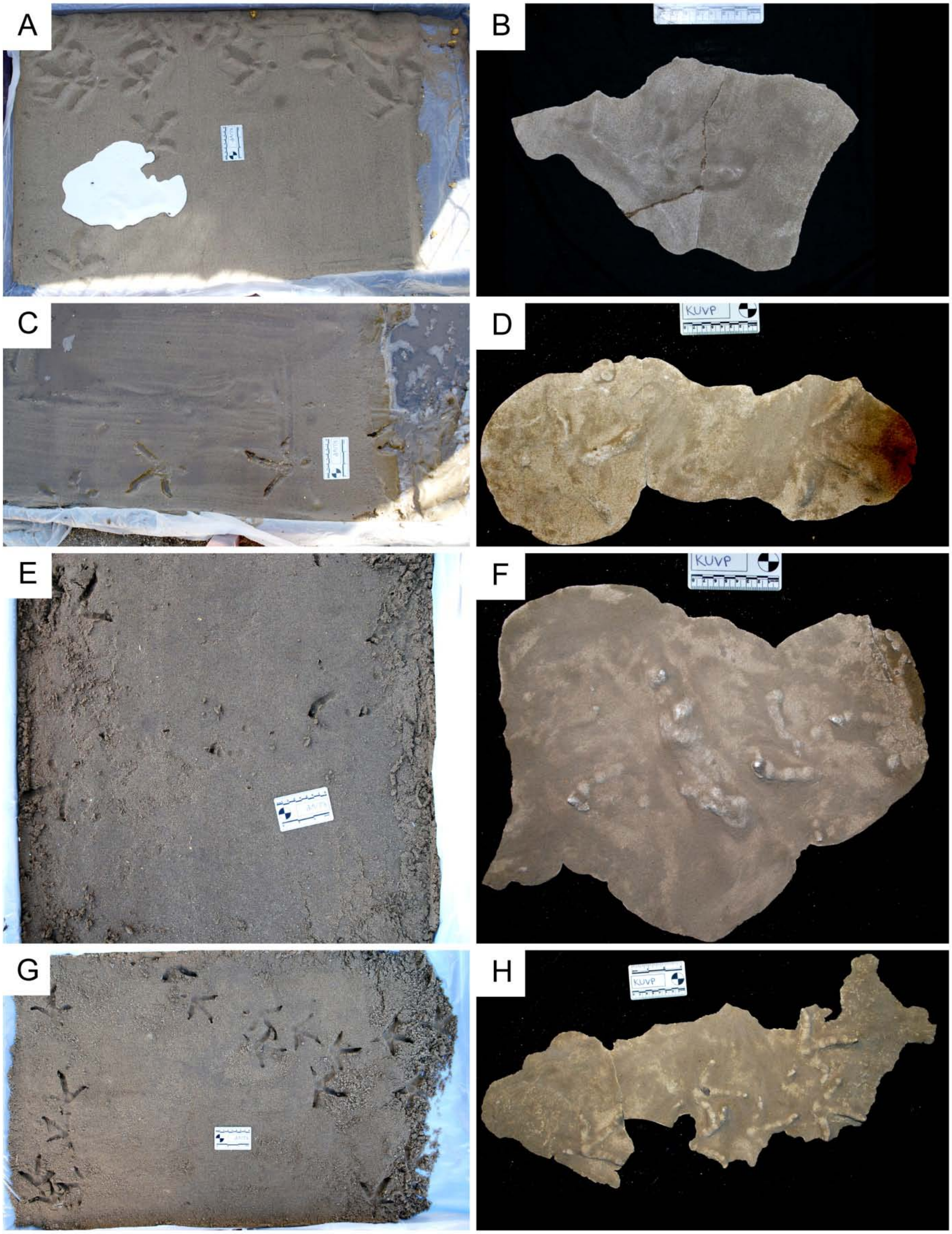

Fig. 4: Medium sand runs, and plaster casts produced. A.) Medium sand run, dry. B.) Plaster cast produced (seen in A). C.) Medium sand run wet. D.) Plaster cast produced of the wet medium sand run. E.) First moist medium sand

run. F.) Plaster cast produced of the first moist medium sand run. G.) Second moist medium sand rum. H.) Plaster cast produced of the second moist medium sand run.

Only one track was cast in the dry medium sand run. The length of toe III was 61.8 mm, the width of toe III was 38.2 mm, and the FL:FW ratio was 0.8. In the wet sand run, two tracks were measured. The average toe III length was 71.4 mm, the average toe III width was 18.8 mm, and the average FL:FW ratio was 0.75.

In the third medium sand run, there were three tracks measured from one trackway. The average toe III length was 58.3 mm, the average toe III width was 14.3 mm, and the average FL:FW ratio was 0.76. In the fourth medium sand run, six tracks were cast, however, due to multiple chickens being used, not all tracks were averaged together to compare to the third run. In the fourth medium sand run, only tracks 1 and 2 were produced by the same chicken from the third run. The average toe III length was 57.5 mm, and the average toe III width was 13.9 mm. The average FL:FW ratio was 0.83. Only one FW was recorded for this run (Table 3).

Medium sand dry (Run 1)							
Track 1:	L	Toe I:	38.6				
		Toe II:	58.43				
		Toe III:	61.82				
		Toe IV:	47.09				
	W	Toe II:	24.37				
		Toe III:	38.23				
		Toe IV:	34.52				
	AoD	II-III:	68				
		III-IV:	74				
		II-IV:	142				
	FL:	102.8					
	FW:	128.6					
Medium sand wet (Run 2)							
Track 1:	L	Toe I:	14.79				
		Toe II:	37.26				
		Toe III:	69.13				
		Toe IV:	56.34				
	W	Toe II:	8.48				
		Toe III:	14.96				
		Toe IV:	12.06				
	AoD	II-III:	57.4				
		III-IV:	72.3				
		II-IV:	129.8				
	FL:	100.29					
	FW:	129.6					
Track 2:	L	Toe I:	N/A				
		Toe II:	44.58				
		Toe III:	73.69				
		Toe IV:	50.33				
	W	Toe II:	22.35				
		Toe III:	22.55				
		Toe IV:	13.6				
	AoD	II-III:	68				
		III-IV:	83.7				
		II-IV:	151.7				
	FL:	100.16					
	FW:	137.91					

Medium sand moist 1 (Run 3)							
Track 1:	L	Toe I:	N/A		Pace length:	1-2:	66.83
		Toe II:	33.09			2-3:	176.2
		Toe III:	57.33		Pace width:	1-2:	57.89
		Toe IV:	47.07			2-3:	53.64
	W	Toe II:	11.12		Stride length:	1-3:	247.39
		Toe III:	11.76				
		Toe IV:	9.08				
	AoD	II-III:	66.8				
		III-IV:	65.5				
		II-IV:	132.3				
	FL:	79.7					
	FW:	105.4					
Track 2:	L	Toe I:	N/A				
		Toe II:	34.96				
		Toe III:	59.32				
		Toe IV:	48.7				
	W	Toe II:	12.01				
		Toe III:	17.31				
		Toe IV:	8.75				
	AoD	II-III:	67.2				
		III-IV:	65.5				
		II-IV:	132.7				
	FL:	82.83					
	FW:	105.04					
Track 3:	L	Toe I:	N/A				
		Toe II:	25.28				
		Toe III:	58.14				
		Toe IV:	36.81				
	W	Toe II:	11.42				
		Toe III:	14.57				
		Toe IV:	6.27				
	AoD	II-III:	59.2				
		III-IV:	65.1				
		II-IV:	124.3				
	FL:	76.65					
	FW:	104.05					

Medium sand moist 2 (Run 4)							
Track 1:	L	Toe I:	N/A				
		Toe II:	N/A				
		Toe III:	58.16				
		Toe IV:	43.44				
	W	Toe II:	N/A				
		Toe III:	14.13				
		Toe IV:	10.26				
	AoD	II-III:	N/A				
		III-IV:	49.9				
		II-IV:	N/A				
	FL:	81.32					
	FW:	N/A					
Track 2:	L	Toe I:	N/A				
		Toe II:	37.67				
		Toe III:	56.9				
		Toe IV:	38.66				
	W	Toe II:	12.68				
		Toe III:	13.74				
		Toe IV:	13.66				
	AoD	II-III:	73.5				
		III-IV:	67.2				
		II-IV:	140.7				
	FL:	82.36					
	FW:	99.17					
Track 3:	L	Toe I:	15.54				
		Toe II:	39.3				
		Toe III:	56.34				
		Toe IV:	46.16				
	W	Toe II:	13.22				
		Toe III:	12.71				
		Toe IV:	14.2				
	AoD	II-III:	61.4				
		III-IV:	52.4				
		II-IV:	113.8				
	FL:	81.38					
	FW:	99.6					

Track 4:	L	Toe I:	14.38				
		Toe II:	45.36				
		Toe III:	55.7				
		Toe IV:	39.24				
	W	Toe II:	14.04				
		Toe III:	10.45				
		Toe IV:	12.65				
	AoD	II-III:	62.1				
		III-IV:	65.1				
		II-IV:	127.2				
	FL:	82.44					
	FW:	100.69					
Track 5:	L	Toe I:	N/A				
		Toe II:	41.4				
		Toe III:	47.41				
		Toe IV:	N/A				
	W	Toe II:	9.91				
		Toe III:	11.28				
		Toe IV:	N/A				
	AoD	II-III:	54.9				
		III-IV:	N/A				
		II-IV:	N/A				
	FL:	81.72					
	FW:	N/A					
Track 6:	L	Toe I:	20.74				
		Toe II:	40.97				
		Toe III:	65.81				
		Toe IV:	47.97				
	W	Toe II:	14.46				
		Toe III:	17.25				
		Toe IV:	12.49				
	AoD	II-III:	60				
		III-IV:	72.3				
		II-IV:	142.3				
	FL:	87.16					
	FW:	116.52					

Table 3: Measurements of medium sand runs. All measurements are in mm, unless the measurement is an angle, which are in measured in degrees. L=Length of the toe. W=Width of the toe. AoD=Angle of Divarication between

the toes. II=Toe 2. III=Toe 3. IV=Toe 4. FL=Foot length. FW=Foot width. AoD from Mid=Angle of Divarication from Midline.

Fine sand

Four runs using six chickens were performed. On the dry run, a single chicken produced tracks. On the wet run, two chickens, one of which had produced tracks in the third and fourth medium sand runs, produced tracks. On the third fine sand run, one of the chickens that produced tracks in the wet run was used. On the fourth fine sand run, four chickens produced tracks. Even with video footage, associating which tracks were produced by which chicken was difficult. See Table 4 for all measurements associated with the fourth fine sand run.

Fine sand dry (Run 1)							
Track 1:	L	Toe I:	24.59		Pace length:	1-2:	128.74
		Toe II:	42.75			2-3:	101.03
		Toe III:	68.21		Pace width:	1-2:	49.28
		Toe IV:	50.78			2-3:	27.96
	W	Toe II:	25.66		Stride length:	1-3:	246.92
		Toe III:	34.44				
		Toe IV:	22.29				
	AoD	II-III:	59.2				
		III-IV:	69.3				
		II-IV:	128.5				
	FL:	98.04					
	FW:	114.22					
Track 2:	L	Toe I:	23.16				
		Toe II:	49.66				
		Toe III:	66.67				
		Toe IV:	56.98				
	W	Toe II:	23.82				
		Toe III:	36.22				
		Toe IV:	26.7				
	AoD	II-III:	54.5				
		III-IV:	64.2				
		II-IV:	118.7				
	FL:	92.92					
	FW:	130.17					
Track 3:	L	Toe I:	27.61				
		Toe II:	46.11				
		Toe III:	76.97				
		Toe IV:	54.05				
	W	Toe II:	29.63				
		Toe III:	37.97				
		Toe IV:	32.56				
	AoD	II-III:	53.7				
		III-IV:	69.7				
		II-IV:	123.4				
	FL:	103.32					
	FW:	118.16					

Fine sand wet (Run 2)							
Track 1:	L	Toe I:	N/A		Pace length:	3-4:	159
		Toe II:	32.25			4-5:	163
		Toe III:	57.25		Pace width:	3-4:	<5
		Toe IV:	44.5			4-5:	<5
	W	Toe II:	11.74		Stride length:	3-5:	32.25
		Toe III:	9.25		AoD from Mid:	3-	4.89
		Toe IV:	17			4-	15.21
	AoD	II-III:	90.03			5-	4.45
		III-IV:	73.84				
		II-IV:	163.87				
	FL:	82.25					
	FW:	110					
Track 2:	L	Toe I:	18.75				
		Toe II:	38				
		Toe III:	63.5				
		Toe IV:	34.75				
	W	Toe II:	7.5				
		Toe III:	17.5				
		Toe IV:	17.75				
	AoD	II-III:	70.84				
		III-IV:	74.96				
		II-IV:	145.8				
	FL:	88.75					
	FW:	101.75					
Track 3:	L	Toe I:	21.75				
		Toe II:	20				
		Toe III:	47.25				
		Toe IV:	22.5				
	W	Toe II:	7.75				
		Toe III:	7.75				
		Toe IV:	10.75				
	AoD	II-III:	63.64				
		III-IV:	54.64				
		II-IV:	117.97				
	FL:	65					
	FW:	55.75					

Track 4:	L	Toe I:	21				
		Toe II:	25.25				
		Toe III:	49.25				
		Toe IV:	28.25				
	W	Toe II:	11.25				
		Toe III:	5				
		Toe IV:	8.75				
	AoD	II-III:	46.94				
		III-IV:	83.53				
		II-IV:	130.16				
	FL:	65.25					
	FW:	61.5					
Track 5:	L	Toe I:	25.75				
		Toe II:	24.25				
		Toe III:	40				
		Toe IV:	25.75				
	W	Toe II:	16				
		Toe III:	12				
		Toe IV:	13				
	AoD	II-III:	76.03				
		III-IV:	63.34				
		II-IV:	139.37				
	FL:	55.25					
	FW:	64					

Fine sand moist 1 (Run 3)							
Track 1:	L	Toe I:	N/A		Pace length:	1-2:	145.24
		Toe II:	27.19			2-3:	147.8
		Toe III:	42.17		Pace width:	1-2:	<2
		Toe IV:	29.58			2-3:	<2
	W	Toe II:	5.41		Stride length:	1-3:	289.03
		Toe III:	8.71				
		Toe IV:	7.16				
	AoD	II-III:	65.1				
		III-IV:	67.2				
		II-IV:	132.3				
	FL:	51.26					
	FW:	63.77					
Track 2:	L	Toe I:	10.3				
		Toe II:	25.56				
		Toe III:	41.86				
		Toe IV:	28.63				
	W	Toe II:	8.22				
		Toe III:	10.25				
		Toe IV:	5.51				
	AoD	II-III:	47.3				
		III-IV:	43.9				
		II-IV:	91.1				
	FL:	58.25					
	FW:	55.79					
Track 3:	L	Toe I:	N/A				
		Toe II:	24.67				
		Toe III:	42.3				
		Toe IV:	25.55				
	W	Toe II:	7.63				
		Toe III:	6.15				
		Toe IV:	7.51				
	AoD	II-III:	54.9				
		III-IV:	49.4				
		II-IV:	104.3				
	FL:	51.92					
	FW:	61.67					
Track 4:	L	Toe I:	13.78				
		Toe II:	26.69				
		Toe III:	37.1				
		Toe IV:	30.65				
	W	Toe II:	8.36				
		Toe III:	8.6				
		Toe IV:	6.96				
	AoD	II-III:	41				
		III-IV:	47.7				
		II-IV:	88.7				
	FL:	55.77					
	FW:	59.33					

Fine sand moist 2 (Run 4)							
Track 1:	L	Toe I:	18.88				
		Toe II:	48.36				
		Toe III:	63.76				
		Toe IV:	46.78				
	W	Toe II:	14.46				
		Toe III:	11.54				
		Toe IV:	13.75				
	AoD	II-III:	47.7				
		III-IV:	62.1				
		II-IV:	109.8				
	FL:	92.29					
	FW:	96.39					
Track 2:	L	Toe I:	N/A				
		Toe II:	37.63				
		Toe III:	56.64				
		Toe IV:	45.31				
	W	Toe II:	8.17				
		Toe III:	14.58				
		Toe IV:	10.72				
	AoD	II-III:	33				
		III-IV:	60.8				
		II-IV:	93.8				
	FL:	69.17					
	FW:	98.49					
Track 3:	L	Toe I:	N/A				
		Toe II:	36.91				
		Toe III:	45.81				
		Toe IV:	40.05				
	W	Toe II:	13.31				
		Toe III:	17.18				
		Toe IV:	9.59				
	AoD	II-III:	78.6				
		III-IV:	76.9				
		II-IV:	155.5				
	FL:	75.74					
	FW:	110.68					
Track 4:	L	Toe I:	19.17				
		Toe II:	43.13				
		Toe III:	69.9				
		Toe IV:	54.94				
	W	Toe II:	11.21				
		Toe III:	17.71				
		Toe IV:	13.04				
	AoD	II-III:	62.5				
		III-IV:	87				
		II-IV:	149.5				
	FL:	88.01					
	FW:	128.68					

Table 4: (Opposite page) Measurements of fine sand runs. All measurements are in mm, unless the measurement is an angle, which are in measured in degrees. L=Length of the toe. W=Width of the toe. AoD=Angle of Divarication between the toes. II=Toe 2. III=Toe 3. IV=Toe 4. FL=Foot length. FW=Foot width. AoD from Mid=Angle of Divarication from Midline.

The chicken that made the dry run tracks was similar in size to the chicken of the first through third coarse sand run. One trackway composed of three tracks was produced (Fig. 5). The average toe III length was 70.6 mm, the average toe III width was 36.2 mm, and the average FL:FW ratio is 0.81.

Two chickens produced trackways during the wet fine sand run. The chicken that produced tracks in the medium sand runs produced two tracks in the wet fine sand run. The average toe III length was 60.3 mm and average toe III width was 13.4 mm. The average FL:FW ratio was 0.81. The small chicken produced three tracks with an average toe III length of 45.5 mm, an average toe III width of 8.25 mm, and a FL:FW ratio of 1.02.

The third fine sand run used the same small chicken from the wet fine sand run. Four tracks were produced, three of which were in one trackway. The average toe III length was 40.9 mm, the average toe III width was 8.4 mm, and the average FL:FW ratio was 0.9. Chickens that produced tracks in previous runs could not be identified positively from video from the fourth fine sand run.

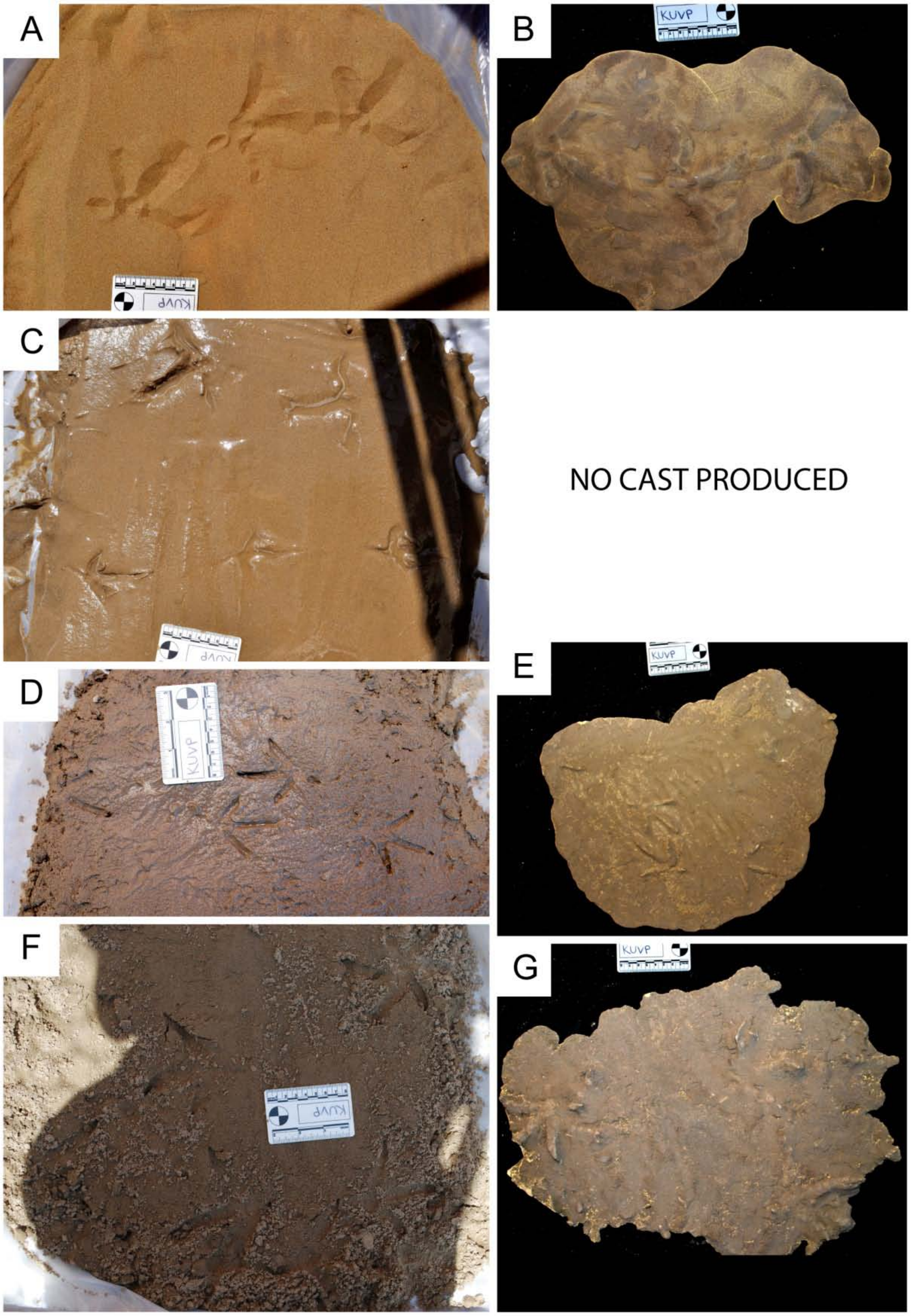

Fig. 5: Fine sand runs, and plaster casts produced. A.) Fine sand run, dry. B.) Plaster cast produced from the dry fine sand run. C.) Fine sand run, wet. D.) First moist fine sand run. E.) Plaster cast produced from the first moist fine sand run. F.) Second moist fine sand run. G.) Plaster cast produced from the second moist fine sand run.

Mud

No dry run was performed with mud. See Table 5 for all measurements from the mud runs. The first run used a medium-sized chicken that had not been previously used. There is little accompanying video footage (first track only) due to a camera malfunction (see video: Mud run 1). The average toe III length was 59.1 mm, the average toe III width was 11.3 mm, and the average FL:FW ratio was 0.79.

Mud 1							
Track 1:	L	Toe I:	12.72				
		Toe II:	50.38				
		Toe III:	64.13				
		Toe IV:	56.71				
	W	Toe II:	10.71				
		Toe III:	12.65				
		Toe IV:	7.08				
	AoD	II-III:	51				
		III-IV:	74				
		II-IV:	125				
	FL:	92.64					
	FW:	124.9					
Track 2:	L	Toe I:	15.72				
		Toe II:	41.05				
		Toe III:	52.21				
		Toe IV:	46.2				
	W	Toe II:	9.71				
		Toe III:	9.86				
		Toe IV:	8.92				
	AoD	II-III:	54				
		III-IV:	73				
		II-IV:	127				
	FL:	83.85					
	FW:	99.58					
Track 3:	L	Toe I:	22.66				
		Toe II:	41.21				
		Toe III:	60.81				
		Toe IV:	48.05				
	W	Toe II:	8.95				
		Toe III:	11.27				
		Toe IV:	9.39				
	AoD	II-III:	50				
		III-IV:	61				
		II-IV:	111				
	FL:	82.51					
	FW:	101.79					

Mud 2							
Track 1:	L	Toe I:	15.81		Pace length	1-2:	122.38
		Toe II:	25.8			2-3:	91.68
		Toe III:	41.45		Pace width:	1-2:	<5
		Toe IV:	30.27			2-3:	31.71
	W	Toe II:	7.57		Stride lengt	1-3:	211.9
		Toe III:	7.43		AoD from l	1-	3.01
		Toe IV:	5.91			2-	23
	AoD	II-III:	53.74			3-	12.43
		III-IV:	47.44				
		II-IV:	101.36				
	FL:	55.16					
	FW:	61.07					
Track 2:	L	Toe I:	N/A				
		Toe II:	28.81				
		Toe III:	36.83				
		Toe IV:	31.71				
	W	Toe II:	6.32				
		Toe III:	7.21				
		Toe IV:	5.81				
	AoD	II-III:	43.08				
		III-IV:	67.24				
		II-IV:	110.32				
	FL:	50.76					
	FW:	64.1					
Track 3:	L	Toe I:	12.94				
		Toe II:	25.7				
		Toe III:	39.67				
		Toe IV:	33				
	W	Toe II:	7.04				
		Toe III:	8.83				
		Toe IV:	7.9				
	AoD	II-III:	51.82				
		III-IV:	43.86				
		II-IV:	95.68				
	FL:	56.38					
	FW:	58.74					

Track 4:	L	Toe I:	13.38				
		Toe II:	28.86				
		Toe III:	40.05				
		Toe IV:	29.72				
	W	Toe II:	7.22				
		Toe III:	7.21				
		Toe IV:	6.75				
	AoD	II-III:	57.69				
		III-IV:	49.97				
		II-IV:	104.28				
	FL:	42.03					
	FW:	61.8					
Track 5:	L	Toe I:	12.52				
		Toe II:	27.99				
		Toe III:	40.15				
		Toe IV:	33.46				
	W	Toe II:	7.17				
		Toe III:	7.41				
		Toe IV:	7.19				
	AoD	II-III:	53.75				
		III-IV:	44.47				
		II-IV:	97.24				
	FL:	56.81					
	FW:	61.14					
Track 6:	L	Toe I:	N/A				
		Toe II:	28.86				
		Toe III:	43.5				
		Toe IV:	29.54				
	W	Toe II:	6.68				
		Toe III:	7.36				
		Toe IV:	6.34				
	AoD	II-III:	51.59				
		III-IV:	41.05				
		II-IV:	92.86				
	FL:	57.86					
	FW:	61.91					

Table 5: Measurements of mud runs. All measurements are in mm, unless the measurement is an angle, which are in measured in degrees. L=Length of the toe. W=Width of the toe. AoD=Angle of Divarication between the toes. II=Toe 2. III=Toe 3. IV=Toe 4. FL=Foot length. FW=Foot width.

The second run used the same small chicken used in multiple fine sand runs. Pad impressions were clearly visible (Fig. 6). The average toe III length was 40.3 mm and the average toe III width was 7.6 mm. The average FL:FW ratio was 0.865. The third mud run did not produce definable tracks, only a single metatarsal pad impression and a few claw impressions (Fig. 6).

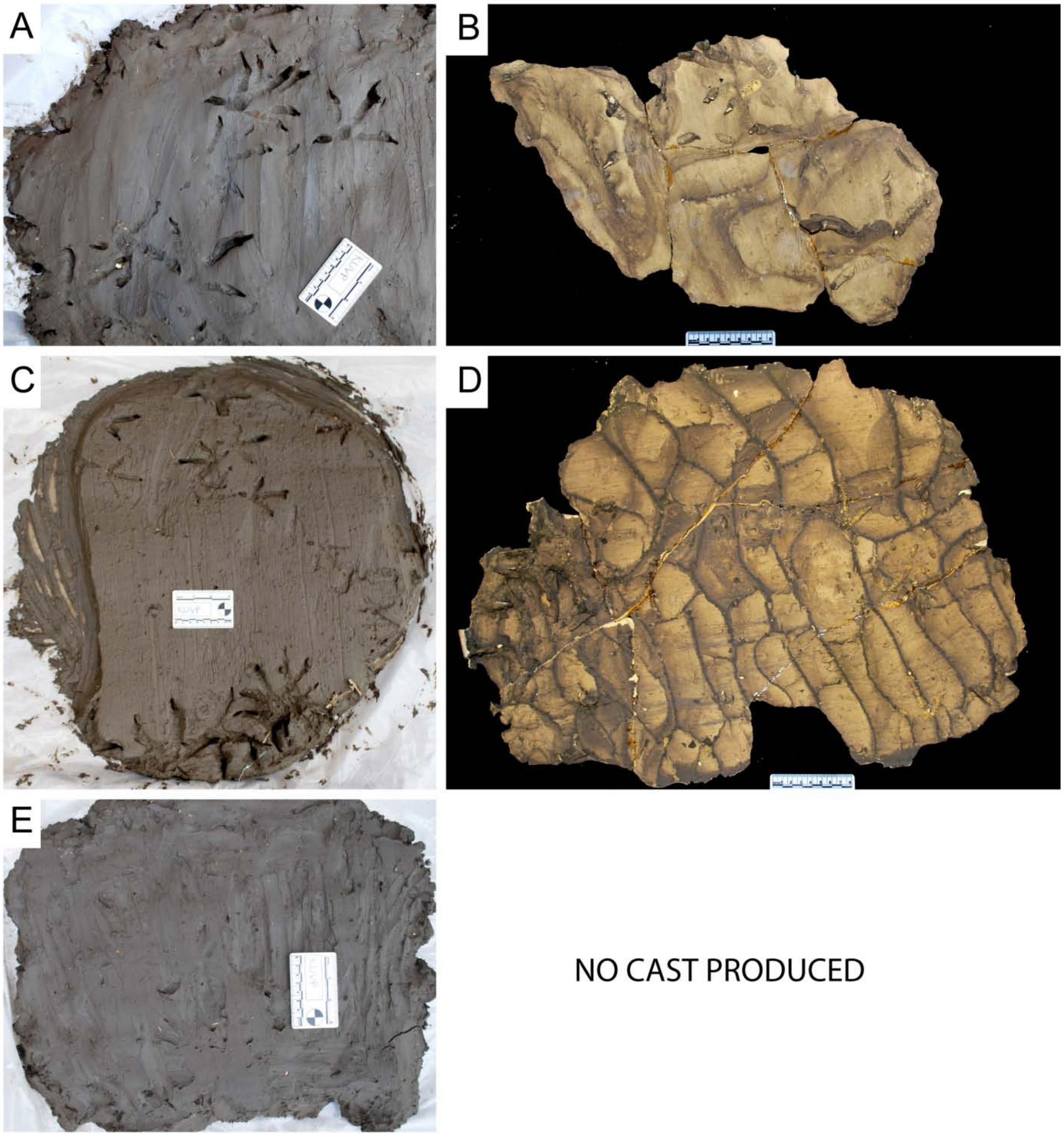

Fig. 6: Mud runs, and plaster casts produced. A.) Mud run 1. Arrow indicates track seen on plaster cast. B.) Plaster cast produced from mud run 1. Arrow indicates track highlighted in A. C.) Mud run 2. D.) Plaster cast produced from mud run 2. E.) Mud run 3.

Mixed sand

Although no moisture data is available for the mixed sand runs, these runs captured valuable behavioral data. Two runs (dry and first moist run) were performed with the same chicken. The wet mixed sand run was performed with the same chicken that was used in the medium sand dry and wet runs. The final mixed sand run used a new chicken. The multitrack measurements of the final mixed sand run are summarized in Table 6.

Mixed sand dry (run 1)								
Track 1:	L	Toe I:	18.14			Pace length:	1-2:	133.36
		Toe II:	47.93				2-3:	146.03
		Toe III:	66.72			Pace width:	1-2:	60.62
		Toe IV:	53.04				2-3:	48.7
	W	Toe II:	19.1			Stride length:	1-3:	268.48
		Toe III:	34.38			AoD from Mid:	1-	30.94
		Toe IV:	30.64				2-	<5
	AoD	II-III:	67				3-	11.04
		III-IV:	79					
		II-IV:	146					
	FL:	91.4						
	FW:	117.65						
Track 2:	L	Toe I:	21.76					
		Toe II:	47.1					
		Toe III:	63.1					
		Toe IV:	44.91					
	W	Toe II:	31.38					
		Toe III:	38.01					
		Toe IV:	26.27					
	AoD	II-III:	65					
		III-IV:	69					
		II-IV:	134					
	FL:	86.35						
	FW:	109.25						
Track 3:	L	Toe I:	18.46					
		Toe II:	44.28					
		Toe III:	61.39					
		Toe IV:	52.1					
	W	Toe II:	15.68					
		Toe III:	32.96					
		Toe IV:	28.7					
	AoD	II-III:	71					
		III-IV:	65					
		II-IV:	136					
	FL:	83.41						
	FW:	114.42						

Mixed sand wet (Run 2)								
Track 1:	L	Toe I:	30.83			Pace length:	1-2:	144.2
		Toe II:	52.43				2-3:	111.2
		Toe III:	75.89				3-4:	75.2
		Toe IV:	63.17			Pace width:	1-2:	51.6
	W	Toe II:	15				2-3:	41
		Toe III:	22.62				3-4:	55.2
		Toe IV:	16.39			Stride length	1-3:	251
	AoD	II-III:	58.7				2-4:	188.8
		III-IV:	74.8			AoD from Mid:	1-	46.25
		II-IV:	133.5				2-	38.92
	FL:	108.84					3-	<5
	FW:	144.18					4-	<5
Track 2:	L	Toe I:	23.5					
		Toe II:	48.78					
		Toe III:	67.52					
		Toe IV:	61.27					
	W	Toe II:	20.92					
		Toe III:	30.05					
		Toe IV:	20.82					
	AoD	II-III:	79.9					
		III-IV:	57.9					
		II-IV:	137.8					
	FL:	94.78						
	FW:	144.21						
Track 3:	L	Toe I:	N/A					
		Toe II:	46.86					
		Toe III:	72.7					
		Toe IV:	64.65					
	W	Toe II:	17.84					
		Toe III:	19.71					
		Toe IV:	16.16					
	AoD	II-III:	77.3					
		III-IV:	59.6					
		II-IV:	136.9					
	FL:	105.09						
	FW:	143.62						
Track 4:	L	Toe I:	22.25					
		Toe II:	41.51					
		Toe III:	73.88					
		Toe IV:	59.69					
	W	Toe II:	19.56					
		Toe III:	25.81					
		Toe IV:	18.93					
	AoD	II-III:	64.2					
		III-IV:	63					
		II-IV:	127.2					
	FL:	113						
	FW:	148.42						

Mixed sand moist 1 (Run 3)								
Track 1:	L	Toe I:	N/A	Depth:		Pace length:	3-4:	232.95
		Toe II:	42.68	<5			4-5:	173.28
		Toe III:	59.69	5.03			5-6:	77.56
		Toe IV:	43.71	<5		Pace width:	3-4:	109.77
	W	Toe II:	14.4				4-5:	94.51
		Toe III:	13.12				5-6:	64.45
		Toe IV:	9.98			Stride length:	3-5:	408.83
	AoD	II-III:	65.5				4-6:	251.54
		III-IV:	60.8			AoD from Mid:	3-	
		II-IV:	126.3				4-	
	FL:	83.54					5-	
	FW:	114.51					6-	
Track 2:	L	Toe I:	N/A					
		Toe II:	30.2	<5 mm				
		Toe III:	60.65	>10				
		Toe IV:	50.58	<5				
	W	Toe II:	14.32					
		Toe III:	16.53					
		Toe IV:	10.87					
	AoD	II-III:	60.4					
		III-IV:	63.4					
		II-IV:	123.8					
	FL:	86.1						
	FW:	109.28						
Track 3:	L	Toe I:	N/A					
		Toe II:	29.1	<5				
		Toe III:	65.13	10				
		Toe IV:	52.05	7				
	W	Toe II:	13.44					
		Toe III:	17.91					
		Toe IV:	15.22					
	AoD	II-III:	62.5					
		III-IV:	70.1					
		II-IV:	132.6					
	FL:	88.28						
	FW:	101.2						
Track 4:	L	Toe I:	22.11					
		Toe II:	38.18	8				
		Toe III:	65.72	12				
		Toe IV:	N/A	-				
	W	Toe II:	16.98					
		Toe III:	22.74					

		Toe IV:	N/A					
	AoD	II-III:	61.3					
		III-IV:	N/A					
		II-IV:	N/A					
	FL:	83.93						
	FW:	N/A						
Track 5:	L	Toe I:	22.44					
		Toe II:	50.55	14				
		Toe III:	64.41	17				
		Toe IV:	45.94	12				
	W	Toe II:	29.19					
		Toe III:	21.57					
		Toe IV:	14.23					
	AoD	II-III:	68					
		III-IV:	52.8					
		II-IV:	120.8					
	FL:	82.89						
	FW:	119.21						
Track 6:	L	Toe I:	N/A					
		Toe II:	38.06	16				
		Toe III:	57.99	18				
		Toe IV:	38.65	6				
	W	Toe II:	13.57					
		Toe III:	19.15					
		Toe IV:	17.23					
	AoD	II-III:	61.3					
		III-IV:	64.6					
		II-IV:	125.9					
	FL:	85.09						
	FW:	98.01						

Mixed sand moist 2 (Run 4)								
Track 1:	L	Toe I:	18.83	Depth:		Pace length:	1-2:	92.45
		Toe II:	36.71	18			2-3:	143.1
		Toe III:	46.97	23			3-4:	161.83
		Toe IV:	39.16	18			4-5:	134.03
	W	Toe II:	17.28				6-7:	223.88
		Toe III:	14.05				7-8:	40.04
		Toe IV:	13.82			Pace width:	1-2:	77.85
	AoD	II-III:	66.3				2-3:	80.18
		III-IV:	85.8				3-4:	55.18
		II-IV:	152.1				4-5:	<5
	FL:	72.31					6-7:	37.09
	FW:	99.1					7-8:	66.69
Track 2:	L	Toe I:	20.97			Stride length:	1-3:	232.35
		Toe II:	38.63	23			2-4:	311.66
		Toe III:	47.4	18			3-5:	296.03
		Toe IV:	39.32	13			6-8:	270.03
	W	Toe II:	22.57					
		Toe III:	14.76					
		Toe IV:	16.48					
	AoD	II-III:	54.5					
		III-IV:	73.5					
		II-IV:	128					
	FL:	79.24						
	FW:	99.49						
Track 3:	L	Toe I:	13.18					
		Toe II:	35.66	<5				
		Toe III:	52.06	5				
		Toe IV:	33.89	<5				
	W	Toe II:	12.56					
		Toe III:	14.17					
		Toe IV:	10.09					
	AoD	II-III:	64.2					
		III-IV:	68.9					
		II-IV:	133.1					
	FL:	73.21						
	FW:	85.33						
Track 4:	L	Toe I:	N/A					
		Toe II:	39.99	<5				
		Toe III:	52.92	5				
		Toe IV:	43.68	<5				
	W	Toe II:	12.48					
		Toe III:	12.34					
		Toe IV:	9.86					
	AoD	II-III:	60.4					
		III-IV:	69.3					
		II-IV:	129.7					
	FL:	77.93						
	FW:	101.68						

Track 5:	L	Toe I:	N/A					
		Toe II:	36.85	<5				
		Toe III:	56.7	7				
		Toe IV:	45.85	5				
	W	Toe II:	9.8					
		Toe III:	14.92					
		Toe IV:	12.57					
	AoD	II-III:	63					
		III-IV:	64.6					
		II-IV:	127.6					
	FL:	78.95						
	FW:	102.44						
Track 6:	L	Toe I:	18.34					
		Toe II:	39.99	5				
		Toe III:	52.67	5				
		Toe IV:	45.49	<5				
	W	Toe II:	15.15					
		Toe III:	14.95					
		Toe IV:	11.51					
	AoD	II-III:	48.6					
		III-IV:	71.8					
		II-IV:	120.4					
	FL:	79.65						
	FW:	100.18						
Track 7:	L	Toe I:	21.42					
		Toe II:	38.34	10				
		Toe III:	48.49	19				
		Toe IV:	37.65	20				
	W	Toe II:	14.27					
		Toe III:	16.77					
		Toe IV:	14.11					
	AoD	II-III:	62.5					
		III-IV:	67.6					
		II-IV:	130.1					
	FL:	74.97						
	FW:	95.47						
Track 8:	L	Toe I:	21.66					
		Toe II:	33.35	19				
		Toe III:	48.35	26				
		Toe IV:	35	14				
	W	Toe II:	16.04					
		Toe III:	22.65					
		Toe IV:	14.22					
	AoD	II-III:	60					
		III-IV:	74.4					
		II-IV:	134.4					
	FL:	75.71						
	FW:	92.02						

Table 6: (Opposite page) Measurements of mixed-sand run resulting in takeoff and landing traces. All measurements are in mm, unless the measurement is an angle, which are in measured in degrees. L=Length of the toe. W=Width of the toe. AoD=Angle of Divarication between the toes. II=Toe 2. III=Toe 3. IV=Toe 4. FL=Foot length. FW=Foot width. AoD from Mid=Angle of Divarication from Midline.

The dry run produced 3 tracks in a single trackway, and had an average toe III length of 63.7 mm and an average toe III width of 35.1 mm. The average FL:FW ratio was 0.77. The third run used three chickens, one of which was the same chicken used in the dry run. The third run contained a takeoff trace (Fig. 7; www.ichnology.ku.edu). The average toe III length of the larger chicken tracks was 63 mm, the average toe III width was 20.3 mm, and the average FL:FW ratio was 0.8. The tracks representative of takeoff, tracks 5 and 6, were significantly deeper than those in the trackway. The third toe impressions of tracks 3 and 4 were 10 and 12 mm, respectively, whereas the takeoff tracks (5 and 6) were 17 and 18 mm deep. Other tracks, belonging to different chickens, have toe III depths of $\leq$ 5 mm (Table 6).

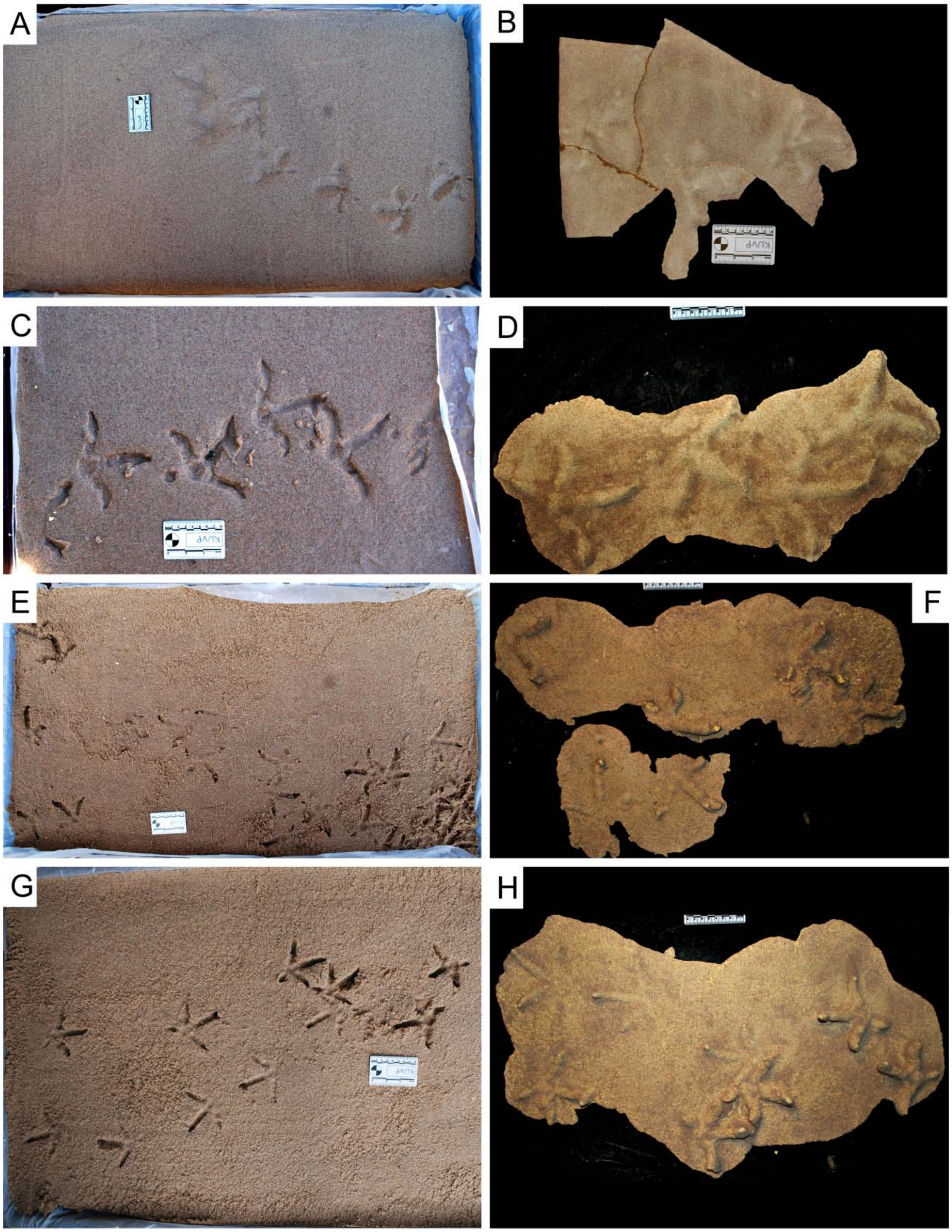

Fig. 7: Mixed sand runs, and plaster casts produced. A.) Mixed sand run, dry. B.) Plaster cast produced from the dry mixed sand run. C.) Mixed sand run, wet. D.) Plaster cast produced from the wet mixed sand run. E.) First moist mixed sand run. F.) Plaster cast produced from the first moist mixed sand run. G.) Second moist mixed sand run. H.)

Plaster cast produced from the second moist mixed sand run. Note takeoff and landing traces. See online video "Mixed sand run 4" to view takeoff and landing behavior.

The wet run did not show any new and significant behaviors. The average toe III length was 54.3 mm, and the average toe III width was 24.5 mm. The average FL:FW ratio was 0.75.

The fourth run contained landing, walking, running, and takeoff traces (Fig. 7D; supplemental data; www.ichnology.ku.edu). The average toe III length was 50.7 mm, and the average toe III width was 15.6 mm. The average FL:FW ratio was 0.79. The landing tracks had toe III depths of 23 and 18 mm (Table 6), whereas the walking trackway tracks had much shallower depths (Table 6). The walking trackway pace lengths are variable, but shorter than the running trackway pace length. The takeoff tracks are also significantly deeper than the walking and running tracks (19 and 26 mm, Table 6). The running tracks are slightly deeper than the walking tracks, although it is not significant (Table 6).

Behaviors observed and quantified

Behaviors observed included stop-start walking, sinuous walking, and running. Takeoff and landing were the two most significant behaviors observed. All of the locomotion behaviors observed in this study can be quantified. There have been no studies, however, that specifically suggest how to quantify trackways that are variably sinuous. We suggest that trackways should be classified as straight, symmetrical, asymmetrical, or irregular, based results herein and trackway patterns from both modern and ancient avian examples (e.g., Elbroch and Marks, 2001; Genise et al., 2009; Lockley and Harris, 2010; Melchor et al., 2012; Falk et al., 2014). Straight trackways have little or no curvature (Fig. 7B, 8A) and are observed in modern and many fossil examples (e.g., the Lower Cretaceous Haman Formation, Republic of Korea). Symmetrical trackways are symmetrical about an axis drawn from the start to the end of the trackway (Fig. 3, 8B) and have been observed in modern bird trackways (e.g., Elbroch and Marks, 2001; Genise et al., 2009). Asymmetrical trackways are asymmetrical about an axis drawn from the start to the end of the trackway (Fig. 8C), and have been observed in both modern and fossil tracks (e.g., Elbroch and Marks, 2001; Falk et al., 2014). Irregular trackways have tortuous and circuitous pathways that may self cross one or more times (Fig. 8D) and have been observed in modern tracks (e.g., American Robins in snow, Mourning Doves in a feeding tray). These types of trackways have likely been preserved in the fossil record as well, however, they may be difficult to identify as a single trackway, especially on isolated float blocks (e.g., from the Gyeongsamnado Institute of Science Education, Republic of Korea).

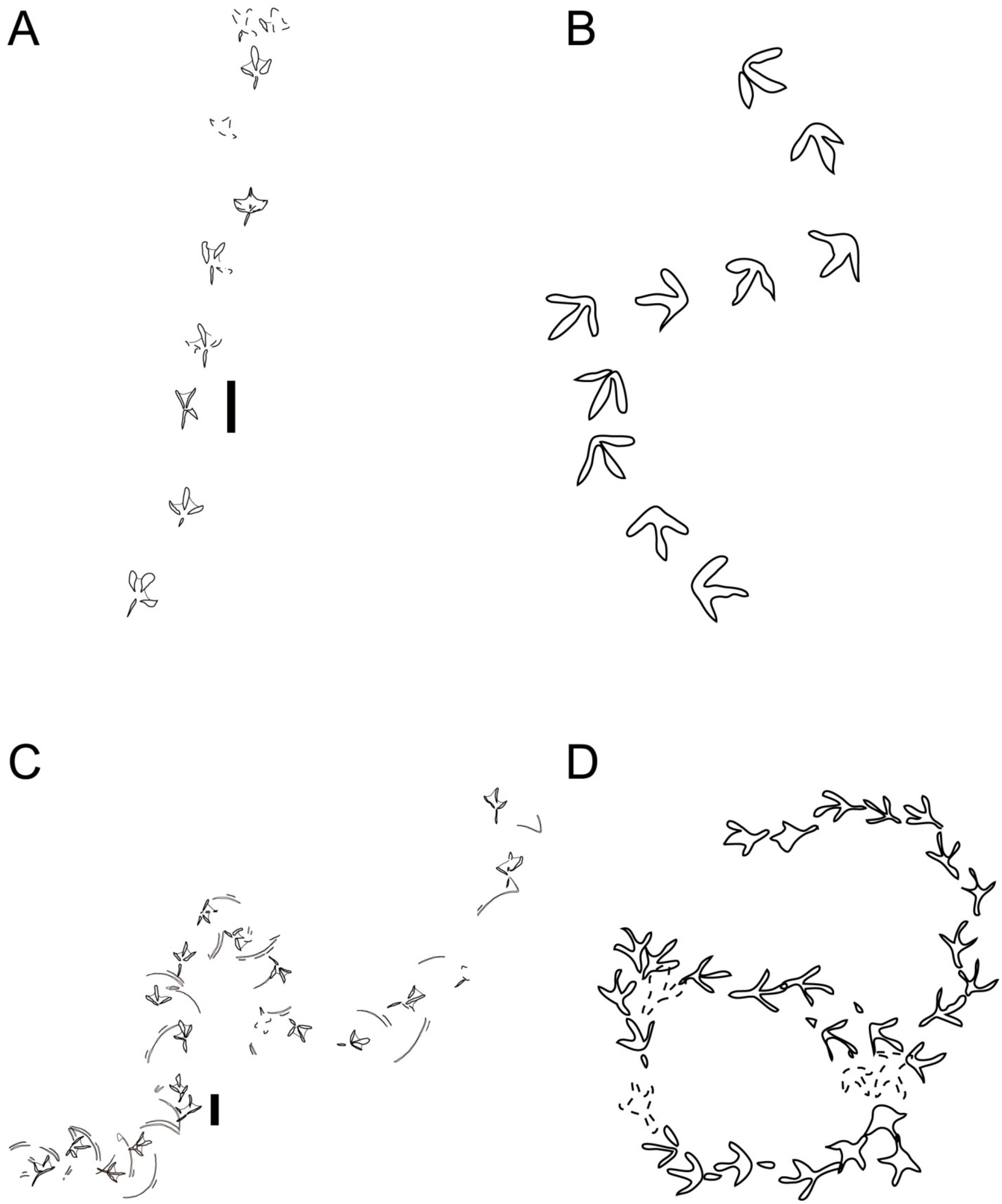

Fig. 8: Differing sinuosities of bird trackways. A.) Straight. Modified from Chapter 1 (Falk et al., 2014). Scale bar=8 cm. B.) Symmetrical. Modified from Elbroch and Marks, 2001. C.) Asymmetrical. Modified from Chapter 1 (Falk et al., 2014). Scale bar=8 cm. D.) Irregular. Modified from photgraph provided by M. J. Will.

These trackway patterns can be quantified using a sinuosity index (SI), which we define as the length from the beginning of the trackway to the end in a straight line (SL) divided by the total length (TL) of the trackway (SL:TL). The total length of the trackway follows the true midline of the trackway from the base of toe III of the first track to the base of toe III of the final track. This metric is analogous to the sinuosity ratio used in fluvial geomorphology to measure the sinuosity of rivers (Leopold et al., 1995, p. 281) and the tail trace sinuosity measurement for tail-bearing tetrapods (Platt and Hasiotis, 2008). In order to measure sinuosity of asymmetrically sinuous trackways (Fig. 8C, 9), the midline of the track would have to be changed each time the trackway deviated from a simple sine curve. The SI removes the necessity of changing the midline of the track, by measuring the length from the beginning of the trackway to the end in a straight line, and then using ImageJ© or a string to measure the total length of the trackway including the curves (Fig. 9). If a ratio is close to 1, the sinuosity is low; if a ratio is close to 0 the sinuosity is high.

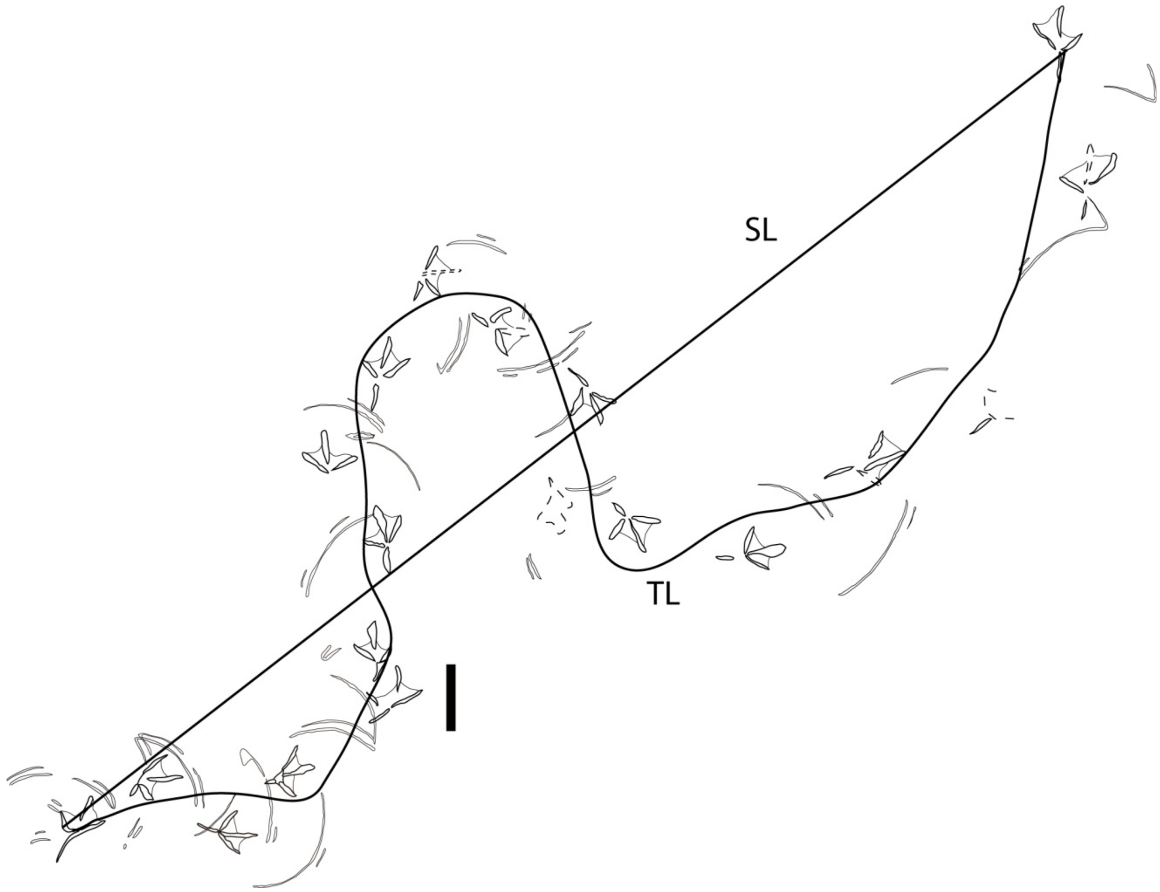

Fig. 9: The sinuosity index used to measure sinuous bird trackways. SL=Straight line length. TL=Total length.

Start-stop walking is best represented in the wet coarse sand trackway. The same trackway also represents sinuous walking, exhibited in the S curves (Fig. 3B). The sinuosity of the trackway is 0.64. There were no side-by-side footprints that represented a stoppage in movement. Running was observed in several runs but is best observed in the final mixed-sand run, where the bird ran and took off.

Three different takeoffs are observed, two from the same chicken, all three from the mixed-sand runs. Unfortunately, the first takeoff occurred in the dry sand run, and essentially obliterated any detail (Fig. 7A). The takeoff tracks appear, however, to be roughly parallel. The second takeoff occurred in a moist sand run and, therefore, exhibited better detail. The takeoff tracks are significantly deeper than the preceding tracks (Table 6). The takeoff tracks, however, are not parallel, but staggered, with a pace length of 77.6 mm (Fig. 7B). The third takeoff trace was produced in the final mixed-sand run. Similar to the previous takeoff trace, the tracks are not parallel, with a pace length of 40 mm (Fig. 7C), however, they are closer together than the previous takeoff trace. They are also much deeper (by up to 21 mm) than the running trackway preceding them (Table 6).

The final mixed-sand trackway also exhibited a landing trace. The landing trace is similar to the takeoff trace, except that rather than appearing at the terminus of a trackway it appears at the beginning. The tracks are not parallel (pace length of 92.4 mm), and significantly deeper than the tracks that follow (Table 6). Both takeoff and landing traces tend to have relatively wide pace widths (Table 6), although they are not always the widest pace widths of the trackway. The digit III impression on the very first track in the landing trace is shorter than the average (Table 6; Fig. 7D), likely due to the toe entering the sediment at a more vertical angle than is normal.

Behaviors of Mourning Doves observed include landing, takeoff, feeding, sinuous walking, and charging (territorial defense) (Video: Mourning dove dry sand, Fig. 10). Landing, takeoff (Fig. 10A, B), and sinuous walking trackways were similar in morphology to those reported for the domestic chicken. Irregular walking, where the dove crossed its own trackway multiple times, was also observed. Pecking was the only feeding behavior observed, and no clear traces were produced, likely due to the lack of moisture in the sediment. Some divots in the sand may be attributable to pecking (Fig. 10C). Charging behavior was also observed, where one dove drove another dove away from the food source. As one dove landed on the left side of the tray, another landed near the middle of the tray. As the dove from the left approached the center of the tray, the dove present in the center charged a short distance at the dove from left, stopping short of any actual contact. This caused the approaching dove to leave the tray. The end of this encounter is represented in Figure 14A. Note the staggered paired tracks at the terminus of one of the trackways, directly to the left of the dove in the center of the tray—these represent the takeoff of the dove that was charged.

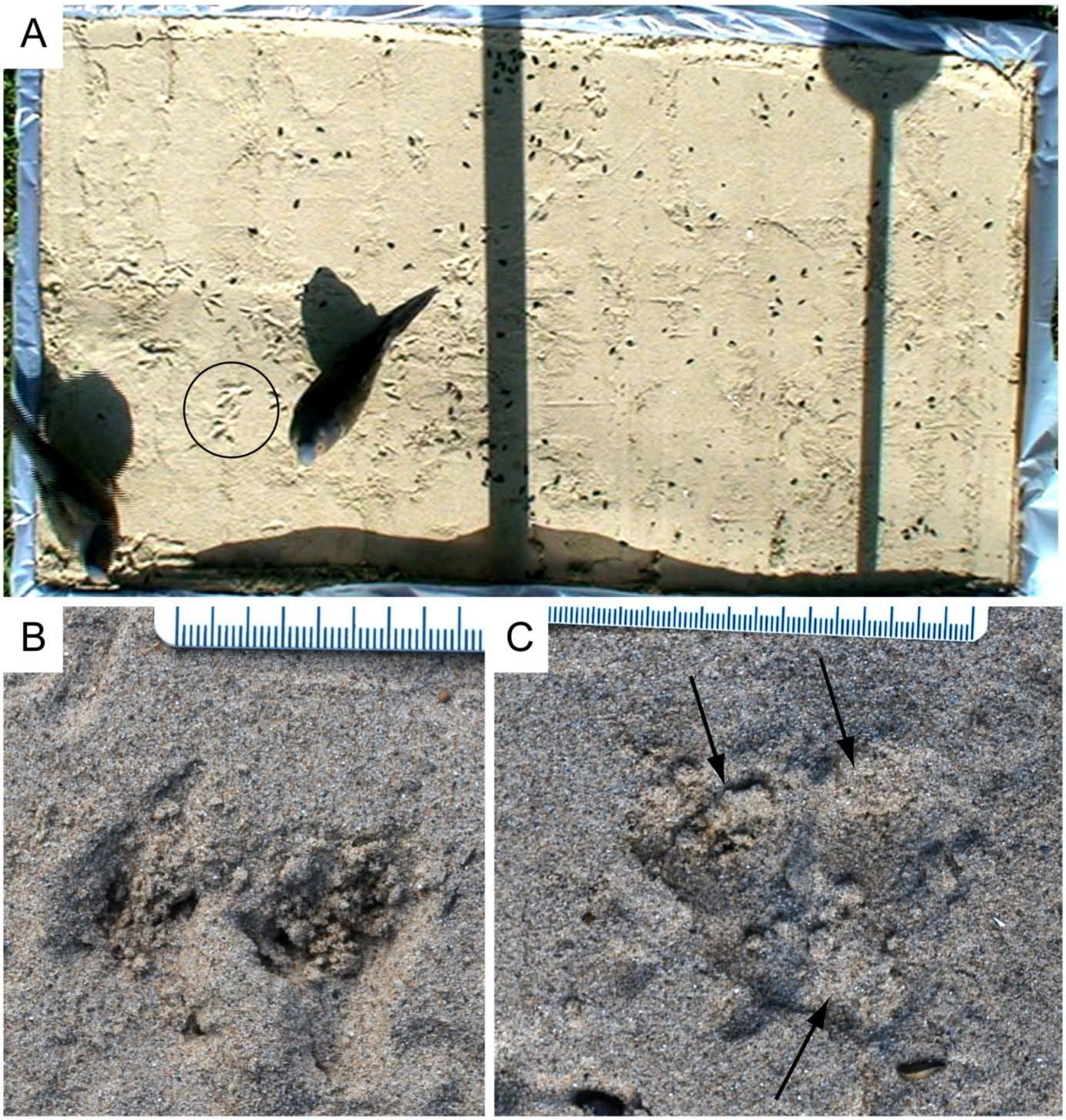

Fig. 10: Screenshot of Mourning Doves (*Zenaida macrocura*) on the tray and traces left behind. A.) Aftermath of the charging incident, where the dove near the center charged and drove off another dove. Directly to the left of the

center dove are the paired tracks that represent the takeoff trace of the dove that was charged. Note, the left-hand dove in this photograph is not the dove that was charged. B.) A pair of tracks at the terminus of a trackway representing takeoff. C.) Circle-shaped divots in the sand likely left by pecking behaviors, indicated by arrows.

DISCUSSION

The portability and simplicity of this experimental setup makes it ideal for observing trackway production both in controlled settings and in the field with the use of remotely controlled with a digital video camera. The experimental setup requires no human influence beyond setting the tray up in the field and adding sediment and water. The runs performed in this study demonstrates that this setup is capable of collecting data on behavior and track and trackway morphology, and how they change with media consistency. Using this setup, traces produced by specific behaviors can be quantitatively analyzed by casting the tracks with plaster, and then measuring the tracks and trackways using standard measurements (Fig. 1), or by photographing the tray with a scale and measuring the tracks and trackways using computer software (e.g., ImageJ®). Note that multiple different chickens were used in these runs, therefore, the exact measurements reflect difference in size and breed of chicken, and not always the influence of media properties. Certain measurements (e.g., FL:FW ratio, angle of divarication) may be more strongly representative of variation in media properties than such measurements as toe length.

Variation of track morphology with media consistency

Despite using different chickens in several different runs, track morphology clearly varies with media consistency. Tracks produced in dry sand lack any detail, including distinct pad impressions, and have very wide and long toe impressions (e.g., Fig. 3A), formed by the sand collapsing as the foot is pulled out of the sand. For example, despite using the same chicken in the dry, wet, and one of the moist coarse sand runs, the average length of toe III of dry sand track was 0.7 mm longer than the wet sand toe III, and 1.8 mm longer than the toe III of the moist sand run (Table 2). The width of the digit impressions was also significantly longer than the actual toe. The dry coarse sand toe III width was 16.6 mm wider than the moist coarse sand toe III width (Table 2).

Tracks produced in wet sand possessed more detail than tracks produced in dry sand (Fig. 11). The toes were thinner, closer to the actual toe width of the bird (e.g., 1.1 mm wider in the wet coarse sand vs. the moist coarse sand), and taper distally instead of terminating in blunt tips (Fig. 11A–B). They possess a strong metatarsal pad impression, as do the tracks produced in dry sand. Tracks produced in wet sand, however, still lack fine detail, including claw impressions and pad impressions.

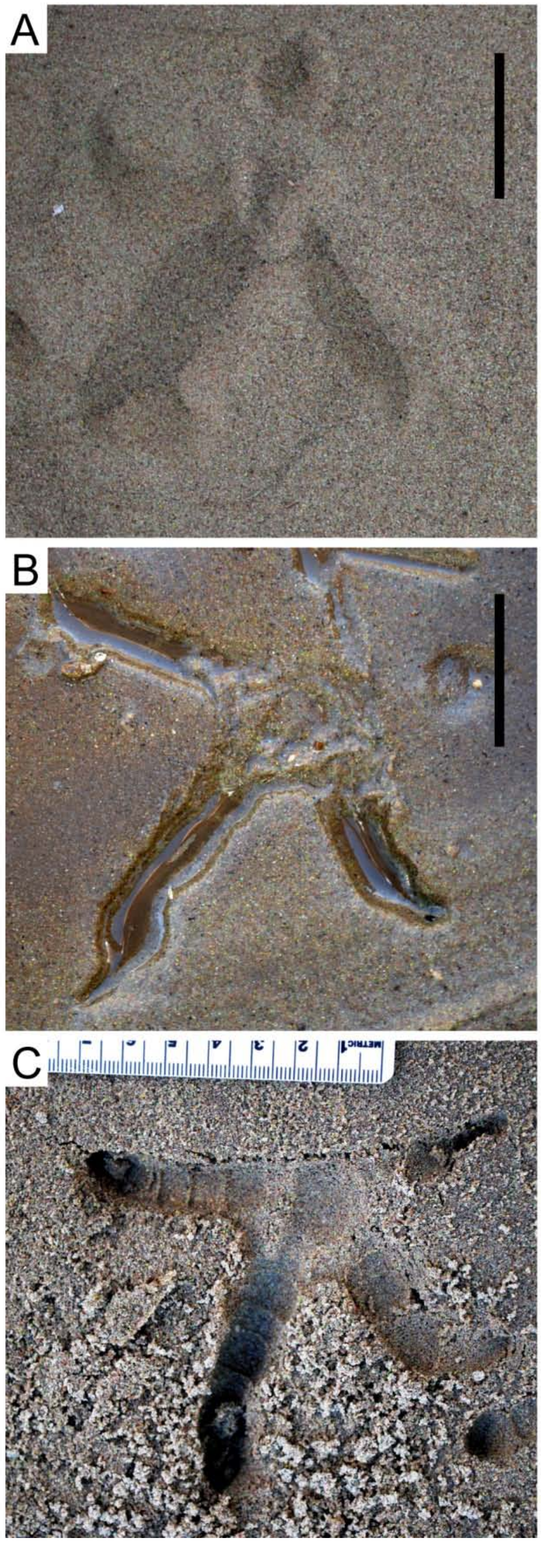

Fig. 11: Comparison of traces produced in dry, wet, and moist mediun-grained sand. A.) Dry sand. Note wide, blunt digit impressions and collapsed morphology. Scale bar 4 cm. B.) Wet sand. Moisture content 8.8%. Scale bar 4 cm. C.) Moist sand. Moisture content 3.6%.

Tracks produced in moist sand (3.2–5.3% moisture content in these runs, Table 1) generally preserve better detail than dry or wet sand. Grain size seems less important in dry and wet sand, however, grain size becomes more important for determining the level of detail in sand runs with this range of moisture content. Coarse sand does not produce tracks with fine detail as medium or fine sand (Fig. 12). Pad impressions are barely visible in coarse sand (Fig. 12A), however, in medium sand they are clearly visible (Fig. 12B). In fine sand, the pad impressions are even clearer than in medium sand (Fig. 12C). The lower the moisture content in the moist sand, the lower the amount of detail (Fig. 13).

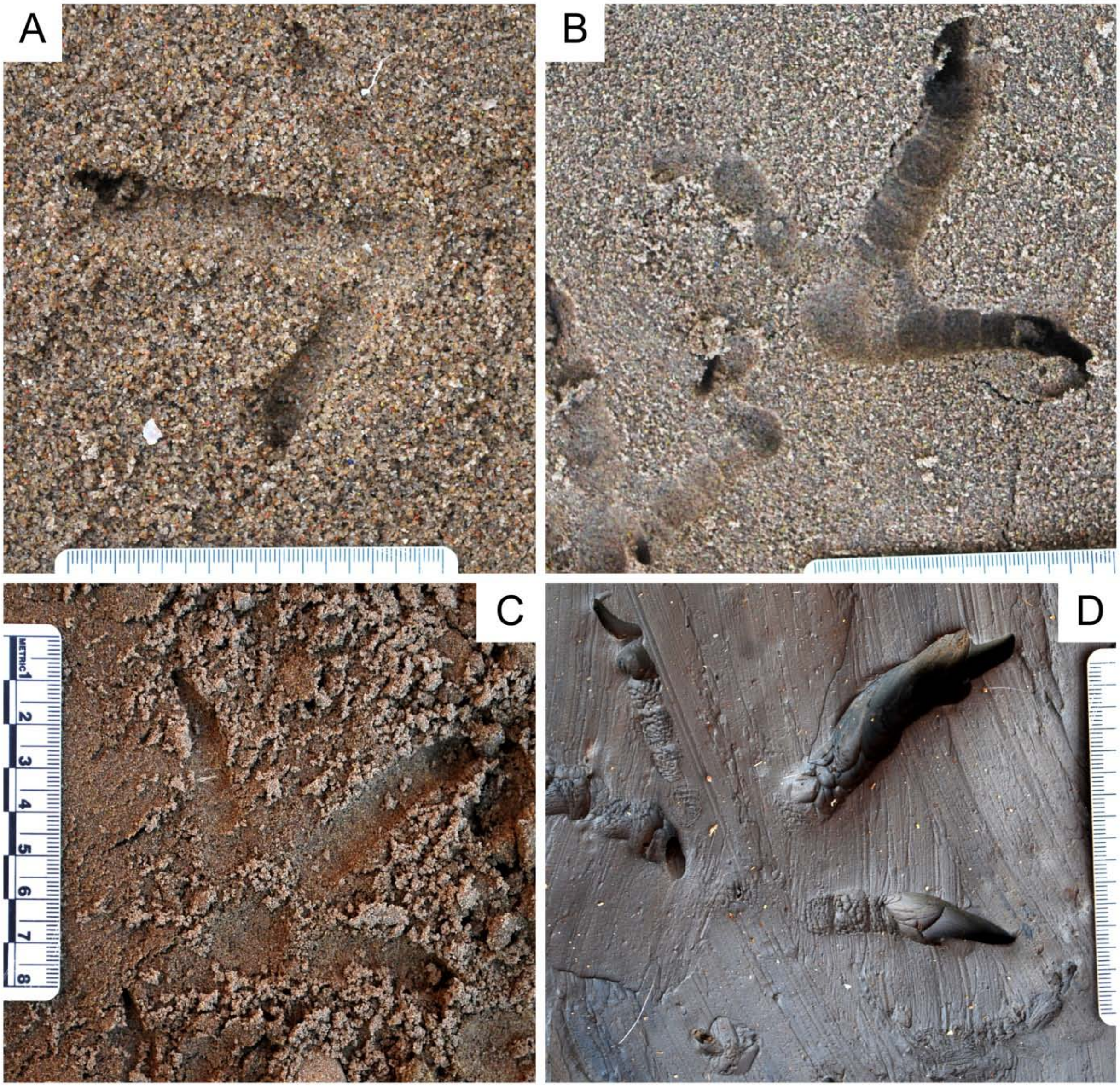

Fig. 12: Comparison of traces produced in coarse, medium, and fine sand, and mud. A.) Coarse sand, moist, 3.2% moisture content. B.) Medium sand, moist, 4.6% moisture content. C.) Fine sand, moist, 3.4% moisture content. D.) Mud, moist, 10.8% moisture content.

Tracks produced in mud (illite-smectite clay) preserve a great amount of detail (Fig. 12D). Claw, pad, and scale impressions are present in mud with moisture content of 10.8% and 15.6%. No tracks were produced in mud with a moisture content of 13.9% (Fig. 6). This could be due to the weight of the chicken—the chicken that produced tracks in mud with a moisture content of 10.8% was likely heavier than the chicken that was used in the run with 13.9% moisture content. Once the mud becomes soupy, tracks will not be preserved due to the collapse of the track, or they will not be produced because the birds refuse to walk across this kind of medium.

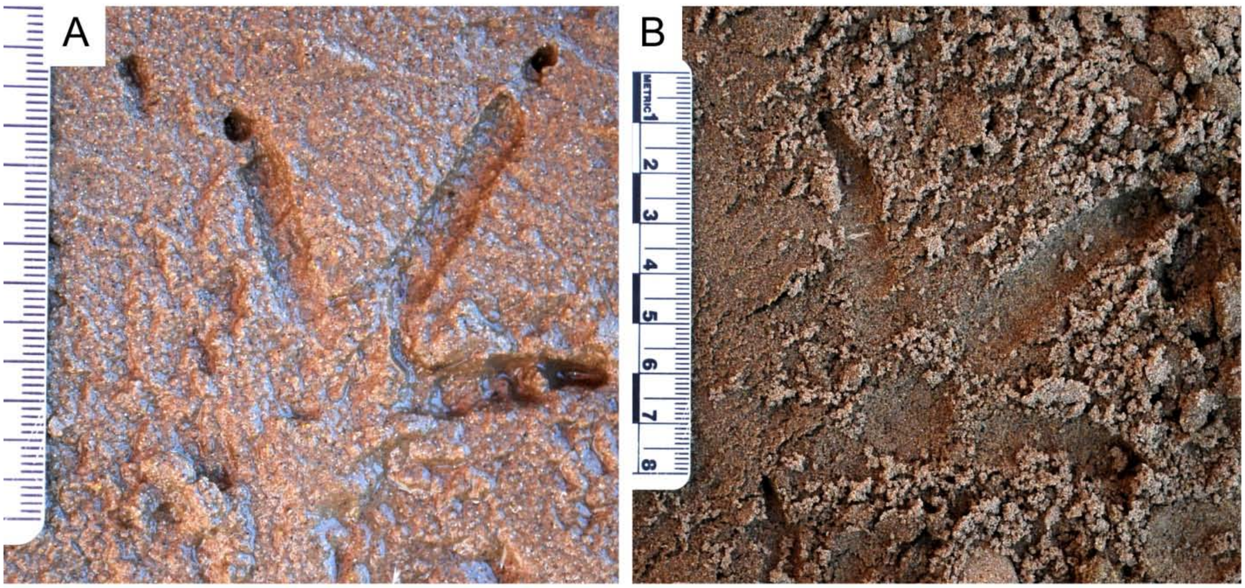

Fig. 13: Comparison of detail in fine sand runs 3 and 4. A.) Fine sand run 3. Moisture content 5.3%. B.) Fine sand run 4. Moisture content 3.4%.

Trackway preservation potential based on media consistency

In general, the finer grained the sediment, the better preserved the tracks and trackways. The lowest value for media moisture content reported in this study was 3.4% in fine sand, and there was a noticeable lack of fine detail (e.g., pad and claw impressions). If the moisture content of a media is too low, fine detail will not be preserved. If sediment is too wet, the fine detail will also not be preserved, due to a breakdown in cohesion between sediment grains. In some cases, such as mud, if the sediment is too soupy the tracks will not preserve and collapse. The birds may actively refuse to cross such sediment as well. The amount of fine detail that will be preserved is linked to the amount of moisture present, however, the amount of moisture necessary for fine detail preservation will vary based on grain size. For fine sand, moisture contents < 4%, will result in loss of fine detail, for medium sand, <3%, and for mud, <10% (see Table 1). Coarse sand does not preserve fine detail regardless of sediment moisture content.

Most bird tracks are found in water-margin environments (e.g., lake shores, river pointbars and sand bars, coastal dunes, and wet interdunes) (Lim et al., 2002). Even these environments have areas where the exposed sediment is completely dry. The preservation potential and amount of detail that will be preserved is very low. Unless there is some form of moisture, either from precipitation—which may wash away the tracks—or condensation from the air (dew or fog; e.g., Lancaster, 1989; Hasiotis, 2004, 2008), tracks produced in strictly dry sediment have very little chance of being preserved.

Tracks found in water are likewise vulnerable to destruction. Wave action and further bioturbation can destroy tracks before burial. If the sediment is too saturated, even further deposition of sediment may distort the trackways. For example, no cast of the tracks was produced for the wet fine sand run because the plaster obliterated the tracks as it covered them, despite being poured away from the tracksite. Too much water was present, and the cohesion between the sand grains broke down. Even the minor disruption of a plaster pour, which in almost all other cases did not affect track morphology, was enough to completely destroy the tracks.

Bird tracks produced subaerially will usually become unrecognizable within 11 days (Cohen et al., 2001). As seen in this study, however, tracks with too much water content may be unrecognizable soon after being produced. The number of days that a track remains recognizable is surely variable—from hours to years, depending on biophysicochemical conditions (e.g., Hasiotis et al., 2012; Hasiotis and Platt, 2012). Falkingham et al (2011) discussed a "goldilocks effect", a narrow range of environmental conditions which must be "just right" for track production. This same effect would also apply to track preservation. Tracks can obviously be produced in a wide variety of sedimentological conditions, however, which conditions will be conducive to track preservation is dependent upon multiple factors.

Comparison with previous studies on avian tracemaking behavior

Genise et al. (2009) reported that takeoff tracks should be significantly deeper than tracks produced by walking or running. This study confirms that criteria, and also provides evidence that landing traces, at least in some cases, should also be deeper than traces produced by walking or running. Landing traces with elongated hallux drag marks, reported by Genise et al. (2009) may not be subject to this criteria.

Genise et al. (2009) reported stopping and standing as a clear pair of side-by-side tracks (Genise et al, 2009, fig. 7). During standing and feeding (Video: Chicken Coarse Sand Run 4, Fig. 14), the chicken does appear to stand with its feet side by side, however, the tracks are difficult to distinguish in a semitrampled area (Fig. 4). In general, in this study, when the birds paused in walking, the feet were not held side by side, but the bird literally paused in mid-stride. Furthermore, Genise et al. (2009) also illustrated takeoff as a trackway terminating in paired, parallel trackways (Genise et al. 2009, fig. 7). In the observations of both the domestic chicken and the Mourning Dove, however, takeoffs were noted as subparallel, with significantly long pace lengths (Figs. 7, 12), contrary to what is reported in previous studies. Landing traces may also result in nonparallel tracks, which has previously been shown only in a landing trace with the feet directed forwards, resulting in long hallux drag marks (Genise et al., 2009, fig. 7).

Fig. 14: Screenshot of chicken standing and feeding in coarse sand run 4.

Distinguishing between a fast walk and running in birds is difficult based on the knee-driven locomotion found in birds (e.g., Farlow et al., 2000). The pace and stride length observed during running is significantly longer than in walking in the domestic chicken (Table 6), and the tracks are slightly deeper. Determining high-speed running from slow walking should not be difficult in birds, however, walking speed and transitions in speed (e.g., from a fast walk to a slow run) are difficult to determine. In many cases, pace and stride lengths will vary without changing the walking speed, depending on the bird—this was also observed in the final mixed-sand run as well (Table 6, Fig. 7). For example, the pace length between tracks (not including the landing) varies from 134 mm to 161.8 mm with no change in the speed of the bird. This can make interpreting speed from stride length difficult in birds.

Comparison with some fossil bird tracks for morphology and behavior

Two different types of fossil tracks with unique morphology are compared to the modern tracks in this study to determine the sedimentological and/or behavioral characteristics that influence the ancient track production. *Pullornipes*, described from the Lower Cretaceous Tuchengzi Formation in western Liaoning Province, China (Lockley et al., 2006), has relatively wide toes (Table 7) and are compared to domestic chicken tracks produced in dry mixed sand run (Fig. 15). The ratio of toe III length to width for the chicken averages ~1.8 (Fig. 15B). The ratio of toe III length to width in *Pullornipes* averages ~3.5 (Fig. 15A). The toes of *Pullornipes* are not as relatively wide as those of tracks produced in dry mixed sand, however, the tracks do have generally blunt, rounded distal ends, and share the same characteristic collapsed morphology. *Pullornipes* trackways also have toe drag marks (Lockley et al., 2006), something that was not seen in the tracks of the domestic chicken in dry mixed sand. The level of detail present between *Pullornipes* and the chicken tracks is approximately the same; *Pullornipes* was also preserved in a mixed coarse- and medium-grained sandstone. The likelihood that *Pullornipes* was produced in dry sand is quite small—there are ripples present on the sandstone, and the formation itself has typical interbedded sand and mudstones typical of fluvial sequences (Lockley et al., 2006). The morphology, however, is similar to tracks produced in dry sand; perhaps similar morphology can occur in wet sediment in the correct conditions, or the water level fell after ripple production and the tracks were made in the dried sediment on the tops of ripples.

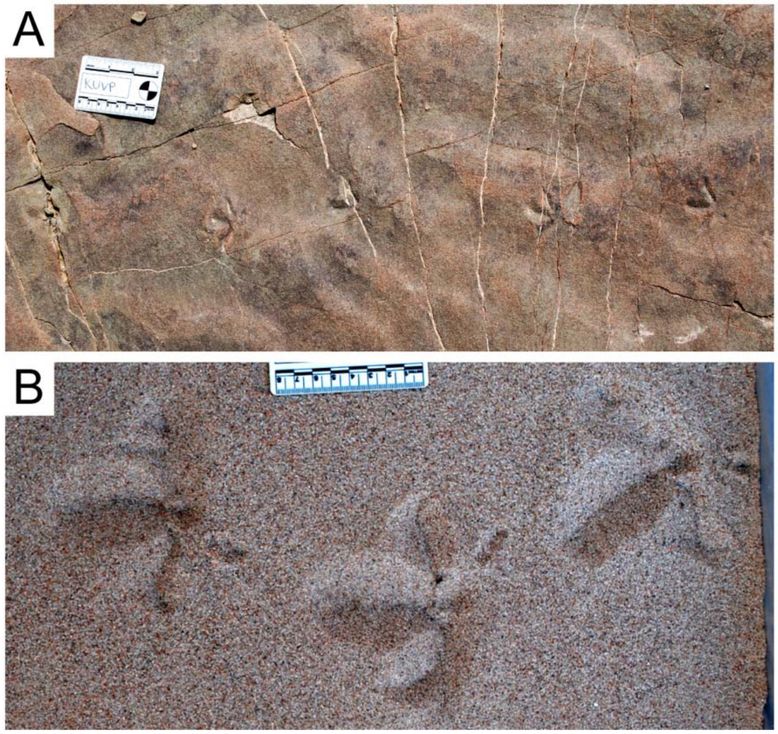

Fig. 15: Photographs of *Pullornipes* from the Early Cretaceous of western Liaoning Province compared to dry sand tracks from *Gallus*. A.) *Pullornipes*. B.) *Gallus*.

Trackway A									
	LII	LIII	LIV	WII	WIII	WIV	FL	FW	Hallux
1	20.92	N/A	18.37	3.55	N/A	4.54	N/A	26.28	-
2	15.47	23.61	20.44	5.06	7	4.68	29.47	39.33	-
3	19.95	22.85	21.44	3.2	7.99	5.28	30.84	38.59	-
4	19.48	24.67	20.31	4.79	7.58	2.36	29.82	40.58	4.24
5	20.42	24.58	22.55	3.47	9.48	7.42	32.22	48.97	6.31
6	22.92	24.74	17.72	4	5.94	5.02	36.32	45.59	7.76
7	23.72	27.8	N/A	5.48	6.47	N/A	38.13	N/A	4.75
8	18.17	24.57	24.51	5.31	9.08	5.03	39.04	45.18	6.45
9	N/A	N/A	N/A	N/A	N/A	N/A	38.33	51.16	-
10	19.6	26.81	21.8	2.64	5.43	3.01	34.14	40.34	4.28
11	15.63	25.69	23.17	3.21	3.2	3.01	37.9	37.54	-
12	14.75	21.37	21.07	3.93	3.69	4.44	31.34	36.99	-
13	19.48	24.98	23.24	5.99	6.25	5.26	34.88	44.48	-
Break									
1	13.47	24.94	21.83	5.58	6.49	7.1	34.38	42.79	10.67
2	14.9	25.43	20.38	4.74	8.91	2.04	33.24	43.37	5.98
3	16.26	25.95	22.03	4.69	4.11	2.97	31.38	40.87	3.6
4	20.55	21.53	23.11	N/A	8.05	4.2	32.02	49.61	-
5	20.22	19.76	25.33	3.26	5.36	3.81	28.59	48.33	5.49
6	17.85	23.85	22.27	2.63	5.58	4.25	28.08	45.59	4.04
7	14.58	22.84	21.4	4.65	7.39	6.27	28.87	45.62	-
8	14.13	21.94	20.67	3.05	4.98	3.25	26.43	46.68	3.03
9	20.73	18.7	21.74	3.44	9.02	2.71	28.05	45.58	6.39
10	14.13	22.59	22.54	3.24	5.02	5.87	29.05	43.58	7.14
11	20.73	19.39	18.49	8.3	9.22	5.96	26.44	43.59	10.99
12	19.97	25.79	19.37	5.15	10.62	8.29	30.86	44.74	10.75
13	21.73	N/A	N/A	6.26	N/A	N/A	N/A	N/A	20.82
14	21.23	N/A	21.82	6.52	N/A	4.53	N/A	47.06	13.96
		23.6687			6.82		3.47048		
Trackway B									
1	15.34	21.72	19.3	6.94	6.31	4.6	28.36	37.82	-
2	14.78	26.57	21.17	6.3	9.19	5.95	29.29	37.24	-
3	17.47	28.01	23.31	5.69	6.85	5.41	37.6	38.3	-
4	18.49	27.29	22.9	7.82	9.59	9.68	36.8	39.54	-

Table 7: Mophometric data of fossil tracks assigned to *Pullornipes.*

Typical *Koreanaornis* tracks from the Haman Formation of South Korea may or may not possess a hallux and a metatarsal pad, have a large angle of divarication, and slender toes. Atypical *Koreanaornis* tracks appear somewhat smeared, have a strong metatarsal pad impression, generally posses a hallux impression, and have larger than average angle of divarication (Fig. 16A–B). These tracks are similar to the tracks produced by a small chicken moving relatively quickly through wet fine sand (Fig. 16C). These atypical *Koreanaornis* tracks are, however, often preceded or followed by tracks with normal morphology (Fig. 16B). These atypical tracks may represent a change in speed (e.g., a very fast run) or a change in media consistency.

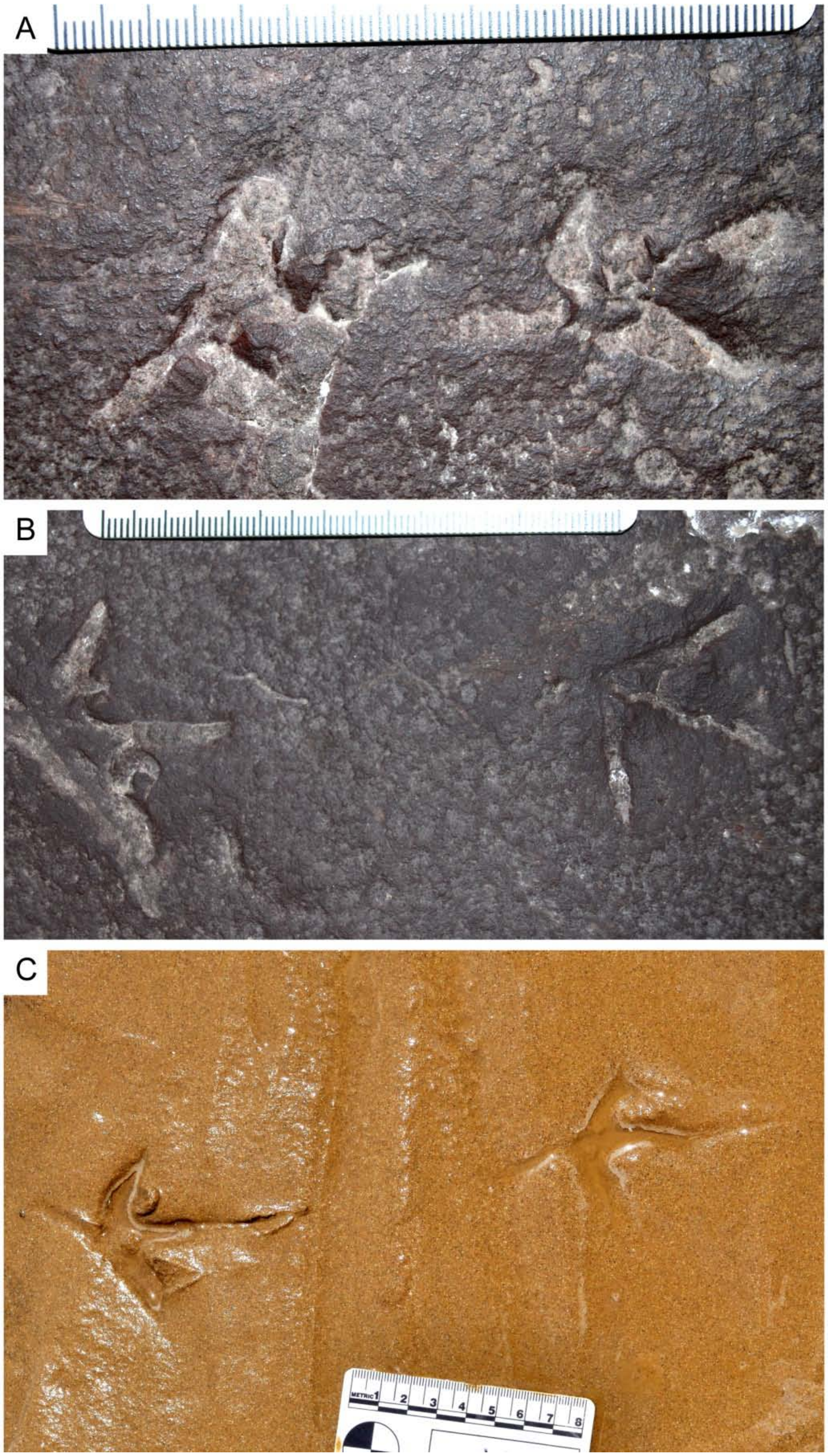

Fig. 16: Photographs of *Koreanaornis* (KS064) from the Haman Formation showing abnormal morphology, compared to tracks produced in wet fine sand from *Gallus*. A.) *Koreanaornis* showing abnormal morphology.

Tracks are a left and a right moving from the left side of the photograph. B.) *Koreanaornis* showing normal morphology. Tracks are a left and a right moving from the left side of the photograph. C.) Tracks of *Gallus* produced in wet fine sand (moisture content 6.7%). Tracks are a right and a left moving from the left side of the photograph.

The comparison of modern to fossil bird tracks for behavioral interpretation has been performed in multiple studies (e.g., Genise et al., 2009; Falk et al., 2010; Melchor et al., 2013). The morphological comparison between modern bird tracks produced in different media types can also be useful for interpreting paleoenvironmental and paleohydrologic environments. Although these methods may be semiquantitative, bird tracks and traces may be more indicative of paleoenvironment than has been previously discussed.

CONCLUSIONS

An experimental setup using controlled input of media (i.e., grain size and moisture content) and a video camera placed perpendicular to the sediment surface conclusively captures avian tracemaking behavior and trackway morphology during the time of trace production. This setup is portable, and can be used in both controlled field and laboratory settings. The monopod can be used separately from the rest of the setup and placed in a natural setting of interest (e.g., pointbar, sand bar, beach). Larger trays can be used, although multiple cameras may need to be used depending on the lens angle and tray size. Two species of bird in two controlled situations were used—the domestic chicken (*Gallus gallus*) and the Mourning Dove (*Zenaida macrocura*). The experimental setup was placed inside a chicken coop or next to a bird feeder respectively, and the observer left so as not to disturb the birds as they produced traces. Video footage was recorded to link traces with behaviors produced. Tracks were photographed and cast with plaster for quantitative analysis.

The morphology of bird tracks recognizably varies with both amount of moisture and size of sediment grains. The coarser the grains, the smaller the amount of detail preserved. Moist mud is the best for preserving detail; pad, claw, and scale impressions are all preserved. The amount of water present can also greatly affect the amount of detail. Too much water, and the tracks lack detail. Too little, and the detail is faint to nonexistent.

The most critical aspect of this new experimental setup is the ability to capture tracemaking behavior and irrevocably link it to the tracks produced. Qualitative and quantitative analyses of avian tracemaking behavior can be performed using this setup. Bird tracks are often sinuous, and the measurement of their sinuosity can be quantified using the sinuosity index, which is the straight line length of the trackway divided by the total length of the trackway. If the sinuosity index is near 1, the track is relatively straight; if it is near 0, the track is highly sinuous. There are four distinct types of trackways: straight, symmetrical, asymmetrical, and irregular. Straight trackways have little to no curvature, symmetrical trackways are symmetrical about a straight line, asymmetrical trackways are asymmetrical about a straight line, and irregular trackways self cross at least once.

Behaviors observed in this study include walking, running, sinuous walking, stopping and standing, feeding, landing, takeoff, and charging. This study confirms that both takeoff and landing traces should be deeper than traces produced by simple walking and running, and further supports that the pace and stride lengths of walking birds can vary unpredictably, although running birds do have a longer average stride length than walking birds. This study also suggests that start-stop walking does not necessarily result in paired, side-by-side tracks. Birds can, and often do, pause in mid-stride. Furthermore, birds may also land and take off with the feet separated, resulting in a trackway that begins or terminates in nearly normal pace length.

This is a largely preliminary study—this experimental setup will continue to be used to quantify multiple types of bird track morphotypes (e.g., perching birds) and a wider range of avian behaviors than presented here (e.g., probing, pecking, etc.).

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CONCLUSIONS

Avian ichnology and avian paleontology are areas of study within ornithology; however, these are seldom included in ornithological literature. This dissertation bridges the gap between ornithology, avian ichnology and neoichnology, and avian paleontology, laying the foundation for a more encompassing approach to the study of fossil avian behavior, morphology, and evolution, as well as modern avian body and trace morphology and tracemaking behaviors.

The avian tracks of the Lower Cretaceous Haman Formation of the Republic of Korea represent a diversity of avian morphotypes that is largely unknown from the avian body fossil record (Chapter 1). That diversity also extends to the behaviors represented by the tracks and associated traces. Scything, a behavior that is relatively unique to only a few groups of birds, is represented by long, arcuate traces associated with webbed-footed bird tracks. These scything traces are almost identical in morphology to those produced by extant spoonbills (Swennen and Yu, 2004; Lockley and Harris, 2010), except that the footprints associated with them are 43–61% the size of modern Black-faced Spoonbills (*Palatea minor*). Other behaviors include foraging, landing, and following megaherbivores.

Understanding and interpreting behavior and morphology from avian tracks and traces results in new information about depositional environment and avian evolution. The Haman Formation is interpreted as a fluvial system, however, no channels have been described, and mudcracks are common, indicating subaerial exposure (Choi, 1986). The avian tracks, however, must have been produced in the presence of water. Spoonbills and other scything birds do not scythe above water, as the electromagnetic sensory organs in their bills would not function. Modern scything traces, however, are not produced when the water is deeper than 6–7 cm, as the bird will not place its face in the water past a certain point and thus will not interact with the sediment (Swennen and Yu, 2004). Using this information, the water depth at the time of Haman Formation deposition can be interpreted as < 5 cm. Furthermore, as the avian tracemakers of the Haman Formation were ornithurine birds (due to their ground-to-air takeoff ability), the diversity of track morphologies and behaviors represents a hidden diversity (*sensu* Hasiotis, 2004, 2008) of ornithurine birds not seen elsewhere during the Early Cretaceous.

The soft tissue of birds is poorly understood relative to the underlying osteology, which adds difficulty in reconstructing the soft tissues of fossil birds. Also, the relationship between soft-tissue morphology and trace morphology is poorly known. The length of the osteological toe and fleshy toe, however, is not significantly different (Chapter 2), which suggests that there is no significant difference between the osteology of the avian foot and the traces that foot produces. The width of the toe at the joint is significantly different between osteological and soft-tissue specimens, however, only toe length is used when studying tracks, not toe width. Furthermore, there is no evidence that ethanol storage causes specimens to shrink, as there is no statistically significant pattern between subzero and ethanol storage.

The soft-tissue morphology of avian feet reflects their life habit. Birds that inhabit arboreal environments (e.g., perching birds) tend to have expanded, fleshy phalangeal pads and reduced or absent interphalangeal pads. Birds in the order Passeriformes also incorporate a portion of their proximal phalanxes into the metatarsal pad. Birds that inhabit water-margin environments tend to have expanded interphalangeal pads and reduced phalangeal pads. Their pads are also not fleshy and tend to be thin. Webbed-footed and lobed-footed birds do not possess true phalangeal or interphalangeal pads. Ground-dwelling birds (e.g., Galliformes) tend to have expanded interphalangeal pads, however, their interphalangeal and phalangeal pads are large and fleshy. Arboreal birds require the ability to grasp, which is likely the reason for the expanded phalangeal pad and reduced interphalangeal pad. Ground-dwelling birds do not need to grasp branches, however, and do not reduce their interphalangeal pads. Furthermore, ground-dwelling birds that live in upland habitats walk on firmground, whereas ground-dwelling birds that inhabit water-margin environments must contend with media that may be unstable and, therefore, need a more even surface for weight distribution. Large, fleshy pads create areas of pressure that could puncture through an unstable surface. This may be the reason for the relatively few number of pad impressions preserved in fossil bird tracks. Using the relationship between life habit and foot morphology recorded in Chapter 2, reconstructions of fossil bird feet can be performed.

The total hindlimb (foot + three separate hind limb elements) is one of the most variable structures in avian anatomy. The foot of birds, however, is more widely variable than the three hind limb elements (Chapter 3). Furthermore, as previous studies have shown, principal component analysis can establish both ecological niche modeling and evolutionary patterns in birds (Bell and Chiappe, 2011; Wang et al., 2011; Benson and Choiniere, 2013). None of these previous studies, however, have included the foot, and have only focused on the hind limb elements, discarding a series of critical data points. Chapter 2 illustrated the importance and diversity of the feet of modern birds, and Chapter 3 illustrated the overwhelming influence that the length of the toes, specifically toe I, has on the overall morphology of the hindlimb.

The use of PCA to establish a hypothetical morphospace in which to view clustering of modern and fossil birds established a primitive foot morphotype, with a relatively robust, reflexed hallux, but without the extreme elongation of the hallux seen in Passeriform birds, zygodactyl birds, and some wading birds. Additionally, enantiornithines often form their own cluster within the morphospace, further separating them from ornithurine birds. Some ornithurine birds have already developed a modern leg morphology and positioning by the Early Cretaceous, including *Gansus* and *Hongshanornis*. Other birds retain a primitive femoral positioning, indicating that the femur was not bound to the body wall with muscle, and the hind limb locomotion was hip driven, not knee driven as in modern birds.

Confuciusornis, a primitive, beaked bird, is among those primitive birds that fall into the primitive hind limb posture. *Confuciusornis* has several distinct characteristics, including a large deltopectoral crest with a large foramen, a unique pygostyle, and paired elongate tail feathers that may represent sexual dimorphism (Martin et al., 1998; Chiappe et al., 1999). Using laser fluorescence in combination with special camera filters, previously undescribed soft tissues, including scales and skin-muscle tissue complexes, are visualized (Chapter 4). The scales on the feet of two *Confuciusornis* specimens are entirely reticulate with no evidence of scutillate scales. Furthermore, on one specimen (IVPP V 13156), enlarged phalangeal pads are visible on the feet, indicating that *Confuciusornis* had a foot morphology similar to that of modern arboreal birds. The hind limb of IVPP V 13156 also preserves the outline of the tibiotarsal muscle tissue as a pinkish halo. This outline is likely the *m. gastrocnemius*, the main muscle in the lower leg, and it is relatively small, another indication of aboreality (Earls, 2000).

Previous interpretations of the flight ability of *Confuciusornis* have suggested that, because of thin, weak primary feather rachises, it was likely unable to perform flapping flight (Nudds and Dyke, 2010). *Confuciusornis* had a keel that was relatively small and previously interpreted to be restricted to the caudal half of the keel (Zhou and Farlow, 2001), however, it may have been slightly more expanded than previously suggested (Chapter 4). The idea that *Confuciusornis* had weak primary rachises has been refuted (Zheng et al., 2010), and the data presented here also shows that *Confuciusornis* had primary rachises >1.5 mm thick, which is comparable to modern birds. *Confuciusornis* has relatively long primaries in comparison to its ulna, which is usually the case seen in fast-flying birds (e.g., swifts) (Wang et al., 2011). The 10th (outermost) primary of *Confuciusornis*, however, is relatively short—the 8th and 7th primaries are actually the longest primaries. The secondaries are also relatively long in relation to the primaries, unlike the secondaries of modern fast-flying birds, resulting in a much broader wing surface than is found in fast-flying birds. *Confuciusornis* likely relied on a broader, more maneuverable wing shape.

In order to understand the production and behavior of fossil avian tracks and traces, observation, recording, and morphologic measurements of modern bird tracks must occur. Although a handful of previous studies have examined modern bird tracks, either morphologic measurements and/or media analysis (sediment grain size and moisture content) was not performed (Swennen and Van Der Baan, 1959; Cadhee, 1990; Genise et al., 2009; Melchor et al., 2012). The morphology of bird tracks is significantly influenced by not only grain size, but also by sediment moisture content (Chapter 5). Tracks produced in dry sediment appear blunt and wide toed, without any detail preserved. Tracks in saturated sand preserve the outline of the toe (i.e., a tapered digit impression), however, fine detail is not preserved. In wet or moist sand, pad impressions can be preserved; if the sand becomes too dry, they will not be preserved. Claw impressions can be found in wet or moist sand, and in mud. Scale impressions are only preserved in mud.

Although Genise et al. (2009) suggested that takeoff traces should be deeper than the surrounding traces, no data were presented to support this statement. Traces produced by both takeoff and landing result in tracks that are 10–20 mm deeper than simple walking traces. Although the sample size is small, traces left by a running bird also appear to be slightly deeper

(2–4 mm) than traces left by a walking bird. Furthermore, the stop-start walking described by Genise et al. (2009) as resulting in paired, side-by-side tracks, was not observed. Instead, start-stop walking that resulted in a normal-looking trackway, where the bird stopped in midstride, was recorded. Takeoff and landing traces, both of which Genise et al. (2009) illustrated as being parallel, paired trackways, are often staggered and non-parallel.

This dissertation represents a fundamental need for collaboration between avian ichnologists, paleontologists, and ornithologists. Chapter 1 indicates that the diversity of ornithurine birds was higher in the Early Cretaceous than previously supposed, and that the types of behaviors are already advanced, modernlike behaviors. The osteological and soft-tissue morphology of the foot is tied closely to the life habit of the bird (Chapter 2), and is also tied in to the types of tracks and traces produced, although soft-tissue morphology does not influence the gross morphology of the track. The results of Chapter 3 indicate that, without understanding the foot morphology of a bird, the variation throughout the hindlimb cannot be understood. The reconstructions of the foot, hindlimb, and soft tissues of *Confuciusornis* in Chapter 4 could not have been performed accurately without the information from Chapters 2 and 3. Finally, Chapter 5 begins to move towards a synthesis of observation and morphologic data collection using a new experimental setup to link observations and morphometric analysis to catalog modern avian tracks and traces. Data presented indicates that although the width at the joint is significantly different between the osteology and soft tissue of birds (Chapter 2), the width of the digit impressions varies strongly depending on media consistency.

This is only the beginning of our understanding of how avian foot morphology and behavior has evolved through time. Several Lower Cretaceous avian trace fossil localities in China represent track densities and diversities almost as great as the Geyongsamnado Institute of

Science Education in the Republic of Korea (Chapter 1), however, there has been no behavioral analysis of these tracksites. Laser fluorescence as used in Chapter 4 should be applied to many more Jehol Group specimens to examine them for soft-tissue preservation. The experimental setup and methodology used for collecting modern avian tracks in Chapter 5 has been shown to work in an uncontrolled setting at a bird feeder, however, it should be applied in other laboratory and field settings to obtain a complete record of birds performing a variety of behaviors from all avian foot morphotypes.

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Appendix I

	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
Trackway 1	1	60	37	97	23	38	34.5	7.7	9.5	5	48	57	0.842	17	L
	2	53	40	93	26	40	34.2	7	7.7	5.5	49.2	59.7	0.824	25	R
	3	87	40	127	21	33	24.7	9	6.2	4	40	62	0.645	14	L
	4	62	51	113	20.5	30	20	6.5	4.5	8.2	36.7	64.7	0.567	26.5	R
	5	80	56	136	12	35	17.5	10	11	8.2	46	48	0.958	19.5	L
	6	72	44	116	25	43	36	6	8.2	6.7	48.2	57	0.846	29.7	R
	7	84	53	137	26	30	29.7	13.7	9.2	7.7	46.5	64.7	0.719	14	L
	8	57	46	103	24.7	38.5	32.5	5.2	9.5	11.7	51.5	54	0.954	25.5	R
	9	51	99	160	21.2	26.2	20.7	10	12.5	5	45	56.7	0.794	18	L
	10	54	35	89	29	26	33.5	8	9	6	47.2	62.5	0.755	16	R
	11	58	46	104	24	39.5	22	13.7	7.2	5.7	48.5	59	0.822	36	L
	12	55†	35	90	23	39.5†	32.5†	4.5	9.5	6†	51.5†	54†	0.954	23.5	R
	13	65	56	121	22.2	28.5	29.2	7.5	6	7	51.2	61.2	0.837	21.7	L
	14	52	63	115	26.2	36.2	28.2	9.7†	11.5	8.7	53.5	60.7	0.881	22.2	R
	15	46	58	104	20.5	36.2	33.5	8.5	9.5	6.5	57	61	0.934	31.5	L
	16	42	36	78	22.5	33	34.2	8.2	7	6.2	51.2	70.1	0.73	25.7	R
	17	78†	58	136	28	35.5	23	6	11.2	10.5	47.5	52.5	0.905	32.7	L
	18	73	48	121	27.7	35.5	29.5	7.5	3.5	6	45	55.5	0.811	31.5	R
	19	46	32	78	14.5	30.5†	29	8	7.2	6.5	41	50.1	0.818	-	L
	20	40	37	77	22.5	42†	24.5	8	7	5	59†	52.2	1.13	13.5	R
	21	22†	48	70	25.5†	35†	27.5	6.5†	10.5	12	46.5	59.2	0.785	30.2	L
	22	82	-	-	20.5*	28	27†	9	8.7	-	52	63.5†	0.819	32.2	R
Trackway 2	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	0	25	56	81	17.5	24.5	24.5	5.5	6.5	4.5	37.5	45.5	0.824	21.5	L
	1	35	53	88	15.5	27.5	26.5	10.5	8.2	5	44.2	48.5	0.911	17.5	L
	2	39	45	84	16.2	28.5	22.7	12.5	9	5	41	55	0.745	20.7	R
	3	42	60	102	21.2	29.2	28.2	9.2	6.7	6.2	44.5	51.2	0.869	19	L
	4	30	64	94	23.5	29.7	17.5	8	9	5.2	44.7	48.5	0.923	7.5	R
	5	35	74	109	22.7	25.5	22.5	6.5	9.5	6.2	41.5	52	0.798	24	L
	6	37†	89	126	19	26.5	24.7	7.5	13	7	39.5	49.5	0.798	-	R
	7	26†	94	120	17.5†	33.5	17†	-	-	-	42†	50†	0.84	27	L
	8	63	65	128	16.2	36.5†	26.5	7	4	6.2	41†	51.2	0.801	-	R
	9	40	59	119	19	24.5	19.5	6.5	8.5	4†	43	50.7	0.848	-	L
	10	39†	59	98	16†	29.5	25.5†	10.5†	5.5†	6.5	36.5†	57	0.64	20	R
	11	67	20	87	19	30	29	5.2	7.5	5	43	46.7	0.921	27.2	L
	12	51	88	139	16.5	27.7	23.5	7	10.2	11	38.2	49	0.78	12.5	R
	13	26	71	97	21.2	29.7	22.2	5.5	8	5.5	38.9	52	0.794	13	L
	14	77	78	155	17.5	26.5	24.7	16.2	5.2	5.5	45.2	54	0.837	36	R
	15	51	55	106	15.7	28	20	10.5	6.2	7.7	39	44.2	0.882	21.2	L
	16	58	65	123	25	27	23.2	3.5	8.5	5.5	41.2	53	0.777	17.5	R
	17	39†	91	130	18.5	19.2	20.5	5	5	7.5	34.7	40.5	0.857	19.2	L
	18	64	83	147	20.5	28.5	27	6	8	6.7	47.5	60	0.792	-	R
	19	44	59	103	16.5	22.5	24	6.2	8.7	5.7	39.7	50.7	0.783	19.5	L
	20	37	73	110	14.2	26.2	23	5.5	6	4	39	61	0.639	22.7	R
	21	30	79	109	20.2	25	25.5	12	11	3.5	37.2	63.5	0.586	20	L
	22	36	86	122	13.5	24	19	7.2	14	8.2	36	45.2	0.796	7.5	R
	23	-	-	-	24†	-	-	-	-	-	-	-	-	18.7	L
Trackway 3	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	57	46	103	24.2	27.5	19	7	8.5	5.7	44.5	54.2	0.821	11.7	R
	2	50	45	95	21	36.5	29.5	6.5	12	7	50.5	58.2	0.868	10	L
	3	23†	73	96	31	37	29	9	-	-	45	62	0.726	28.5	R
	4	42†	52	94	21.2†	29	23	6	5.5†	6	39.5	64	0.617	11.5	L
	5	74†	90	164	16†	25.5*	20.5	10.5†	12.5	9.5	43.5	57.2	0.76	22.7	R
	6	62	64	126	20.5	22	20.5	9	16	12	42.7	60	0.712	-	L
	7	58	94	152	21.5†	28.2	21.2	9.5	17.7	8.5	43	57.2	0.752	-	R
	8	41	57	98	22	34.7	28.5	3.5	14.5	7	43.2	57.5	0.751	23.5	L
	9	61	67	128	26.5	30.5	16	7.7	9.2	5.5	43	56	0.768	14.5	R

	15	49	79	128	26.2	34.5	25.7	8.2	5.5	4.5	49	51	0.961	19.2	R
	16	51	76	127	23.2	31.5	24.5	4.7	13	7.5	41	51.7	0.793	7.7	L
Trackway 4	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	61	46	107	24.5	35	33	9.5	7	6.2	47.2	61.5	0.767	29.7	R
	2	56	59	115	22	29.5	38.5	5.7	7.5	6	44.2	64	0.691	8.5	L
	3	88	76	164	15	25.5†	24.5	5.5	6.5†	3	37.2	50	0.744	-	R
	4	54	49	103	27.7	34.5†	34	5.2	5.5	3	41.5	56	0.741	14.5	L
	5	91	41	132	12.7†	34.5	32.5	6.5	5.5	5.5	44.5	55†	0.809	-	R
	6	45	52	97	18.5	30	27	6.5	4.5	6	41	56.2	0.73	28	L
	7	71	43	114	22.5	38.7	31.5	5.5	5	5.5	48	60	0.8	15.2	R
	8	81	-	-	15.8	28.2*	-	-	-	-	39.5	-	-	18.5	L
	9	48	41	89	22	27.2	30.5	8†	4.5	4.5	42.2	62.7	0.673	12.5	R
Trackway 5	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	51	55	106	22.5	31.7	24.5	6.2	5.2	3	43	46.7	0.921	-	L
	2	42	43†	85	23*	33†	30.5*	4*	5	5.5*	41.5*	49.5*	0.838	-	R
	3	57	50	107	20	32.2	23	5.2	8	6.5	48.5	60.5	0.802	23.7	L
	4	50	46	96	25.5	34.2	28.7	7.2	6	6	44	57.2	0.769	20.2	R
	5	42	53	95	20	30.5	29.2	6.7	5.7	5.7	39.5	57	0.693	20.5	L
	6	48†	51	99	23.5	29.2†	24†	8.5	6.5†	9.5†	47†	56.2	0.836	18.5	R
	7	43	55	98	26	35	27.7	8.5	7	4.5	40.5	57	0.711	18.7	L
	8	60	41	101	22.7	33.2	34.5	9.5	10	6.7	47.5	60	0.792	17.2	R
	9	48	61†	109	16.5†	22.7†	25†	9	6.7	8.5†	41	60	0.683	-	L
	10	58	44	102	19	24.5	24	5	9.7	3.7	44.2	54.5	0.811	26.5	R
	11	41†	59†	100	28.5	36.5	34†	7.2	8.5	9.5†	45.2	56.2	0.804	35.2	L
	12	56	-	-	17	29.7	28†	10	5	-	41	64	0.641	26.7	R
	13	25	51	76	25.2	35.2	37.5	9.5	6.2	5	49.5	60.2	0.822	26.2	L
	14	38	28†	66	20.5	30	-	5.5	7.5	-	53	-	-	21.5†	R
	15	-	56	-	-	37.5*	21.7	-	-	7	53†	-	-	29	L
	16	50†	31†	81	29*	30.5†	19*	4.5	2.5	4.5	-	-	-	-	R
Trackway 6	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	-	-	-	-	21.2	-	-	-	-	-	-	-	-	L
	2	-	93†	-	-	22.2	12.8*	-	8	3	-	-	-	-	R
	3	-	-	-	-	22	34.7	11.2	8.2	-	36.2	-	-	-	L
	4	4	71	75	22	24.5	21	7.5	9	5.2	37.5	39.5	0.949	8	R
	5	58	28	86	17	22	15	8	12.5	3.2	34	45.2	0.752	12.5	L
	6	50	47	97	26	29.7	27.2	8.5	11.2	5.2	43.2	48.5	0.891	17.5	R
	7	35	57	92	20.5	27.5	22.5	7	10.2	9	43	47.2	0.911	9.5	L
	8	50	61	111	17.5	27.5	23.5	7	8.5	10	50	53.5	0.935	13	R
	9	50	64	114	20.5	26.7	25	11.5	10.5	8.7	40	50.5	0.8	15.5	L
	10	36†	68	104	20.5	28.5	29	7	8.5	3.5	48†	45.5	1.05	-	R
	11	60	55	115	17	25.2	19	6.5	8.7	5.5	39	47.2	0.826	15.2	L
KS049	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	54	37	91	25.85	40.47	27.66	6.37	8.46	4.44	41.64	44.62	0.933	16.49	L
	2				22.11	32.77†	16.7	4.46	-	7.64	38.85†	46.69	0.832	15.28	R
	3	47	53	100	18.49	34.15	25.39	5.26	8.98	5.7	43.66	47.54	0.918	19.9	L
GS021	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	
	1	24	66	90	33.22	39.34	36.37	10.84	9.04	14.59*	52.35	59.91	0.874	32.63	-
	2	41	41	82	25.98	40.31	34.64	11.48	9.34	9.41	51.22	57.65	0.888	34.11	-
	3	44	25	69	35.46	39.04	31.49	11.45*	5.89†	7.66†	43.09	61.6	0.7	25.48	-
GS012	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	26	51	77	27.76†	43.02†	28.04	-	10.81	7.44	49.38	61.03	0.809	25.5	L
GS018	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	75	79	154	24.4	25.96	23.82	10.31	6.85	5.35	33.9	59.47	0.57	22.58	L
	2	61	63	124	19.26	34.76	31.46	7.64	15.8	8.19	43.07	56.85	0.758	14.06	R
	3	47	72†	119	22.32	29.05	30.93	12.2†	11.41	12.58	40.19	60.95	0.659	27.95	L
	4	68	85	153	20.78	32.27	30.21	5.46	-	5.58	39.71	62.42	0.636	9.89*	R
	5	-	-	166†	24.36	22.85†	33.72	-	-	-	38.95	57.86	0.673	31	L
	6	47	83†	130	25.23	34.03	27.39	7.81	10.17	-	45.41	51.78	0.877	28.84	R

	3	63	46	109	21.2	35.91	34.97	9.64	10.14	11.03	47.79	58.64	0.815	18.38	R
	4	30	76	106	32.14	25.7*	31.6*	7.7	8.6	12.17	45.24	60.56	0.747	27.73	L
	5	76	45	121	31.58	32.81*	37.4	10.61	11.05	8.24	44.04	61.1	0.721	13.35	R
	6	64	39	103	18.84	37.36*	34.16	4.86	11.43	6.87	49.01*	56.31	0.87	29.72	L
		II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	

Table 1: Single-track measurements taken of all spoonbill-like footprints (assigned to *Ignotornis gajinensis*) from the GISE. II=Toe II, III=Toe III, IV=Toe IV, LII=Length of toe II, LIII=length of toe III, LIV=length of toe IV, WII=width of toe II, WIII=width of toe III, WIV=width of toe IV, FL=foot length, FW=foot width, R=right, L=left. †=estimated length or width, *=digit impression that was incomplete, usually due to the broken edge of the slab. All measurements are in millimeters unless stated otherwise.

KS064	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	L/R
	1	61	50	111	12	21.2	13.2	3	3.5	2.5	25	31.7	0.789	-	R
	2	89	54	143	10.5	16.7	17	7.2	4.5	3	19.5	35.2	0.554	-	R
	3	54	70	124	11.7	18	16.2	4	2.7	3	26.2	35.5	0.738	-	R
	4	73	41	114	13†	20	18.2	2.5	4.2	5	25.5	36	0.708	-	L
	5	57	42	99	10.5	20.2	18.2	2.5	3.2	2	22.2	34.2	0.649	7.2	R
	6	61	60	121	11.9	20.5	12.2	3.5	2.2	3	22	30.2	0.728	-	R
	7	40	64	104	14.5	19	14	4.2	2.5	4	24.5	28.2	0.869	5	L
	8	57	39†	96	12.7†	18.9	16.5†	4	4.5	5.2	23.9	36.2†	0.677	10†	L
	9	36	52	88	12.7	22.7	16.5	5.2	3.2	6.2	28.2	29.5	0.956	12	L
	10	48	48	96	12.9	18.5	16.7	4	6	5	28.7	28.5	1.01	13.5	R
	11	48	63	111	9.7	20.5	18	2.2	1.5	3.5	28	30.2	0.927	-	L
	12	47	44	91	15	25.2	19	3.5	3	3.5	30	34.2	0.877	5.5	R
	13	40	81	121	12.2	15.2	13.2	3.9	3	4	23.2	36.5	0.636	-	L
	14	49	52	101	16.2	22	15.5†	4	4	2.9	30	34.5	0.87	-	L
	15	65†	60	125	14†	19.5	13.5	2.9	1.9	3.2	23.7	30.5	0.777	-	R
	16	38	45	83	10.5	15.5	14.5	3.2	3.2	3.2	20.5	28.7	0.714	3?	R
	17	32	75	107	7.7†	14.7	12.5	3.7†	2	4	18.2	29.9	0.609	-	R
	18	47	41	88	9.5*	11	11	2.2†	3	3	16.2	21.2	0.764	-	L
	19	39	56	95	14	18.2	15.2	5.7	2.2	1.5	24.7	30.5	0.81	-	R
	20	61	27†	88	17.2	21.5	14.2†	3.9	3.2	3.2	24.5	36†	0.681	-	L
	21	73	45	118	13.5	20	19.9	4.5	3.5	4.5	25	41.5	0.602	-	R
	22	52	58	110	18.5	20.5	14.2	4.5	2.2	2.9	29.2	40.9	0.714	8.5	L
	23	39	49	88	8.7†	14	9.5	3	3.5	1.2	24.2	26.5	0.913	10.5	R
	24	61	53	114	15.5	18†	17	4	4	3	27	41.9	0.644	10.5	R
	25	56	60	116	19	21.2	20.2	3.5	3.5	3	30.2	39	0.774	6.2	L
	26	65	46	111	15.7	22.2	20	4	3.9	3.9	26.7	42	0.636	9	R
	27	64	47	111	12.5	18.5	15.5	3	4	3	26.2	36	0.728	-	L
	28	111	37	148	7.5	19.2	14.5	2	3	2.2	23.5	28.2	0.833	11.5	R
	29	76	36	112	7.2	16.2	10.5	3.7	2.7	3.5	22.9	25.2	0.909	9.5	L
	30	61	51	112	8.2	18.9	12.5	2.5	4.2	2.5	27	29	0.931	7.2	R
	31	47	60†	107	17†	21.5	12.7	2.2	7.2†	5†	26.2	32	0.819	11	L
	32	83†	46	129	8†	16.5	12.9	2.5	2.5	2.5†	21.2	25.2†	0.841	-	R
NHC-IC-002A	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	L/R
	1	73	44	120	14.5	20.5	16.5	5	4	4.5	25	35	0.714	7	R
	2	60	41	101	21.5†	24	20	8.5	4	7.5	29	38†	0.763	12	R
	3	-	78	-	-	20*	13*	-	4.5	2.5	-	-	-	-	L?
	4	46	84	130	11.5	13	17.5	2.5	3	4	21	32	0.656	-	R
	5	71	70	141	13	18†	15	2.5	2.5	2	23†	32	0.719	5	L
	6	44	71	115	16	22	12	2	4	2	23.5	26	0.904	10	R
	7	56	-	-	15	24	-	6	3	-	33	-	-	6.5	R
	8	70	58	128	14	20	18	5	4	2.5	25	38	0.658	13	L
	9	45	126	171	10.5	23.5	20	5.5	3	2.5	26	31	0.839	11	L
	10	40	65	105	16.5	20	20	3	3	2	25	40	0.625	5.5	R
	11	67	73	140	14	15	17.5	6	3	2.5	23	37	0.621	6.5	L
	12	50	74	124	13	17	15	4.5	2	3	24	27.5	0.873	-	L
	13	83	42	125	12.5	17	14.5	3.5	2.5	3	21	30	0.7	10.5	R
	14	67	52	119	14	20	15	4	2	3.5	25	32.5	0.769	6	L
	15	56	62	118	13	21.5	17.5	6	4	4.5	25	34	0.735	3.5	R
	16	61	68	129	15	18	21	4	1.5	3.5	26	38.5	0.675	9.5	R
	17	65	53	118	16	15	17	5	3	3	20	36.5	0.548	6.5	L
	18	73	58	131	11	19	18	4.5	3	3	24	34	0.706	-	R

	19	64	78	142	10.5	15	16.5	5	3.5	3.5	23.5	31.5	0.746	7.5	L
	20	73	45	118	19	23	20.5	6	4.5	3	30	44	0.682	9	R
	21	62	61	123	12	18†	13.5	4.5	1.5	3.5	24	35	0.686	11†	L
	22	63	72	135	12	17	19	4	4	3.5	24	24.5	0.98	-	L
	23	71	110	>180	16	20.5	19	4.5	3	3	26	37.5	0.693	5.5	R
	24	51	55	106	13.5	22	12.5	4.5	9	3.5	24	32.5	0.738	5.5	L
	25	72	-	-	-	18.5†	12.5	-	5	3	-	-	-	9.5	R
	26	59	40	119	11†	19	15.5	2	3	2	26	29†	0.897	4	R
	27	63	67	130	11	17	16	4	3.5	4.5	22	38	0.579	-	L
	28	51	43	114	11.5*	23.5	19.5	2.5	3	2	26	34	0.765	-	R
	29	77	53	130	14	17.5	18	2.5	2	3.5	25	38	0.658	10	R
	30	46	70	116	17	22	19	5	3	2	25	39	0.641	-	L
	31	45	69	134	8.5†	20	18.5	5	2	4	23.5	33	0.712	-	R
	32	86	50	136	13	19.5	12	1.5	1	2	24	33	0.727	8.5	R
	33	59	65	124	9	23	16	5	2	3	25	35	0.714	6	L
	34	31	49	80	15.5	23	16.5	3	5	3	26.5	36	0.736	7	R
	35	69	71	140	18	21.5	16	4	2	4	26	36	0.722	6	L
	36	56	82	138	19	20	21	4.5	4.5	4	26	48	0.542	10.5	R
	37	64	78	142	14	13	15.5	3.5	2	2.5	21	38	0.553	-	R
	38	61	38	119	10	23	20	3	2	4.5	24	29	0.828	-	L
	39	86	60	146	17	20.5	15	8	2.5	3.5	27	39	0.692	4.5	L
	40	82	51	133	14	20	13.5	9.5	7	8	25	41	0.61	-	L
	41	48	55	103	13	20	19	6.5	3	3	29	32	0.906	4.5	R
	42	55	56	111	16	20	17.5	2.2	3.2	4.5	23	34.2	0.673	-	R
	43	63	75	148	15.5	20	16.7	6	3.5	4	28	38.7	0.724	9	R
	44	46	72	118	7.7	17.5	14.5	4.2	3	3.7	22.2	34.5	0.643	18.5	L
	45	88	63	151	12	12.5	10	3	3.5	5	17.7	24.5	0.722	4.5	L
	46	75	65	140	17	17	18	5	3.2	3.5	24.5	39.5	0.62	10.5	R
	47	54	56	111	14	19	21	5.5	3.2	4	23	36	0.639	5.2	L
	48	71	59	130	19.2	18	19.2	6.2	1.5	2.2	24.2	42.2	0.573	14	L
	49	59	85	144	8.5	17	13.2	4	4.2	3	21	37.5	0.56	-	R
	50	56	64	120	13.7	19.5	16	4	3	3	24.7	34.2	0.722	4	L
	51	55†	64	119†	12.7	15*	-	3	3.5	-	-	-	-	-	R
	52	48	34	82	10.5	17	17.2	4	2	2.5	21	25	0.84	8	R
NHC-IC-003a	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	L/R
	1	34	62	96	13.2	14*	16.2	5.5	6.7†	5†	19*	39.5	0.481	13	R
	2	63	43	106	13.7	17.7	17	5.2	2.7	5.5	26	37.2	0.699	6.5	L
	3	47†	71	118	12†	16.2	16.2	4.5†	5.5	3.5	27.2	32.5†	0.837	4	R
	4	60	49	109	13	18.2	13.7	4.5	3	4.2	25	28.5	0.877	-	L
	5	42	111	153	14.5	18.5	10	1.5	3.5	2.2	19.5	28	0.696	8.5†	R
	6	74	47	121	15.7	17.5	13	2.7	3	2	25	33	0.756	6.7	R
	7	62	51	113	11	15.2	14	1.7	5	2.5	22.2	36	0.617	-	R
	8	67	38	105	12	19.2	15.5	2	3	2.2	25	34.5	0.725	-	L
	9	53	57	110	15.5	15.5*	19	3.2	1.5	3	25.5†	32	0.797	6	R
	10	55	59	114	13†	22	15.7	3.7†	3	5.2	25	27†	0.926	-	L?
	11	64	58	122	11.2	18.2†	15	4.2	5.5	7	24†	32.5	0.738	-	L
	12	43	64	107	12	17.5	17.2	3.7	3	4.5	23.5	30.5	0.77	5.7*	L
	13	18	74	92	16.5	24.7	18	5.2	6.2	4.5	34.5	33.5	1.03	8†	R
	14	44	53	97	10.5†	18	14.7	4.5	2.5	9.5	27.7	30†	0.923	12	L
	15	63	52	115	15	17	13.5	5.7	3.5	4.5	23.5	34	0.691	7.5	R
	16	49	44	93	12.5	15.5	13	3	3.7	2	22.2	28.5	0.779	9.2	L
	17	73	79	152	13.2	14.5	17.7	4.5	3	4	18.2	37	0.492	-	L

	18	55	47	102	10	16.5	12.5	2	1.2	3	23.5	27	0.87	7	L
	19	74	54	138	11	18.2	15	9	2	3	21.2	31.5	0.673	14.2	R
	20	65	86	151	11	17.7	16.5	5.5	3	5.5	25.2	33	0.764	-	L
	21	55	79	134	15.5	15	12.2	2.5	3.7	3.7	21.2	37	0.573	6	R
	22	44	53	97	12.5	24†	14.2	2.2	3†	3.5	27.7	27.2	1.02	9	R
	23	51	69	120	10	17	14.7	3	3.2	3	25.5	30	0.85	-	R
	24	58	52	110	8.5*	18	15	4	3	2.5	22	33.5*	0.657	-	L
	25	98	54	152	13.5	9.7†	19	3.5	5	3.2	22†	35	0.629	12	L
	26	62	47	109	13.7	17.2	15.5	4.5	2.5	3	22.2	32.5	0.683	5.2	L
	27	50	66	116	13.7	16.5	18.2	4.5	1.5	5.5	27.2	36.5	0.745	-	R
	28	57	49	106	11	17	15.5	3.2	2.5	4.7	22	28	0.786	9.2	L
	29	62†	36	98	13.3†	16.2†	17.5	?	2.7	2.5	20.7†	32†	0.647	10.2	R
	30	35	69	104	13.5	15.5	13.2	4	4	3	25.2	30.2	0.834	10	L
	31	65	50	115	14	18.7	17.2	4	3.5	3.2	25	33.5	0.746	-	R
	32	46	81	127	13	16.7	14	3.5	4.5	3.2	23	34.2	0.673	-	R
	33	31	64	95	13	20.5	19	3.5	3.5	2.2	30.5	33.5	0.91	6.2	L
	34	40	49	89	12.5	20.5	16.5†	3	3.5	3	29	36†	0.806	-	L
	35	62	70	13.2	9.2	15	11	3.7	3.7	3.2	21	30.5	0.689	-	R
	36	54	59	113	10	14.5	13	3.7†	2	3	20.2	33	0.612	10	R
	37	73	53	126	12.5	19.5	14.2†	3.5	1.2	2	26.5	30†	0.883	-	L
	38	44	55	99	12	14	11.5	2.5	2.7	2.2	19.5	27.2	0.717	5.5	L
	39	59	71	130	10.2	18	13*	4.5	2.7	3.5	26	28.2†	0.923	8	L
	40	48	50	98	11.2	18.2	17.5	5	3.7	3.5	26.5	29.2	0.908	7.5	L
	41	45	106	151	10.5†	18.2	17.2	2.7	2	2.5	22.5	31.2	0.721	8.2	L
	42	62	61	123	12	19.7	13	3.5	4.7	2.5	22	31	0.71	-	R
	43	55	55	110	12.5	19	18	2.2	2.7	3.7	25.2	28	0.9	10.5	R
	44	76	48	124	11.2	17.2	13	4.7	2.5	4.7	26	29	0.897	8.7	R
	45	61	58	119	9	11	12	3	5	3.5	19.5	26.7	0.73	5	R
	46	55	73	128	6.2	17.5	13	2.2	2.2	1.7	22	26.7	0.824	6	L
	47	59	49	108	12	21	13	1.5	2.2	2.2	26.5	29	0.914	7	L
	48	96	40	136	8	13	13	2.2	3.7	2.5	18.5	32.2	0.574	10.2	R
	49	71	84	155	8.2	21.5	15.2	6	3.5	4.5	26	29	0.897	8.2	L
	50	50†	39	89	-	20.5	13.5	-	3.2	3.2	24.2	-	-	-	R
	51	64	53	119	13.5	20	17	2.5	2.5	3	26.5	32	0.828	10.7	R
	52	78	45	123	10.5	18.2	19	3.2	1.7	4	25	34	0.735	-	L
	53	52	65	117	10.5	20.7	17	2	1.5	4.5	23.5	34	0.691	-	R
	54	80	65	145	9	13	11.7	3	2	2	20	30	0.667	-	R
	55	60	49	109	10	14.5	10	4	4	1.7	20.5	28.5	0.719	-	R
	56	55	50	105	13	18	13.5*	2.5	4	3.2	25.5	27.7*	0.92	2.2	R
	57	50	71	121	13.7	17	11†	11	2.5	4	25.7	27.2†	0.945	11.5	R
	58	45	64	109	12	19.5	14	4	4	6.5	24	32	0.75	-	R
	59	66†	34	100	10.5*	20.7	14	-	4	2.5	25.7	-	-	-	L
	60	89	49	138	18.7	18.5	15	2.5	3	2.7	23	31	0.742	5.5	L
NHC-IC-004	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	65	85	150	15.91	17.71*	16	2.67	3.85	6.08	23.87	39.42	0.606	-	R
	2	66	69	135	13.96	20.74	18.93	4.07	2.73	3.85	25.78	38.6	0.668	-	L
	3	66	70†	136	19.03	25.04	17.49*	7.88	6.17	4.34†	30.33	35.96*	0.843	13.55	R
	4	76	69	145	17.73	16.97†	18.86	3.9	3.58	5.32†	23.22	42.78	0.543	13.69	L
	5	64	68	134	15.84*	21	19.27	5.59†	4.52	5.92	26.97	38.77†	0.696	-	L
	6	74	51†	125	15.64†	18.82	16.13	3.51	-	4.83†	26.11	31.5	0.829	-	L

	7	47	49	96	15.35	23.01	18.95	7.52	4.49	1.99	29.81	33.27	0.896	8.2	R
	8	82	45	127	14.01	19.77	19.83†	4.22	1.29	1.42	24.89	37.01	0.673	7.58	L
	9	34	-	-	9.61*	20.67*	1.53*	3.91	3.53	-	-	29.92	-	-	L
	10	43†	50	93	17.06†	19.94	16.8	<1	3.61	1.49	23.09	32.06	0.72	-	R
	11	46	72	118	17.54	19.97	15.96*	3.12	4	2.77	28.2	42.36	0.666	-	L
	12	59	63	122	15.95	19.98	15.74*	5.54	4.66	5.52	27.67	39.52	0.7	-	L
	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L

Table 2- Single-track measurements from selected samples of *Koreanaornis* from GISE and GISE specimens found in outside repositories.

#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
0	34	75	109	21.9	24.83	18.42	5.84	4.74	5.04	34.73	45.5	0.763	20.56	L
1	87	67	154	17.21	24	19.99	4.58	1.95	4.44	30.16	46.8	0.644	13.08	R
2	63	57	120	16.94	26.88	24.46	4.21	4.66	4.39	30.76	48.1	0.64	12.51	L
3	73	71	144	18.5	28.02	20.91	6.54	3.21	6.29	30.83	44.18	0.698	9.62	R
4	51	85	136	24.03†	25.22†	24.17†	9.75	8.1	5.79	30.07†	58.04†	0.518	12.02*	L
5	82	62	144	13.13	23.46	18.61	5.57	2.81	2.22	30.22	39.91	0.757	13.94	R
6	58	62	120	17.26	29.09	17.47	4.16	4.67	3.37	33.56	42.37	0.792	11.91	L
7	70	64	134	17.35	22.47	20.83	3.08	5.03	3.45	29.05	51.25	0.567	-	R
8	85	69	154	26.52†	25.66	21.68	5.78	5.55	3.82	29.51	50.74	0.582	7.18?	L
9	35	81	116	14.42	23.96	18.33	3.51	6.07	4.2	32.25	43.95	0.734	10.44	R
10	60	61	121	20.67	27.25	21.49	5.42	6.03	4.45	34.17	45.77	0.747	-	L
11	68	61	129	16.22	27.92	20.05	7.3	4.11	5.38	35.37	43.37	0.816	19.77	R
12	55	67	122	19.74	27.64	19.37†	7.27	3.63†	4.67†	34.2	36.28	0.943	13.16	L
13	76	82	158	15.54†	23.15	16.64	5.8	10.09	5.8	29.77	41.35	0.72	-	R
14	79	70	149	14.85	21.65*	16.81	4.73	7.84	8.67	26.66*	39.38	0.677	-	L
15	74	83	157	18.24	23.99	20.37	7.67	4.85	4.25	31.29	45.38	0.69	14.05	L
16	63	64	127	14.82	24.25	14.7	4.94	5.67	2.72	30.17	34.29	0.88	9.13	R
17	46	-	-	18.79	27.92	-	2.9	3.15	-	35.53	-	-	-	R
18	67	65	121	11.36*	27.29	22.51	3.81†	2.79	3.97	30.21	41.31	0.731	-	L
19	44	50	94	17.22	28.31	18.74†	4.33	6.18	4.68†	32.39	37.63†	0.861	-	R
20	56	66	122	18.88	27.31	19.34	4.81	2.99	5.25	30.83	43.73	0.705	6.9?	L
21	59	53	112	19.55	23.72	17.46	7.4	5.44	3.92	30.44	42.7	0.713	8.54	R
22	70	60	130	19.12	28.68	19.31	6.84	3.76	5.92	39.57	45.91	0.862	-	R
23	59	59	118	20.52	27.4	20.48	5.83	4.84	5.03	35.86	45.74	0.784	7.19	L
24	49	67	116	17.69	27.13	23.13	6.02	6.94	3.83	33.94	40.39	0.84	14.32	R
25	57	58	115	15.23†	24.63	18.81	4.38	3.28	5.17	32.59	42.94	0.759	-	L
26	80†	46	126	16.3	20.17*	18.8	6.64	5.2	3.48	27.93*	39.46	0.708	9.0?	R
27	60	68	128	16.14	22.5	19.3	6.15	6.67	5.08	29.56	40.98	0.721	7.72	R
28	50	73	123	16.76	24.71	18.57	5.77	6.6	3.28	29.85	41.95	0.712	6.86	L
29	52	41	94	13.52	18.66	14.76	3.83†	3.15	6.65	30.66	39.7	0.772	7.3	L
30	40	73	113	16.71	23.09	18.61	1.91	4.33	3.93	32.18	40.73	0.79	-	R

Table 3- Single-track measurements of all *Geoseongornipes* tracks from Exhibit Hall 2.

KS005	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	63	47	110	19.95	26.33	22.45	4.09	3.95	4.31	32.75	47.37	0.691	7.57	L
	2	76	48	124	23.6	24.86*	24.74	3.71	3.86	2.54	33.13*	53.16†	0.648	13.47	R
	3	44	53	97	24.82	24.52	17.85	4.57	3.65	4.5	35.87*	47.08	0.762	-	L
	4	70	51	121	18.44	21.92	24.84	5.84	3.08	3.74	33	46.71	0.706	8.3	R
	5	48	83†	131	17.68	23.27	13.43*	3.22	3.15	4.59	33.66	40.26*	0.836	-	L
	6	75	48	123	16.73	23.11	18.8	3.81	3.94	1.97	31.1	45.82	0.679	6.33	R
GS073	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	60†	50	110	19.12	26.92	20.72	4.61†	3.86	5.18	36.62	37.22	0.984	-	R
	2	58	58	116	20.47	24.38	21.01	5.38	5.9	3.58	34.31	46.85	0.732	-	R
	3	52	56	108	16.5	24.52	20.4	5.74	4.14	3.27	33.54	45.35	0.74	-	R
	4	82†	55	137	23.57	24.07*	14*	4.8	4.19	3.45	30.08*	44.27*	0.679	-	L
GS068	#	II-III	III-IV	II-IV	LII	LIII	LIV	WII	WIII	WIV	FL	FW	FL:FW	Hallux	R/L
	1	82	57	139	19.07	26.45	20.24	7.57	5.38	7.02	35.1	45.54	0.771	18.96	R
	2	63	65	128	20.38	26.28†	21.32	8.54	5.33	4.91	37.37	48.35	0.773	12.66	L
	3	80	55	135	20.41†	27.25	22.35	10.71	5.04	4.88	32.41	44.33	0.731	-	R
	4	44	87	131	17.42	30.13	21.53	5.3	4.18	9.58	38.1	43.65	0.873	12.75	L

Table 4- Single-track measurements of selected unassigned avian tracks from the GISE.

		Up. Wid.	Low. Wid	Dist Btw.	Up Len.	Low Len.
Storage Room	1	1.9	2.73	8.14	55.48	45
	2	2.33	2.85	4.31	20	30.4
	3	2.39	3.25	7.81	53.12	141.48
	4	1.92	2.85	5.36	20.82	264.41
	5	1.98	2.41	7.1	38.77	59.52
	6	-	2.37	-	-	34.75
	7	3.51	3.6	6.49	23.97	59.46
EH1 #1	1	1.6	2.14	6.64	126.1	127.16
	2	2.2	2.34	4.1	19.67	30.27
	3	2.19	2.66	7.67	147.44	153.44
	4	-	1.64	-	-	74.01
	5	1.68	2.2	6.38	64.43	166.5
	6	1.87	2.4	6.5	24.79	150.5
	7	1.7	3.28	8.8	86.37	95.04
	8	1.8	3.83	6.87	105.91	122.56
	9	-	1.89	-	-	98
	10	2.11	2.58	7.91	95.15	92.56
	11	2.63	2.53	6.48	71.37	69.8
	12	1.92	2.74	6.86	17.41	69.71
	13	1.97	2.28	6.57	10.11	21.69
	14	1.79	2.86	7.66	100.34	116.49
	15	-	3.15	-	-	55.09
	16	1.76	2.21	7.46	31.51	130.74
	17	1.12	2.3	8.19	32.71	86.14
	18	1.51	2.58	7.79	29.21	129.03
	19	-	2.16	-	-	68.12
	20	2.66	2.37	7.98	105.94	213.78
	21	-	2.16	-	-	100.52
	22	1.99	3.9	6.06	19.88	61.67
	23	2.2	2.72	5.83	21.5	30.49
EH1 #4	1	2.5	2.2	8.5	29	82
	2	2	3	9.5	40	114
EH1 #5	1	2.33	3.6	5.56	39.17	56.17
	2	3.32	4.33	6.19	58.59	62.94
	3	2.52	1.94	6.79	15.54	39.38
	4	2.67	2.98	5.4	87.42	98.11
	5	-	2.53	-	-	35.11

	6	2.31	3.15	5.91	31.04	54.75
	7	-	2.52	-	-	89.56
	8	1.64	2.96	6.32	93.01	77.26
	9	-	2.21	-	-	95.25
	10	1.07	3.09	7.91	8.49	84.49
	11	1.69	2.78	7.09	81.51	73.12
	12	2.43	2.05	7.28	95.13	71.29
	13	2.34	3.01	6.26	70.05	74.1
	14	2.62	3.27	5.26	28.2	72.08
		Up. Wid.	Low. Wid	Dist Btw.	Up Len.	Low Len.
EH1 #6	1	1.72	2.8	5.87	90.03	88.98
	2	-	2.32	-	-	91.04
	3	-	2.52	-	-	55.44
	4	2.28	2.73	4.21	36.04	83.86
	5	1.9	2.12	4.37	20.61	108.93
	6	-	1.78	-	-	71.37
	7	1.91	2.44	5.91	27.01	41.5
	8	1.79	2.73	7.61	60.33	72.18
	9	1.75	2.41	6.58	20.67	37.12
	10	1.41	2.22	5.19	15.32	38.67
KS049	1	2.59	2.04	4.88	64.17	81.33
	2	0.91	2.55	5.98	14.65	42.23
GS021	1	-	1.94	-	-	90.79
	2	2.01	3.61	5.11	21.38	56.85
GS012	1	-	2.8	-	-	63.44
	2	1.49	3.03	5.8	25.89	208.28
GS007	1	1.59	2.58	6.51	23.76	138.32
	2	2.4	2.41	9.67	41.38	114.7
	Average	2.04659	2.65047	6.6124	49.2078	86.9214
		Up. Wid.	Low. Wid	Dist Btw.	Up Len.	Low Len.

Table 5: Measurements of arcuate spoonbill-like feeding traces from the GISE site. Up. Wid. = Upper mandible width. Low. Wid. = Lower mandible width. Dist. Btw. = Distance between mandible impressions. Up Len. = Upper mandible impression length. Low Len. = Lower mandible impression length.

Appendix II

Osteological data:

Name	*Anas platyrhynchos*	*Anas platyrhynchos*	*Anas platyrhynchos*	*Anas platyrhynchos*
Specimen #	14150	14149	14151	17182
M/F	M	M	F	M
LoDI	9.83	9.49	9.08	9.51
w/claw	N/A	N/A	N/A	N/A
LoDII	38.57	39.66	35.15	34.9
w/claw	N/A	N/A	N/A	N/A
LoDIII	51.21	51.67	47.47	46.22
w/claw	N/A	N/A	N/A	N/A
LoDIV	50.01	52.54	45.68	45.46
w/claw	N/A	N/A	N/A	N/A
W@Pjoint II	2.85	3.4	2.86	2.93
W@Pjoint III	4	4.3	3.64	3.73
W@Pjoint IV	3.3	3.1	3.1	3.06
W@2joint III	2.93	3.17	2.83	3.01
W@2joint IV	2.55	2.93	2.57	2.63
W@3joint IV	2.15	2.41	2.06	2.09
LoPhI,II	22.28	22.69	20.85	19.97
LoPhII,II	17.14	17.81	15.34	15.63
LoPhI,III	23.09	23.22	21.27	21.24
LoPhII,III	16.37	16.47	15.11	14.86
LoPhIII,III	13.64	13.86	12.54	12.02
LoPhI,IV	18.53	19.06	16.77	16.55
LoPhII,IV	13.04	13.49	12.11	11.93
LoPhIII,IV	9.82	11.03	9.83	9.58
LoPhIV,IV	11.38	12.04	9.94	9.78
WoPhI,II	2.27	2.71	2.25	2.19
WoPhII,II	1.91	2.25	1.62	1.94
WoPhI,III	2.99	3.03	2.6	2.75
WoPhII,III	2.52	2.68	2.25	2.33
WoPhIII,III	2.04	2.22	1.89	2.08
WoPhI,IV	2.09	2.49	1.98	2.07
WoPhII,IV	2.06	2.17	1.75	1.81
WoPhIII,IV	1.77	1.83	1.51	1.51
WoPhIV,IV	1.46	1.57	1.29	1.34
Foot Length	69.95	65.51	59.25	58.79
Lotmt	46.74	48.26	43.92	43.75
Lott	83.11	86.69	78.25	77.2
LoFem	51.25	55.52	48.59	46.93
Wotmt@prox	9.5	10.22	9.26	9.31
Wotmt@cond	9.35	9.89	8.73	8.58
Wott@prox	12.15	13.26	11.76	10.63
Wott@mid	5.47	6.17	5.36	4.96
Wott@cond	9.09	9.77	8.53	8.71
Wofem@cond	11.77	12.32	10.83	10.75

Name	*Anas platyrhynchos*	*Anas platyrhynchos*	*Anas platyrhynchos*	*Pelecanus erythrorl*
Specimen #	21652	AVERAGE	STDEV	15011
M/F	F			M
LoDI	N/A	9.4775	0.307394969	37.66
w/claw	N/A			50.52
LoDII	39.38	37.532	2.324988172	60.19
w/claw	N/A			75.86
LoDIII	51.36	49.586	2.546316948	102.47
w/claw	64.15			111.82
LoDIV	49.89	48.716	3.06163845	98.43
w/claw	73.56			107.14
W@Pjoint II	3.03	3.014	0.2274423	6.77
W@Pjoint III	4.18	3.97	0.283019434	9.05
W@Pjoint IV	3.33	3.178	0.126570139	7.45
W@2joint III	3.73	3.134	0.355640268	7.24
W@2joint IV	3.23	2.782	0.293462093	6.47
W@3joint IV	2.22	2.186	0.139391535	4.99
LoPhI,II	22.53	21.664	1.195232195	41.65
LoPhII,II	17.58	16.7	1.139583257	28.06
LoPhI,III	23.91	22.546	1.219069317	46.2
LoPhII,III	16.77	15.916	0.867052478	35.29
LoPhIII,III	12.9	12.992	0.763360989	25.62
LoPhI,IV	19.12	18.006	1.252409677	32.12
LoPhII,IV	13.06	12.726	0.672108622	26.61
LoPhIII,IV	9.92	10.036	0.569763109	21.39
LoPhIV,IV	10.66	10.76	0.957287836	20.25
WoPhI,II	2.36	2.356	0.207074866	4.75
WoPhII,II	1.86	1.916	0.225233212	3.76
WoPhI,III	2.69	2.812	0.188997354	6.08
WoPhII,III	2.38	2.432	0.169911742	5.06
WoPhIII,III	2.3	2.106	0.159937488	3.5
WoPhI,IV	2.13	2.152	0.196773982	5.57
WoPhII,IV	1.91	1.94	0.174068952	4.76
WoPhIII,IV	1.76	1.676	0.153883072	4.21
WoPhIV,IV	1.39	1.41	0.109316056	2.88
Foot Length	55.33	61.766	5.865243388	119.11
Lotmt	46.53	45.84	1.949166489	120.87
Lott	82.97	81.644	3.89351769	177.11
LoFem	52.34	50.926	3.340438594	112.72
Wotmt@prox	10.05	9.668	0.439738559	23.77
Wotmt@cond	10.25	9.36	0.720832852	24.28
Wott@prox	12.7	12.1	0.998073144	32.37
Wott@mid	5.24	5.44	0.450166636	16.32
Wott@cond	9.27	9.074	0.487729433	23.6
Wofem@cond	11.87	11.508	0.687982558	32.05

Name	*Pelecanus erythrorl*	*Pelecanus erythror*	*Pelecanus erythrorl*	*Pelecanus erythrorl*
Specimen #	13825	20394	21614	86017
M/F	M	F	F	M
LoDI	37.73	37.26	37.82	34.35
w/claw	N/A	N/A	N/A	N/A
LoDII	68.32	66.32	66.46	60.01
w/claw	N/A	N/A	81.61	N/A
LoDIII	103.58	99.14	96.65	88.57
w/claw	N/A	N/A	112.84	N/A
LoDIV	95.39	96.1	90.7	83.28
w/claw	N/A	N/A	102.54	N/A
W@Pjoint II	5.91	6.06	6.79	5.28
W@Pjoint III	8.7	8.48	8.91	6.81
W@Pjoint IV	7.49	7.63	7.57	6.17
W@2joint III	5.96	5.8	7.26	5.03
W@2joint IV	5.59	5.81	6.65	4.59
W@3joint IV	4.3	4.27	5.13	3.53
LoPhI,II	40.41	39.79	40.32	36.34
LoPhII,II	29.27	27.45	30.8	25.04
LoPhI,III	45	43.7	43.03	38.91
LoPhII,III	35.31	33.85	34.1	29.33
LoPhIII,III	26.15	24.35	25.85	21.82
LoPhI,IV	31.2	30.9	31.78	27.94
LoPhII,IV	26.87	26.4	26.63	22.88
LoPhIII,IV	21.63	21.72	21.28	17.88
LoPhIV,IV	19.73	19.68	17.6	16.44
WoPhI,II	4.16	4.69	4.88	3.52
WoPhII,II	3.3	3.87	3.91	2.83
WoPhI,III	5.76	6.15	6.21	4.86
WoPhII,III	4.97	5.51	5.59	4.1
WoPhIII,III	3.67	3.71	4.18	3.15
WoPhI,IV	5.19	5.49	6.25	4.49
WoPhII,IV	4.57	5.13	5.78	3.89
WoPhIII,IV	4.1	4.23	4.47	3.27
WoPhIV,IV	3	3.06	3.3	2.47
Foot Length	115.43	110.07	104.79	101.51
Lotmt	125.32	118.23	122.54	107.9
Lott	174.05	170.76	175.65	151.79
LoFem	115.87	110.17	114.83	101.57
Wotmt@prox	23.72	24.12	23.68	20.8
Wotmt@cond	23.64	24.71	23.52	20.16
Wott@prox	33.42	32.57	32.47	28.02
Wott@mid	15.32	16.88	15.95	14.57
Wott@cond	23.03	22.77	22.47	19.81
Wofem@cond	32.71	31.34	31.4	27.4

Name	*Pelecanus erythrorhynchos*	*Pelecanus erythrorh*	*Branta canadensis*	*Branta canadensis*
Specimen #	AVERAGE	STDEV	21973	21294
M/F			?	F
LoDI	36.964	1.476864923	12.27	15.13
w/claw			N/A	21.97
LoDII	64.26	3.87925895	59.89	58.64
w/claw	78.735		N/A	71.44
LoDIII	98.082	5.98186175	75.9	75.81
w/claw	112.33		N/A	89.75
LoDIV	92.78	6.006941818	74.9	74.5
w/claw	104.84		N/A	87.79
W@Pjoint II	6.162	0.635586343	4.9	5.52
W@Pjoint III	8.39	0.909202948	7.34	7.48
W@Pjoint IV	7.262	0.614426562	5.62	6.35
W@2joint III	6.258	0.971452521	5.61	5.89
W@2joint IV	5.822	0.818119796	4.49	5.09
W@3joint IV	4.444	0.643257336	3.53	3.63*
LoPhI,II	39.702	1.999292375	34.69	35.55
LoPhII,II	28.124	2.147307617	26.47	24.88
LoPhI,III	43.368	2.774071016	35.14	35.27
LoPhII,III	33.576	2.465903486	23.75	24.65
LoPhIII,III	24.758	1.779851117	20.54	19.14
LoPhI,IV	30.788	1.662203357	28.27	28.23
LoPhII,IV	25.878	1.684182294	19.82	19.22
LoPhIII,IV	20.78	1.630812681	15.47	14.87
LoPhIV,IV	18.74	1.638093404	15.52	16.29
WoPhI,II	4.4	0.563249501	3.93	4.55
WoPhII,II	3.534	0.462525675	3.12	3.12
WoPhI,III	5.812	0.559794605	5.25	5.41
WoPhII,III	5.046	0.594163277	4.66	4.27
WoPhIII,III	3.642	0.37318896	4.02	3.62
WoPhI,IV	5.398	0.638686151	3.97	4.46
WoPhII,IV	4.826	0.697946989	3.75	3.82
WoPhIII,IV	4.056	0.459652042	3.02	3.18
WoPhIV,IV	2.942	0.304991803	2.52	2.37
Foot Length	110.182	7.272215618	92.24	93.62
Lotmt	118.972	6.703914528	90.6	86.68
Lott	169.872	10.37999133	143.34	144.72
LoFem	111.032	5.721732255	82.53	81.69
Wotmt@prox	23.218	1.36294534	17.99	18.32
Wotmt@cond	23.262	1.800338857	18.53	20.3
Wott@prox	31.77	2.13746345	21	21.82
Wott@mid	15.808	0.894745774	10.48	10.34
Wott@cond	22.336	1.471930705	16.16	17.49
Wofem@cond	30.98	2.077269843	20.42	21.06

Name	*Branta canadensis*	*Branta canadensis*	*Branta canadensis*
Specimen #	23403	22569	64772
M/F	M	M	?
LoDI	15.78	10.86	14.42
w/claw	N/A	N/A	N/A
LoDII	60.19	51.54	58.37
w/claw	N/A	64.61	N/A
LoDIII	79.04	65.19	74.83
w/claw	94.31	79.15	N/A
LoDIV	76.38	62.66	70.48
w/claw	86.8	64.59	N/A
W@Pjoint II	5.22	4.78	5.09
W@Pjoint III	7.5	7	6.99
W@Pjoint IV	5.88	5.1	5.26
W@2joint III	5.58	4.91	5.07
W@2joint IV	4.28	3.94	3.96
W@3joint IV	3.69	3.23	3.22
LoPhI,II	36.14	30.33	34.66
LoPhII,II	26.13	21.88	24.89
LoPhI,III	35.9	30.49	34.58
LoPhII,III	25.47	20.86	23.31
LoPhIII,III	20.67	16.43	19.57
LoPhI,IV	29.35	24.47	27.47
LoPhII,IV	20.05	15.84	18.03
LoPhIII,IV	15.68	12.61	13.63
LoPhIV,IV	15.48	12.85	14.54
WoPhI,II	4.37	4.37	4.6
WoPhII,II	3.58	2.87	3.27
WoPhI,III	5.35	5.09	5.67
WoPhII,III	4.45	4.55	3.93
WoPhIII,III	3.57	3.37	2.92
WoPhI,IV	4.58	4.23	4.3
WoPhII,IV	3.76	3.59	3.57
WoPhIII,IV	3.08	2.89	2.82
WoPhIV,IV	2.46	2.2	2.25
Foot Length	96.14	81.11	94.17
Lotmt	95.51	84.15	92.38
Lott	155.95	141.72	149.38
LoFem	87.63	77.05	87.17
Wotmt@prox	19.42	18.08	18.94
Wotmt@cond	20.41	18.25	19.64
Wott@prox	23.95 ?	21.72	20.26
Wott@mid	9.08 ?	9.93	11.18
Wott@cond	18.24	16.21	17.09
Wofem@cond	21.86	19.82	21.12

Name	*Branta canadensis*	*Branta canadensis*	*Phalacocorax auritus*	*Phalacocorax aurit*
Specimen #	AVERAGE	STDEV	19906	22862
M/F			?	M
LoDI	13.692	2.061545537	24.45	26.56
w/claw			35.47	39.37
LoDII	57.726	3.545099434	43.23	48.36
w/claw	68.025		53.31	62.71
LoDIII	74.154	5.255333481	61.7	70.2
w/claw	87.73666667		72.46	85.29
LoDIV	71.784	5.548808881	81.35	91.96
w/claw	79.72666667		90.11	104.82
W@Pjoint II	5.102	0.28865204	4.27	4.01
W@Pjoint III	7.262	0.251435877	5.44	5.53
W@Pjoint IV	5.642	0.499519769	5.79	5.84
W@2joint III	5.412	0.407700871	4.26	4.66
W@2joint IV	4.352	0.472302869	5.16	5.4
W@3joint IV	3.4175	0.231714623	4.03	4.22
LoPhI,II	34.274	2.290595992	24.82	27.47
LoPhII,II	24.85	1.808742657	18.09	21.55
LoPhI,III	34.276	2.167839939	24.1	24.95
LoPhII,III	23.608	1.747375174	23.5	24.23
LoPhIII,III	19.27	1.713578128	18.3	21.28
LoPhI,IV	27.558	1.851572305	24.63	27.16
LoPhII,IV	18.592	1.726085166	22.5	25.09
LoPhIII,IV	14.452	1.302658819	17.89	20.7
LoPhIV,IV	14.936	1.320844427	18.07	20.67
WoPhI,II	4.364	0.263969695	2.33	3.11
WoPhII,II	3.192	0.260134581	1.78	2.77
WoPhI,III	5.354	0.214196172	2.89	4.13
WoPhII,III	4.372	0.285692142	2.37	3.82
WoPhIII,III	3.5	0.400936404	1.84	2.72
WoPhI,IV	4.308	0.233173755	2.49	4.55
WoPhII,IV	3.698	0.111220502	1.95	3.77
WoPhIII,IV	2.998	0.144637478	1.66	3.53
WoPhIV,IV	2.36	0.135462172	1.54	2.62
Foot Length	91.456	5.950691556	70.68	84.32
Lotmt	89.864	4.51488981	62.87	68.31
Lott	147.022	5.749714776	102.14	110.04
LoFem	83.214	4.357072412	56.94	63.3
Wotmt@prox	18.55	0.611637147	12.6	14.16
Wotmt@cond	19.426	0.99545467	14.27	16.57
Wott@prox	21.2	0.72535049	15.07	17.64
Wott@mid	10.4825	0.520280373	11.15	12.9
Wott@cond	17.038	0.88151574	11.83	13.1
Wofem@cond	20.856	0.771803084	15.48	17.67

Name	*Phalacocorax aurit*	*Phalacocorax aurit*	*Phalacocorax aurit*	*Phalacocorax aurit*
Specimen #	79131	20015	AVERAGE	STDEV
M/F	?	?		
LoDI	24.88	25.13	25.255	0.914202749
w/claw	N/A	N/A	37.42	
LoDII	43.31	43.27	44.5425	2.545209553
w/claw	N/A	N/A	58.01	
LoDIII	64.12	63.77	64.9475	3.660886732
w/claw	N/A	N/A	78.875	
LoDIV	84.9	83.54	85.4375	4.587667345
w/claw	N/A	N/A	97.465	
W@Pjoint II	4.13	4.54	4.2375	0.227943707
W@Pjoint III	5.1	4.81	5.22	0.33015148
W@Pjoint IV	5.74	5.16	5.6325	0.317634486
W@2joint III	4.54	4.35	4.4525	0.180992633
W@2joint IV	4.94	4.73	5.0575	0.288024883
W@3joint IV	4.71	3.18	4.035	0.637939391
LoPhI,II	25.22	24.47	25.495	1.351850583
LoPhII,II	19.15	19.12	19.4775	1.466910018
LoPhI,III	23.18	24.68	24.2275	0.78321453
LoPhII,III	23.48	23.18	23.5975	0.446346278
LoPhIII,III	19.16	19.54	19.57	1.252464238
LoPhI,IV	24.27	25.58	25.41	1.290916987
LoPhII,IV	23.34	22.97	23.475	1.130206471
LoPhIII,IV	19.51	19.01	19.2775	1.165371901
LoPhIV,IV	19.74	18.55	19.2575	1.174546012
WoPhI,II	3.08	2.76	2.82	0.363042697
WoPhII,II	3.19	3.19	2.7325	0.665150359
WoPhI,III	4.05	3.75	3.705	0.567421066
WoPhII,III	3.54	3.38	3.2775	0.631737023
WoPhIII,III	2.53	2.37	2.365	0.378109332
WoPhI,IV	4.21	4.05	3.825	0.914093358
WoPhII,IV	3.55	3.57	3.21	0.845852627
WoPhIII,IV	3.28	2.83	2.825	0.828914953
WoPhIV,IV	2.69	2.4	2.3125	0.52961464
Foot Length	77.98	76.21	77.2975	5.620061536
Lotmt	64.1	64.16	64.86	2.375584139
Lott	107.13	103.34	105.6625	3.611005169
LoFem	60.6	56.35	59.2975	3.264050398
Wotmt@prox	13.56	13.16	13.37	0.657571289
Wotmt@cond	15.84	14.36	15.26	1.131753801
Wott@prox	11.77	15.9	15.095	2.461794738
Wott@mid	8.39	11.2	10.91	1.866565473
Wott@cond	12.54	12.55	12.505	0.520544587
Wofem@cond	16.19	15.96	16.325	0.944192777

Name	*Grus canadensis*	*Grus canadensis*	*Grus canadensis*	*Grus canadensis*
Specimen #	22201	85906	85890	69234
M/F	F	M	F	F
LoDI	N/A	N/A	11.89	11.21
w/claw	N/A	N/A	N/A	N/A
LoDII	40.28	58.37	53.83	48.45
w/claw	N/A	86.84	N/A	N/A
LoDIII	55.48	80.75	73.74	69.46
w/claw	N/A	107.05	95.72	N/A
LoDIV	43.43	68.1	58.34	58.29
w/claw	N/A	83.79	73.46	N/A
W@Pjoint II	5.13	6.68	5.84	5.62
W@Pjoint III	6.22	7.03	6.76	6.12
W@Pjoint IV	5.47	6.56	5.63	5.31
W@2joint III	5.11	6.44	5.61	5.12
W@2joint IV	4.81	5.71	4.94	4.31
W@3joint IV	4.17	4.73	4.32	3.91
LoPhI,II	22.04	31.82	28.72	25.71
LoPhII,II	20.35	29.62	27.5	24.33
LoPhI,III	25.75	36.88	33.45	31.68
LoPhII,III	17.57	24.8	22.53	21.75
LoPhIII,III	15.4	21.99	20.58	18.98
LoPhI,IV	18.37	27.56	24.39	24.52
LoPhII,IV	10.16	16.12	14.05	13.85
LoPhIII,IV	8.23	12.73	10.45	10.21
LoPhIV,IV	8.68	13.26	12.7	11.63
WoPhI,II	3.85	4.63	4.92	3.99
WoPhII,II	3.75	4.55	4.5	4.02
WoPhI,III	4.57	5.71	5.68	4.93
WoPhII,III	4.08	4.91	4.88	4.04
WoPhIII,III	3.77	4.36	4.46	3.92
WoPhI,IV	3.85	4.61	4.61	4.06
WoPhII,IV	3.76	4.45	4.37	3.96
WoPhIII,IV	3.71	4.12	4.02	3.57
WoPhIV,IV	3.33	3.83	3.61	3.48
Foot Length	75.07	104.22	99.75	96.02
Lotmt	175.83	249.91	244.45	220.73
Lott	202.07	276.64	263.75	250.82
LoFem	96.95	127.36	121.87	118.06
Wotmt@prox	18.97	25.13	24.43	22.35
Wotmt@cond	18.11	22.77	19.75	19.78
Wott@prox	21.27	27.06	25.81	24.06
Wott@mid	8.28	11.26	12.87	10.67
Wott@cond	16.45	21.34	19.73	18.82
Wofem@cond	19.77	26.7	24.78	23.9

Name	*Grus canadensis*	*Grus canadensis*	*Grus canadensis*	*Ardea herodias*	*Ardea herodias*
Specimen #	68111	AVERAGE	STDEV	21619	17200
M/F	?			M	F
LoDI	10.4	11.16666667	0.480832611	45.64	42.58
w/claw	N/A			65.03	N/A
LoDII	49.28	50.042	6.747523249	75.78	68.8
w/claw	N/A			89.26	82.33
LoDIII	66.7	69.226	9.334970809	106.89	96.86
w/claw	N/A	101.385		121.04	114.61
LoDIV	56.12	56.856	8.824473355	87.95	79.42
w/claw	N/A	78.625		100.57	95.81
W@Pjoint II	5.94	5.842	0.563045291	5.6	4.66
W@Pjoint III	6.77	6.58	0.391216053	6.23	5.16
W@Pjoint IV	5.26	5.646	0.53115911	6.2	5.09
W@2joint III	5.14	5.484	0.574569404	4.48	4.13
W@2joint IV	4.64	4.882	0.519586374	4.81	4.24
W@3joint IV	3.87	4.2	0.349714169	3.94	3.69
LoPhI,II	26.01	26.86	3.651664004	43.83	40.88
LoPhII,II	24.51	25.262	3.520038352	31.93	28.85
LoPhI,III	30.68	31.688	4.072391189	39.56	37.63
LoPhII,III	21.08	21.546	2.627932648	38.76	36.68
LoPhIII,III	17.98	18.986	2.521721634	27.57	24.54
LoPhI,IV	23.39	23.646	3.336859302	28.13	25.41
LoPhII,IV	13.48	13.532	2.147107356	23.13	21.11
LoPhIII,IV	10.74	10.472	1.602036204	21.14	18.44
LoPhIV,IV	11.49	11.552	1.767305859	18.41	16.24
WoPhI,II	4.33	4.344	0.442470338	3.94	4
WoPhII,II	4.18	4.2	0.3345893	3.24	3.01
WoPhI,III	5.27	5.232	0.489918361	4.16	3.93
WoPhII,III	4.57	4.496	0.419916658	3.86	3.61
WoPhIII,III	4.02	4.106	0.293564303	2.93	2.83
WoPhI,IV	4.29	4.284	0.335827337	3.95	3.69
WoPhII,IV	3.86	4.08	0.310724959	3.77	3.47
WoPhIII,IV	3.62	3.808	0.24692104	3.44	3.14
WoPhIV,IV	3.39	3.528	0.199047733	3.24	2.5
Foot Length	93.24	93.66	11.17962209	136.79	114.17
Lotmt	216.22	221.428	29.35994244	179.85	152.07
Lott	249	248.456	28.22140021	246.68	239.9
LoFem	119.24	116.696	11.60525872	105.73	101.96
Wotmt@prox	21.73	22.522	2.434937371	16.92	15.99
Wotmt@cond	21.07	20.296	1.736571335	17.54	15.96
Wott@prox	23.43	24.326	2.229894616	19.15	18.11
Wott@mid	12.64	11.144	1.847817632	8.57	7.87
Wott@cond	19.37	19.142	1.773378132	15.26	14.58
Wofem@cond	24.03	23.836	2.533166003	18.14	16.93

Name	*Ardea herodias*	*Ardea herodias*	*Ardea herodias*	*Ardea herodias*	*Butorides virescens*
Specimen #	22599	?	AVERAGE	STDEV	24321
M/F	M	?			M
LoDI	45.53	43.75	44.954	1.820145599	21.48
w/claw	68.42	N/A	65.59		N/A
LoDII	76.01	74.29	74.472	3.366343714	32.46
w/claw	89.72	N/A	88.62		41.03
LoDIII	106.88	104.43	104.95	4.890669688	45.68
w/claw	126.75	N/A	122.86		55.84
LoDIV	90.25	86.26	87.152	4.826175504	34.82
w/claw	108.91	N/A	102.4475		43.14
W@Pjoint II	5.02	5.04	5.076	0.336273698	2.7
W@Pjoint III	5.66	5.71	5.732	0.390217888	2.68
W@Pjoint IV	5.49	5.48	5.57	0.40068691	2.49
W@2joint III	4.36	4.61	4.624	0.541691794	2.25
W@2joint IV	4.24	4.45	4.442	0.233388089	2.09
W@3joint IV	3.42	3.75	3.702	0.186198818	1.72
LoPhI,II	44.32	43.09	43.366	1.515595592	18.24
LoPhII,II	31.88	31.32	31.69	2.001536909	15.01
LoPhI,III	41.14	39.18	39.698	1.439347074	15.83
LoPhII,III	40.48	39.81	39.596	2.065969506	17.87
LoPhIII,III	28.13	28.6	27.73	1.965006361	13.77
LoPhI,IV	27.92	27.4	27.564	1.328770108	10.28
LoPhII,IV	24.18	23.64	23.394	1.437264763	9.29
LoPhIII,IV	21.43	19.56	20.338	1.289852705	8.33
LoPhIV,IV	18.77	18.46	18.232	1.166134641	8.82
WoPhI,II	3.84	3.91	3.922	0.057619441	1.74
WoPhII,II	3.04	3.31	3.19	0.156044865	1.32
WoPhI,III	3.97	4.29	4.062	0.156428898	1.74
WoPhII,III	3.54	3.91	3.704	0.168315181	1.56
WoPhIII,III	2.79	3.12	2.906	0.130115333	1.27
WoPhI,IV	3.8	3.83	3.792	0.108719823	1.71
WoPhII,IV	3.66	3.82	3.642	0.158965405	1.63
WoPhIII,IV	3.04	3.44	3.232	0.19318385	1.42
WoPhIV,IV	2.48	2.76	2.704	0.319812445	1.27
Foot Length	127.04	123.37	126.292	8.37665327	54
Lotmt	187.38	195.81	182.644	18.55765556	54.79
Lott	252.38	264	234.768	36.79198989	84.59
LoFem	108.85	103.23	105.398	2.822511293	50.49
Wotmt@prox	16.92	16.91	16.652	0.408007353	7.49
Wotmt@cond	17.91	16.9	17.126	0.747382098	6.91
Wott@prox	19.31	19.15	18.842	0.516836531	8.62
Wott@mid	8.57	9.27	8.594	0.497875486	3.61
Wott@cond	15.55	16.02	15.262	0.559839263	7.09
Wofem@cond	18.36	17.95	17.82	0.550681396	7.4

Name	*Butorides virescens*	*Butorides virescens*	*Butorides virescens*	*Butorides virescens*
Specimen #	15556	14981	22571	14593
M/F	F	M	F	M
LoDI	21.3	20.59	21.22	20.39
w/claw	N/A	33	N/A	N/A
LoDII	31.55	31.77	31.19	30.34
w/claw	N/A	42.29	N/A	N/A
LoDIII	44.72	45.97	43.27	44.08
w/claw	N/A	55.96	N/A	N/A
LoDIV	36.5	36.02	32.94	34.87
w/claw	N/A	42.18	N/A	N/A
W@Pjoint II	2.34	2.43	2.59	2.18
W@Pjoint III	2.44	2.56	2.69	2.41
W@Pjoint IV	2.22	2.43	2.42	2.07
W@2joint III	1.69	1.98	2.2	2.11
W@2joint IV	2.07	2.16	2.14	2.24
W@3joint IV	1.71	1.88	1.91	1.64
LoPhI,II	17.58	19.1	17.79	17.19
LoPhII,II	14.72	14.85	14.24	13.93
LoPhI,III	15.07	15.64	15.26	14.64
LoPhII,III	16.76	17.78	16.75	16.06
LoPhIII,III	13.6	13.49	12.68	14.15
LoPhI,IV	10.61	10.58	10.21	10.4
LoPhII,IV	9.55	9.53	9.85	9.3
LoPhIII,IV	8.9	9.02	7.03	8.05
LoPhIV,IV	8.64	8.72	6.15	8.01
WoPhI,II	1.69	1.73	1.87	1.61
WoPhII,II	1.3	1.45	1.4	1.3
WoPhI,III	1.71	1.81	1.7	1.76
WoPhII,III	1.51	1.64	1.54	1.5
WoPhIII,III	1.2	1.27	1.24	1.32
WoPhI,IV	1.54	1.67	1.56	1.52
WoPhII,IV	1.54	1.73	1.61	1.56
WoPhIII,IV	1.44	1.52	1.47	1.46
WoPhIV,IV	1.23	1.27	1.5	1.24
Foot Length	52.27	51.81	49.32	50.52
Lotmt	50.46	53.56	51.33	47.97
Lott	79.81	83.61	79.4	77.1
LoFem	48.81	51.11	50.6	48.03
Wotmt@prox	7.7	7.29	7.02	7.28
Wotmt@cond	6.48	6.77	6.66	6.56
Wott@prox	7.59	7.87	7.82	7.2
Wott@mid	3.1	3.57	3.96	3.13
Wott@cond	6.56	6.71	6.44	6.33
Wofem@cond	6.78	7.38	7.53	7.26

Name	*Butorides virescens*	*Butorides virescens*	*Eudocimus albus*	*Eudocimus albus*
Specimen #	AVERAGE	STDEV	30246	24899
M/F			F	F
LoDI	20.996	0.47668648	21.33	22.37
w/claw			N/A	N/A
LoDII	31.462	0.779660182	40.57	43.65
w/claw	41.66		N/A	N/A
LoDIII	44.744	1.117286892	56.25	62.4
w/claw	55.9		N/A	N/A
LoDIV	35.03	1.376481021	49.97	53.86
w/claw	42.66		N/A	N/A
W@Pjoint II	2.448	0.204621602	2.88	3.27
W@Pjoint III	2.556	0.130499042	3.63	4.01
W@Pjoint IV	2.326	0.175584737	3.15	3.46
W@2joint III	2.046	0.223897298	2.68	3.02
W@2joint IV	2.14	0.06670832	2.64	2.95
W@3joint IV	1.772	0.116918775	2.15	2.4
LoPhI,II	17.98	0.731812818	22.9	24.67
LoPhII,II	14.55	0.450277692	10.08	19.42
LoPhI,III	15.288	0.470605992	22.03	24.36
LoPhII,III	17.044	0.768003906	19.42	22.05
LoPhIII,III	13.538	0.540989834	15.79	17.67
LoPhI,IV	10.416	0.177285081	17.16	18.17
LoPhII,IV	9.504	0.229085137	11.43	13.14
LoPhIII,IV	8.266	0.798266873	10.26	11.19
LoPhIV,IV	8.068	1.118020572	11.93	12.5
WoPhI,II	1.728	0.094445752	2.21	2.6
WoPhII,II	1.354	0.067675697	1.69	2.2
WoPhI,III	1.744	0.043931765	2.86	3.25
WoPhII,III	1.55	0.055677644	2.25	2.69
WoPhIII,III	1.26	0.044158804	1.77	2.21
WoPhI,IV	1.6	0.084557673	2.27	2.47
WoPhII,IV	1.614	0.07436397	2.24	2.53
WoPhIII,IV	1.462	0.037682887	1.99	2.24
WoPhIV,IV	1.302	0.112116011	1.53	1.86
Foot Length	51.584	1.77598705	70.14	75.24
Lotmt	51.622	2.672296765	87.86	98.64
Lott	80.902	3.116018293	123.37	135.08
LoFem	49.808	1.317657012	58.55	62.4
Wotmt@prox	7.356	0.25461736	10.2	12.31
Wotmt@cond	6.676	0.170088212	10.36	11.77
Wott@prox	7.82	0.519567128	12.06	14.22
Wott@mid	3.474	0.361289358	5.24	6.19
Wott@cond	6.626	0.295347253	8.91	10.56
Wofem@cond	7.27	0.290172363	11.3	13.27

Name	*Eudocimus albus*	*Eudocimus albus*	*Eudocimus albus*	*Eudocimus albus*
Specimen #	55618	55645	55615	AVERAGE
M/F	M	F	F	
LoDI	23.22	22.11	22.16	22.238
w/claw	N/A	N/A	N/A	
LoDII	44.16	41.57	42.64	42.518
w/claw	N/A	N/A	N/A	
LoDIII	63.54	59.33	60.93	60.49
w/claw	N/A	N/A	N/A	
LoDIV	53.93	52.42	51.12	52.26
w/claw	N/A	N/A	N/A	
W@Pjoint II	3.19	2.91	2.94	3.038
W@Pjoint III	4.01	3.77	3.69	3.822
W@Pjoint IV	3.44	3.06	3.2	3.262
W@2joint III	3.15	2.84	2.76	2.89
W@2joint IV	2.87	2.65	2.71	2.764
W@3joint IV	2.38	2.08	2.22	2.246
LoPhI,II	25.08	24.07	24.52	24.248
LoPhII,II	19.65	18.16	18.95	17.252
LoPhI,III	24.98	23.47	23.85	23.738
LoPhII,III	22.54	21.18	21.55	21.348
LoPhIII,III	17.79	16.85	17.07	17.034
LoPhI,IV	19.11	18.73	18.04	18.242
LoPhII,IV	13.11	12.97	12.4	12.61
LoPhIII,IV	11.04	11.18	10.66	10.866
LoPhIV,IV	13.15	11.92	12.49	12.398
WoPhI,II	2.56	2.39	2.37	2.426
WoPhII,II	2.08	1.87	1.88	1.944
WoPhI,III	3.26	2.93	2.86	3.032
WoPhII,III	2.68	2.44	2.41	2.494
WoPhIII,III	2.06	1.88	1.97	1.978
WoPhI,IV	2.53	2.24	2.29	2.36
WoPhII,IV	2.51	2.2	2.31	2.358
WoPhIII,IV	2.11	1.9	2.01	2.05
WoPhIV,IV	1.81	1.53	1.66	1.678
Foot Length	77.02	73.38	74.43	74.042
Lotmt	97.17	87.9	93.53	93.02
Lott	135.94	124.44	129.42	129.65
LoFem	65.22	60.05	61.49	61.542
Wotmt@prox	12.14	11.36	10.56	11.314
Wotmt@cond	12.01	11.45	10.7	11.258
Wott@prox	13.94	13.14	12.78	13.228
Wott@mid	6.14	5.91	5.79	5.854
Wott@cond	10.36	9.62	9.16	9.722
Wofem@cond	13.14	12.07	12.22	12.4

Name	*Eudocimus albus*	*Ajaja ajaja*	*Ajaja ajaja*	*Ajaja ajaja*	*Ajaja ajaja*	*Ajaja ajaja*
Specimen #	STDEV	37549	37548	34659	AVERAGE	STDEV
M/F		?	M	F		
LoDI	0.676143476	27.67	26.76	28.1	27.51	0.6841783
w/claw		N/A	N/A	N/A		
LoDII	1.473590852	51.81	49.81	51.4	51.006667	1.0564248
w/claw		N/A	N/A	N/A		
LoDIII	2.849008599	73.72	70.8	71.24	71.92	1.5742935
w/claw		N/A	N/A	N/A		
LoDIV	1.726137306	65.35	60.47	62.44	62.753333	2.4550424
w/claw		N/A	N/A	N/A		
W@Pjoint II	0.178801566	3.97	3.65	3.86	3.8266667	0.1625833
W@Pjoint III	0.178661691	5.04	4.86	4.84	4.9133333	0.1101514
W@Pjoint IV	0.178941331	4.41	4.16	4.15	4.24	0.1473092
W@2joint III	0.192353841	4.08	3.54	3.66	3.76	0.2835489
W@2joint IV	0.13885244	3.63	3.29	3.5	3.4733333	0.1715615
W@3joint IV	0.140641388	2.91	2.54	2.64	2.6966667	0.1913984
LoPhI,II	0.835625514	31.54	30.57	31.24	31.116667	0.4966219
LoPhII,II	4.049564174	20.59	19.68	20.59	20.286667	0.5253887
LoPhI,III	1.110301761	33.59	32.57	32.47	32.876667	0.6197849
LoPhII,III	1.193721073	23.99	23.05	23.51	23.516667	0.4700355
LoPhIII,III	0.799799975	18.35	17.52	17.74	17.87	0.43
LoPhI,IV	0.743014132	25.67	23.87	24.42	24.653333	0.9224063
LoPhII,IV	0.724051103	15.58	14.67	14.69	14.98	0.5197115
LoPhIII,IV	0.401098492	12.29	11.42	11.62	11.776667	0.455668
LoPhIV,IV	0.507907472	14.17	12.75	13.39	13.436667	0.7111493
WoPhI,II	0.157575379	2.91	2.87	2.74	2.84	0.0888819
WoPhII,II	0.198821528	3.03	2.41	2.26	2.5666667	0.4082075
WoPhI,III	0.205596693	3.74	3.84	3.58	3.72	0.1311488
WoPhII,III	0.188759106	3.24	3.13	3.08	3.15	0.0818535
WoPhIII,III	0.168433963	2.62	2.37	2.31	2.4333333	0.1644182
WoPhI,IV	0.130766968	3.01	2.93	2.74	2.8933333	0.1386843
WoPhII,IV	0.153199217	2.95	2.83	2.69	2.8233333	0.1301281
WoPhIII,IV	0.12980755	2.65	2.4	2.32	2.4566667	0.1721434
WoPhIV,IV	0.153850577	2.32	1.99	2	2.1033333	0.1877054
Foot Length	2.555292547	90.64	89.7	89.23	89.856667	0.7179369
Lotmt	5.047449851	106.38	99.22	97.41	101.00333	4.7434622
Lott	5.824182346	154.76	146.28	139.72	146.92	7.5403979
LoFem	2.522136	79.52	72.36	71.73	74.536667	4.3271738
Wotmt@prox	0.933530931	13.93	13.05	12.49	13.156667	0.7259017
Wotmt@cond	0.703967329	13.28	13.16	12.93	13.123333	0.1778576
Wott@prox	0.875168555	15.55	15.14	16.04	15.576667	0.4505922
Wott@mid	0.380433963	7.39	7.57	7.14	7.3666667	0.2159475
Wott@cond	0.723685014	12.01	11.7	11.56	11.756667	0.2302897
Wofem@cond	0.814831271	15.12	14.83	14.87	14.94	0.1571623

Name	*Gavia immer*	*Gavia immer*	*Gavia immer*	*Gavia immer*	*Gavia immer*	*Gavia immer*	*Gavia immer*
Specimen #	80915	36776	80914	79103	17715	AVERAGE	STDEV
M/F	F	F	M	M	M		
LoDI	29.39	26.44	27.86	27.06	28.25	27.8	1.13262968
w/claw	N/A	N/A	36.56	N/A	N/A		
LoDII	78.84	79.53	84.06	81.62	84.21	81.652	2.48762336
w/claw	N/A	N/A	N/A	N/A	N/A		
LoDIII	95.8	94.19	97.19	95.24	101.81	96.846	2.97856173
w/claw	N/A	N/A	N/A	N/A	N/A		
LoDIV	101.6	98.96	102.55	100.53	106.99	102.126	3.02843689
w/claw	N/A	N/A	N/A	N/A	N/A		
W@Pjoint II	4.15	3.97	4.3	4.18	4.35	4.19	0.14815532
W@Pjoint III	5	4.35	5.38	5.41	5.36	5.1	0.45127597
W@Pjoint IV	4.35	4.38	4.44	4.37	4.68	4.444	0.13612494
W@2joint III	4.04	3.94	4.65	5.11	4.96	4.54	0.52995283
W@2joint IV	4.11	4.08	4.21	4.14	4.12	4.132	0.04868265
W@3joint IV	3.76	3.54	3.82	3.75	4.07	3.788	0.18992104
LoPhI,II	50.88	51.86	53.39	53.39	55.12	52.928	1.62532151
LoPhII,II	28.47	27.94	31.02	28.52	30.18	29.226	1.30884682
LoPhI,III	42.93	43.13	44.41	44.25	47.62	44.468	1.88027126
LoPhII,III	27.96	27.26	28.29	27.83	29.6	28.188	0.87256518
LoPhIII,III	25.65	24.67	26.04	24.98	26.49	25.566	0.74694712
LoPhI,IV	37.33	36.76	37.34	37.42	39.82	37.734	1.19552499
LoPhII,IV	22.3	21.94	22.77	22.36	23.65	22.604	0.6546984
LoPhIII,IV	19.74	19.83	20.12	19.52	21.16	20.074	0.64411179
LoPhIV,IV	23.95	22.69	24.94	23.95	24.86	24.078	0.91020327
WoPhI,II	3.57	3.44	3.97	3.67	3.82	3.694	0.20767763
WoPhII,II	3.07	2.61	2.74	2.93	2.89	2.848	0.17753873
WoPhI,III	4.16	3.75	3.97	4.08	4.16	4.024	0.17184295
WoPhII,III	3.54	4.11	3.92	4.01	3.6	3.836	0.25284383
WoPhIII,III	3.75	3.68	3.74	3.76	3.78	3.742	0.03768289
WoPhI,IV	4.2	3.69	4	4.01	4.15	4.01	0.19887182
WoPhII,IV	3.22	2.85	3.21	3.02	3.55	3.17	0.26143833
WoPhIII,IV	3.17	2.9	3.09	3.15	3.24	3.11	0.12903488
WoPhIV,IV	3.06	2.81	2.91	2.95	2.77	2.9	0.11532563
Foot Length	116.23	116.46	116.81	116.58	123.34	117.884	3.0571768
Lotmt	86.81	84.75	88.82	91.23	92.65	88.852	3.20456237
Lott	132.82	134.14	143.14	141.38	140.27	138.35	4.58574967
LoFem	54.79	52.65	56.61	54.1	54.15	54.46	1.43467766
Wotmt@prox	15.86	15.03	15.98	15.4	16.43	15.74	0.54032398
Wotmt@cond	11.56	10.71	11.05	11.69	11.76	11.354	0.45478566
Wott@prox	12.68	15.78	12.93	12.93	17.93	14.45	2.32556445
Wott@mid	8.48	10.81	8.71	8.73	11.5	9.646	1.40240151
Wott@cond	14.77	14.41	15.42	14.26	15.69	14.91	0.62461988
Wofem@cond	16.44	17.95	18.47	18.48	18.03	17.874	0.83799165

Name	*Aechmorphorus occidentalis*	*Aechmorphorus oc*	*Aechmorphorus*	*Aechmorphorus*
Specimen #	91861	81972	32241	81718
M/F	F	?	M	?
LoDI	N/A	N/A	N/A	N/A
w/claw	N/A	N/A	N/A	N/A
LoDII	52.67	47.91	53.45	50.5
w/claw	N/A	N/A	N/A	N/A
LoDIII	58.09	64.83	59.02	56.22
w/claw	N/A	N/A	N/A	N/A
LoDIV	61.5	71.43	63.7	65.69
w/claw	N/A	N/A	N/A	N/A
W@Pjoint II	4.33	4.36	4.89	4.45
W@Pjoint III	3.9	4.43	3.98	4.23
W@Pjoint IV	4.25	4.71	4.7	4.07
W@2joint III	4.46	4.97	4.82	4.59
W@2joint IV	4.02	4.29	4.27	4.2
W@3joint IV	3.97	4.21	4.07	4.08
LoPhI,II	28.22	30.24	28.81	27.51
LoPhII,II	24.75	17.74	25.08	23.89
LoPhI,III	23.32	25.34	24.66	24.27
LoPhII,III	17.68	20	17.59	17.85
LoPhIII,III	17.5	19.8	17.72	15.27
LoPhI,IV	24.86	27.32	25.02	24.45
LoPhII,IV	12.19	15	13.23	13.11
LoPhIII,IV	12.04	14.9	12.52	12.37
LoPhIV,IV	14.64	16.47	14.87	17.82
WoPhI,II	3.67	3.44	3.71	3.8
WoPhII,II	2.53	2.85	2.52	2.54
WoPhI,III	2.68	2.74	2.7	2.93
WoPhII,III	2.87	2.91	2.87	2.88
WoPhIII,III	2.27	2.55	2.36	2.77
WoPhI,IV	4.07	4	4.3	4.16
WoPhII,IV	2.9	3.19	3.18	3.15
WoPhIII,IV	2.89	2.96	3.06	2.84
WoPhIV,IV	2.75	2.99	2.95	2.37
Foot Length	73.4	81.06	76.28	70.01
Lotmt	69.77	78.3	78.17	70.36
Lott	111.27	125.19	122.35	113.81
LoFem	42	47.29	44.95	42.86
Wotmt@prox	11.47	12.56	12.4	12.03
Wotmt@cond	9.36	9.47	9.8	8.6
Wott@prox	10.3	16.68	11.35	10.26
Wott@mid	6.98	10.05	7.98	7.58
Wott@cond	9.58	10.27	10.65	10.05
Wofem@cond	12.58	13.98	14.23	13.14

Name	*Aechmorphorus*	*Aechmorphorus*	*Aechmorphorus*	*Podiceps auritus*
Specimen #	19592	AVERAGE	STDEV	21229
M/F	?			M
LoDI	N/A			N/A
w/claw	N/A			N/A
LoDII	56.68	52.242	3.284017357	31.85
w/claw	N/A			N/A
LoDIII	60.89	59.81	3.272514324	38.8
w/claw	N/A			N/A
LoDIV	70.71	66.606	4.343642481	48.65
w/claw	N/A			N/A
W@Pjoint II	4.86	4.578	0.274899982	3.52
W@Pjoint III	4.62	4.232	0.301446513	2.75
W@Pjoint IV	4.98	4.542	0.371846743	3.07
W@2joint III	5.26	4.82	0.315673882	3.3
W@2joint IV	4.76	4.308	0.274171479	2.98
W@3joint IV	4.32	4.13	0.136198385	2.48
LoPhI,II	30.55	29.066	1.302201981	17.21
LoPhII,II	27.28	23.748	3.583625259	15.11
LoPhI,III	26.58	24.834	1.219130838	17.3
LoPhII,III	19.54	18.532	1.145587186	11.87
LoPhIII,III	16.52	17.362	1.671562144	10.05
LoPhI,IV	25.98	25.526	1.149121404	18.87
LoPhII,IV	13.88	13.482	1.04089865	9.59
LoPhIII,IV	13.29	13.024	1.14456542	8.76
LoPhIV,IV	20.07	16.774	2.248850818	11.77
WoPhI,II	4	3.724	0.203543607	2.95
WoPhII,II	2.97	2.682	0.21253235	1.92
WoPhI,III	2.89	2.788	0.114324101	1.98
WoPhII,III	3.22	2.95	0.151822265	2.02
WoPhIII,III	3.37	2.664	0.438839378	2.05
WoPhI,IV	4.54	4.214	0.213962614	2.45
WoPhII,IV	3.45	3.174	0.19501282	2.22
WoPhIII,IV	3.36	3.022	0.206203783	2.13
WoPhIV,IV	2.86	2.784	0.249158584	1.87
Foot Length	70.3	74.21	4.604117722	51.12
Lotmt	78.82	75.084	4.592889069	47.71
Lott	126.09	119.742	6.777589542	76.44
LoFem	46.58	44.736	2.289875542	34.84
Wotmt@prox	12.92	12.276	0.552476244	8.32
Wotmt@cond	9.64	9.374	0.463874983	6.33
Wott@prox	16.45	13.008	3.277372423	10.46
Wott@mid	11.56	8.83	1.91368754	7.31
Wott@cond	10.8	10.27	0.487288416	7.35
Wofem@cond	14.61	13.708	0.829921683	9.52

Name	*Podiceps auritus*	*Podiceps auritus*	*Podiceps auritus*	*Podiceps auritus*
Specimen #	21227	21228	AVERAGE	STDEV
M/F	F	M		
LoDI	N/A	N/A		
w/claw	N/A	N/A		
LoDII	34.03	32.86	32.585	1.106661647
w/claw	N/A	N/A		
LoDIII	41.7	41.24	40.1875	1.495222949
w/claw	N/A	N/A		
LoDIV	48.25	46.68	47.285	1.430163161
w/claw	N/A	50.11		
W@Pjoint II	3.81	3.35	3.54	0.194079022
W@Pjoint III	3.12	3	2.96	0.154272486
W@Pjoint IV	3.01	3.44	3.1225	0.215619263
W@2joint III	3.31	3.35	3.255	0.131782649
W@2joint IV	3.04	3.17	3.07	0.080415587
W@3joint IV	3.1	3.07	2.9275	0.298817112
LoPhI,II	17.78	17.21	17.2025	0.477729003
LoPhII,II	16.33	16.07	15.625	0.674166152
LoPhI,III	16.71	16.72	16.5725	0.729171905
LoPhII,III	12.6	12.41	12.2075	0.353683003
LoPhIII,III	12.63	12.49	11.62	1.202497401
LoPhI,IV	19.66	18.9	18.93	0.561842208
LoPhII,IV	10.14	10.06	9.815	0.334315221
LoPhIII,IV	8.97	9.06	8.78	0.325269119
LoPhIV,IV	10.92	10.4	10.86	0.659140855
WoPhI,II	2.95	3.01	2.9375	0.070887234
WoPhII,II	1.91	2.15	2.11	0.258327957
WoPhI,III	2.02	2.14	2.035	0.071879529
WoPhII,III	1.98	2.22	2.0375	0.127115433
WoPhIII,III	1.8	2.14	2.0925	0.239635139
WoPhI,IV	2.45	2.8	2.555	0.16663333
WoPhII,IV	2.15	2.48	2.245	0.161348484
WoPhIII,IV	2.2	2.46	2.2125	0.174618632
WoPhIV,IV	1.99	2.63	2.1125	0.34874776
Foot Length	51.22	50.15	50.4375	0.921461701
Lotmt	48.58	45.88	46.7425	1.715582991
Lott	77.21	72.12	74.1425	3.159687485
LoFem	32.75	32.4	32.9675	1.298495925
Wotmt@prox	7.81	8.55	8.18	0.323006708
Wotmt@cond	6.29	6.12	6.1275	0.255130685
Wott@prox	11.44	12.92	11.1125	1.413963107
Wott@mid	6.51	6.54	6.64	0.472369912
Wott@cond	6.75	6.91	6.9825	0.257082996
Wofem@cond	9.56	9.88	9.52	0.311555239

Name	*Fulica americana*	*Fulica americana*	*Fulica americana*	*Fulica americana*	*Fulica americana*
Specimen #	15254	19163	11517	11402	AVERAGE
M/F	M	F	M	F	
LoDI	22.11	18.56	22.98	19.61	20.815
w/claw	29.56	25.56	N/A	29.68	28.26666667
LoDII	54.85	50.29	59.19	48.97	53.325
w/claw	68.34	55.99	N/A	61.72	62.01666667
LoDIII	68.73	62.41	79.2	62.87	68.3025
w/claw	81.52	67.51	N/A	N/A	74.515
LoDIV	60.24	52.75	70.37	55.2	59.64
w/claw	70.45	60.5	N/A	63.11	64.68666667
W@Pjoint II	3.51	3.32	3.69	3.55	3.5175
W@Pjoint III	4.22	3.89	4.14	3.81	4.015
W@Pjoint IV	4.01	3.57	3.98	3.83	3.8475
W@2joint III	3.26	3.02	3.67	3.07	3.255
W@2joint IV	3.04	2.68	2.99	2.61	2.83
W@3joint IV	2.51	2.24	2.55	2.35	2.4125
LoPhI,II	29.89	27.73	32.31	26.87	29.2
LoPhII,II	26	23.22	27.7	23.4	25.08
LoPhI,III	27	24.49	29.43	24.16	26.27
LoPhII,III	21.43	18.4	23.4	18.6	20.4575
LoPhIII,III	23.64	20.86	27.87	20.96	23.3325
LoPhI,IV	23.61	10.98	26.16	20.49	20.31
LoPhII,IV	13.64	12.12	14.98	12.02	13.19
LoPhIII,IV	10.35	8.73	12.03	9.81	10.23
LoPhIV,IV	16.7	13.67	18.04	14.7	15.7775
WoPhI,II	2.67	2.22	2.48	2.47	2.46
WoPhII,II	1.86	1.56	1.71	1.67	1.7
WoPhI,III	3.03	2.87	2.92	2.81	2.9075
WoPhII,III	2.45	2.39	2.45	2.31	2.4
WoPhIII,III	1.88	2.26	1.7	1.78	1.905
WoPhI,IV	2.45	2.25	2.31	2.4	2.3525
WoPhII,IV	2.39	1.97	2.17	2.19	2.18
WoPhIII,IV	1.87	1.58	1.88	1.81	1.785
WoPhIV,IV	1.43	1.17	1.28	1.32	1.3
Foot Length	83.9	73.76	92.24	73.5	80.85
Lotmt	60.81	56.08	63.62	55.29	58.95
Lott	95.55	89.43	98.07	89.71	93.19
LoFem	56.61	51.96	58.14	52.89	54.9
Wotmt@prox	9.35	8.6	9.6	8.71	9.065
Wotmt@cond	8.58	8.01	9.04	8.18	8.4525
Wott@prox	11.61	9.92	9.34	9.48	10.0875
Wott@mid	5.64	4.68	4.4	4.79	4.8775
Wott@cond	8.86	8.39	8.94	8.21	8.6
Wofem@cond	10.73	9.17	10.29	9.73	9.98

Name	*Fulica americana*	*Recurvirostra amer*	*Recurvirostra amer*	*Recurvirostra*
Specimen #	STDEV	23134	19185	23137
M/F		M	F	F
LoDI	2.073748619	N/A	N/A	N/A
w/claw		N/A	N/A	N/A
LoDII	4.651204145	32.72	31.77	31.99
w/claw		38.34	N/A	N/A
LoDIII	7.813916538	39.93	39.98	39.74
w/claw		47.15	N/A	N/A
LoDIV	7.803388153	35.95	36.83	34.32
w/claw		41.27	N/A	N/A
W@Pjoint II	0.152616076	2.36	2.06	2.07
W@Pjoint III	0.196044213	3.05	2.8	2.87
W@Pjoint IV	0.201059693	2.52	2.4	2.3
W@2joint III	0.295352896	2.5	2.32	2.25
W@2joint IV	0.216487105	2.2	1.91	1.93
W@3joint IV	0.143845982	1.96	1.48	1.61
LoPhI,II	2.431597554	20.08	19.39	19.13
LoPhII,II	2.159691336	12.74	12.72	13.44
LoPhI,III	2.458929306	21.36	20.72	20.84
LoPhII,III	2.400532927	12.48	11.72	11.71
LoPhIII,III	3.287627057	8.47	8.27	8.21
LoPhI,IV	6.638117203	14.27	4.42	13.52
LoPhII,IV	1.404801291	10.04	10.05	9.25
LoPhIII,IV	1.376081393	7.71	7.51	7.09
LoPhIV,IV	1.964049813	6.19	5.61	5.58
WoPhI,II	0.184571576	2.12	1.75	1.9
WoPhII,II	0.124096736	1.55	1.38	1.51
WoPhI,III	0.093229108	2.67	1.94	2.17
WoPhII,III	0.066332496	2.01	1.84	1.88
WoPhIII,III	0.247857486	1.83	1.66	1.66
WoPhI,IV	0.089582364	1.72	1.62	1.67
WoPhII,IV	0.171658576	1.69	1.55	1.66
WoPhIII,IV	0.140118997	1.58	1.44	1.54
WoPhIV,IV	0.107393358	1.31	1.18	1.14
Foot Length	9.006020209	48.77	51.64	51.16
Lotmt	3.953943179	103.48	103.64	99.88
Lott	4.306274492	120.35	118.18	117.2
LoFem	2.949881354	41.08	41.09	40.87
Wotmt@prox	0.486381195	8.14	8.08	8.19
Wotmt@cond	0.458793708	7.25	6.66	6.78
Wott@prox	1.044649064	10.38	10.51	10
Wott@mid	0.534189417	3.51	3.61	3.45
Wott@cond	0.355621522	7.14	6.69	7.15
Wofem@cond	0.677544586	9.97	9.94	9.57

Name	*Recurvirostra*	*Recurvirostra*	*Recurvirostra*	*Larus argentatus*	*Larus argentatus*
Specimen #	73006	AVERAGE	STDEV	31939	17760
M/F	M			F	M
LoDI	N/A			3.98	N/A
w/claw	N/A			8.96	N/A
LoDII	31.89	32.0925	0.42789212	36.2	34.31
w/claw	N/A			N/A	N/A
LoDIII	38.93	39.645	0.48774994	49.45	46.11
w/claw	N/A			N/A	N/A
LoDIV	36.46	35.89	1.10709831	50.12	45.82
w/claw	N/A			58.68	N/A
W@Pjoint II	2.15	2.16	0.13928388	3.19	2.59
W@Pjoint III	2.87	2.8975	0.10688779	3.86	2.37
W@Pjoint IV	2.28	2.375	0.11	3.4	2.71
W@2joint III	2.44	2.3775	0.11324752	3.25	2.76
W@2joint IV	1.85	1.9725	0.15542951	2.77	2.3
W@3joint IV	1.57	1.655	0.21047565	2.17	1.91
LoPhI,II	19.65	19.5625	0.4050823	19.14	18.35
LoPhII,II	12.62	12.88	0.37700575	18.82	16.91
LoPhI,III	20.68	20.9	0.31411251	21.94	20.8
LoPhII,III	10.61	11.63	0.76971856	15.23	14.16
LoPhIII,III	8.26	8.3025	0.11470978	12.98	11.93
LoPhI,IV	14.43	11.66	4.84293988	16.84	16.17
LoPhII,IV	9.78	9.78	0.37478883	13.23	11.83
LoPhIII,IV	7.6	7.4775	0.27097048	11.24	9.91
LoPhIV,IV	6.38	5.94	0.40603777	10.88	9.57
WoPhI,II	1.95	1.93	0.15253415	2.2	1.68
WoPhII,II	1.58	1.505	0.08812869	1.74	1.51
WoPhI,III	2.22	2.25	0.30539592	2.76	2.35
WoPhII,III	2.14	1.9675	0.13598407	2.41	2.1
WoPhIII,III	1.79	1.735	0.08812869	2.19	1.92
WoPhI,IV	1.75	1.69	0.05715476	2.48	1.98
WoPhII,IV	1.61	1.6275	0.06130525	2.25	1.84
WoPhIII,IV	1.49	1.5125	0.06075909	1.96	1.55
WoPhIV,IV	1.27	1.225	0.07852813	1.71	1.37
Foot Length	49.83	50.35	1.30217766	62.23	59.71
Lotmt	105.44	103.11	2.32949208	66.34	60.62
Lott	121.38	119.2775	1.92278227	106.72	95.49
LoFem	42.05	41.2725	0.52816506	60.1	50.96
Wotmt@prox	8.09	8.125	0.05066228	11.1	9.9
Wotmt@cond	7.07	6.94	0.26894857	10.8	9.15
Wott@prox	10.38	10.3175	0.22035955	12.5	10.38
Wott@mid	3.49	3.515	0.06806859	4.7	3.89
Wott@cond	6.8	6.945	0.23530123	10.11	8.67
Wofem@cond	9.61	9.7725	0.21171915	11.99	10.14

Name	*Larus argentatus*	*Larus argentatus*	*Larus argentatus*	*Larus argentatus*
Specimen #	54964	31383	AVERAGE	STDEV
M/F	M	F		
LoDI	N/A	4.25	4.115	0.190918831
w/claw	N/A	11.37	10.165	
LoDII	37.32	36.88	36.1775	1.32751334
w/claw	N/A	N/A		
LoDIII	52.1	48.88	49.135	2.456698326
w/claw	N/A	N/A		
LoDIV	50.88	48.71	48.8825	2.230849987
w/claw	N/A	N/A		
W@Pjoint II	3.21	2.96	2.9875	0.288256252
W@Pjoint III	4.28	3.85	3.59	0.837655458
W@Pjoint IV	3.6	3.15	3.215	0.38370996
W@2joint III	3.65	3.16	3.205	0.365194012
W@2joint IV	3.05	2.59	2.6775	0.314894162
W@3joint IV	2.43	2.02	2.1325	0.225148099
LoPhI,II	20.09	19.15	19.1825	0.711682279
LoPhII,II	18.36	18.06	18.0375	0.814058761
LoPhI,III	24.39	22.89	22.505	1.51961618
LoPhII,III	16.09	15.3	15.195	0.79256966
LoPhIII,III	13.27	11.89	12.5175	0.711588598
LoPhI,IV	18.56	17.62	17.2975	1.029316116
LoPhII,IV	13.17	13.12	12.8375	0.67317036
LoPhIII,IV	11.39	10.98	10.88	0.668480865
LoPhIV,IV	10.42	9.37	10.06	0.711383628
WoPhI,II	2.38	2.25	2.1275	0.307828415
WoPhII,II	1.85	1.89	1.7475	0.170562794
WoPhI,III	3.11	3.09	2.8275	0.356499182
WoPhII,III	2.78	2.71	2.5	0.311234103
WoPhIII,III	2.46	2.42	2.2475	0.248646335
WoPhI,IV	2.59	2.41	2.365	0.267145404
WoPhII,IV	2.5	2.13	2.18	0.274104603
WoPhIII,IV	2.2	1.88	1.8975	0.268623032
WoPhIV,IV	1.9	1.76	1.685	0.224870333
Foot Length	65.77	62.52	62.5575	2.48576447
Lotmt	69.72	70.31	66.7475	4.443702473
Lott	111.16	109.17	105.635	7.00285894
LoFem	60.49	62.33	58.47	5.100228753
Wotmt@prox	12.04	11.2	11.06	0.88075725
Wotmt@cond	10.81	11.09	10.4625	0.885263614
Wott@prox	12.82	12.19	11.9725	1.092378903
Wott@mid	4.83	4.78	4.55	0.443245605
Wott@cond	10.96	10.13	9.9675	0.951363057
Wofem@cond	12.39	12.56	11.77	1.112624525

Name	*Larus delawarenes*	*Larus delawarenes*	*Thalasseus maximu*	*Thalasseus maxim*
Specimen #	AVERAGE	STDEV	38961	55950
M/F			M	M
LoDI	3.18	0.115325626	3.91	5.49
w/claw			7.55	N/A
LoDII	27.3475	0.90223334	16.73	17.84
w/claw			20.2	N/A
LoDIII	35.8625	1.222875709	24.8	26.31
w/claw			31.53	N/A
LoDIV	35.8075	1.178399338	24.53	25.38
w/claw			28.54	N/A
W@Pjoint II	2.115	0.079372539	1.87	1.73
W@Pjoint III	2.81	0.156843871	2.46	2.54
W@Pjoint IV	2.3775	0.134008706	2.17	2.18
W@2joint III	2.355	0.119023807	2.12	2.05
W@2joint IV	1.91	0.139283883	1.91	1.76
W@3joint IV	1.4975	0.163986788	1.59	1.33
LoPhI,II	14.725	0.694382219	9.1	9.99
LoPhII,II	13.2125	0.320559407	7.91	8.63
LoPhI,III	17.4925	0.382219396	11.89	12.1
LoPhII,III	11.1875	0.34769479	8.99	8.52
LoPhIII,III	8.3375	0.555840205	6.65	6.63
LoPhI,IV	12.9225	0.51596996	9.27	9.4
LoPhII,IV	9.3675	0.251975528	6.17	7.15
LoPhIII,IV	7.7875	0.276209462	5.93	4.91
LoPhIV,IV	7.2875	0.389903834	5.09	5.03
WoPhI,II	1.62	0.096953597	1.42	1.22
WoPhII,II	1.3975	0.115866302	1.15	1.15
WoPhI,III	2.17	0.13114877	1.68	1.62
WoPhII,III	1.94	0.158534959	1.74	1.61
WoPhIII,III	1.8825	0.068980674	1.6	1.31
WoPhI,IV	1.815	0.130256158	1.58	1.48
WoPhII,IV	1.615	0.162172747	1.38	1.29
WoPhIII,IV	1.425	0.12396236	1.18	1.16
WoPhIV,IV	1.305	0.050662281	1.19	0.93
Foot Length	46.285	2.013727886	32.33	33.36
Lotmt	55.85	1.239435355	34.53	36.49
Lott	84.2625	2.365972316	68.74	70.88
LoFem	43.64	1.539761886	N/A	42.96
Wotmt@prox	8.3325	0.432078311	7.16	7.07
Wotmt@cond	7.5725	0.30291638	6.51	6.43
Wott@prox	8.7125	0.904963167	5.57	7.74
Wott@mid	3.955	0.250931598	3.48	3.56
Wott@cond	7.5725	0.255391856	6.15	6.45
Wofem@cond	8.8175	0.540331688	6.57	7.52

Name	*Thalasseus maxi*	*Thalasseus maxin*	*Thalasseus maximu*	*Thalasseus maximu*
Specimen #	33293	39864	AVERAGE	STDEV
M/F	F	F		
LoDI	5.29	5.02	4.9275	0.70514183
w/claw	N/A	N/A		
LoDII	17.3	17.79	17.415	0.517590572
w/claw	N/A	N/A		
LoDIII	24.87	26.18	25.54	0.816292431
w/claw	N/A	N/A		
LoDIV	24.22	25.1	24.8075	0.527723097
w/claw	N/A	N/A		
W@Pjoint II	1.68	1.94	1.805	0.120692447
W@Pjoint III	2.47	2.45	2.48	0.040824829
W@Pjoint IV	2.08	2.1	2.1325	0.049916597
W@2joint III	2.15	2.08	2.1	0.043969687
W@2joint IV	1.44	1.77	1.72	0.198829911
W@3joint IV	1.32	1.45	1.4225	0.126326297
LoPhI,II	10.12	9.7	9.7275	0.453679402
LoPhII,II	8.45	8.3	8.3225	0.306308668
LoPhI,III	11.86	11.9	11.9375	0.109658561
LoPhII,III	8.19	8.31	8.5025	0.352455671
LoPhIII,III	6.8	6.48	6.64	0.130894359
LoPhI,IV	9.19	9.46	9.33	0.122474487
LoPhII,IV	6.37	6.69	6.595	0.427512183
LoPhIII,IV	4.96	5.01	5.2025	0.48671518
LoPhIV,IV	4.61	5.53	5.065	0.376430604
WoPhI,II	1.23	1.27	1.285	0.092556289
WoPhII,II	1.12	1.22	1.16	0.042426407
WoPhI,III	1.61	1.72	1.6575	0.051881275
WoPhII,III	1.64	1.61	1.65	0.06164414
WoPhIII,III	1.44	1.46	1.4525	0.118708326
WoPhI,IV	1.47	1.59	1.53	0.063770422
WoPhII,IV	1.27	1.33	1.3175	0.048562674
WoPhIII,IV	1.17	1.2	1.1775	0.017078251
WoPhIV,IV	1.05	1.34	1.1275	0.177082843
Foot Length	33.98	33.26	33.2325	0.680753259
Lotmt	35.52	36.33	35.7175	0.898345702
Lott	68.75	69.25	69.405	1.011747663
LoFem	41.05	43.08	42.36333333	1.138961515
Wotmt@prox	6.98	7.32	7.1325	0.145
Wotmt@cond	6.4	6.69	6.5075	0.130224166
Wott@prox	7.84	7.71	7.215	1.098074072
Wott@mid	3.74	3.75	3.6325	0.134008706
Wott@cond	6.04	6.46	6.275	0.212681295
Wofem@cond	7.51	7.84	7.36	0.548513142

Name	*Sterna paradisaea*	*Sterna paradisaea*	*Sterna paradisaea*	*Sterna paradisaea*
Specimen #	31318	30748	30751	30637
M/F	M	M	M	M
LoDI	N/A	3.17	2.39	2.64
w/claw	N/A	N/A	N/A	N/A
LoDII	9.37	10.64	9.54	9.89
w/claw	13.17	N/A	N/A	N/A
LoDIII	15.1	15.5	15.22	15.04
w/claw	21.89	N/A	N/A	N/A
LoDIV	14.52	14.9	13.8	14.74
w/claw	19.05	20.09	N/A	N/A
W@Pjoint II	1.07	0.99	0.9	0.92
W@Pjoint III	1.47	1.23	1.38	1.48
W@Pjoint IV	1.2	1.06	1	1.22
W@2joint III	1.27	1.02	1.22	1.33
W@2joint IV	1.04	1.06	0.91	0.97
W@3joint IV	0.92	0.85	0.86	0.86
LoPhI,II	5.65	5.78	5.13	5.43
LoPhII,II	5.14	4.93	4.68	4.77
LoPhI,III	6.59	6.75	6.7	6.7
LoPhII,III	4.69	4.81	4.44	4.51
LoPhIII,III	4.25	4.13	3.9	4.23
LoPhI,IV	4.89	5.27	5.09	4.92
LoPhII,IV	4.21	3.91	3.36	4.5
LoPhIII,IV	3.31	3.31	2.89	2.75
LoPhIV,IV	3.37	2.85	2.47	3.03
WoPhI,II	0.62	0.58	0.61	0.64
WoPhII,II	0.63	0.61	0.58	0.61
WoPhI,III	0.87	0.89	0.88	0.9
WoPhII,III	0.94	0.81	0.89	0.92
WoPhIII,III	0.85	0.79	0.88	0.88
WoPhI,IV	0.7	0.68	0.68	0.75
WoPhII,IV	0.74	0.67	0.65	0.91
WoPhIII,IV	0.6	0.61	0.65	0.7
WoPhIV,IV	0.57	0.64	0.61	0.62
Foot Length	18.99	19.88	18.57	19.22
Lotmt	16.23	16.21	14.88	15.01
Lott	36.42	37.14	34.69	N/A
LoFem	23.32	23.43	22.83	23.13
Wotmt@prox	3.95	4.03	4.02	4.1
Wotmt@cond	3.66	3.72	3.62	3.65
Wott@prox	4.3	4.81	4.23	N/A
Wott@mid	1.78	1.85	1.66	N/A
Wott@cond	3.66	3.67	3.42	N/A
Wofem@cond	4.2	4.31	4.31	4.12

Name	*Sterna paradisaea*	*Sterna paradisaea*	*Himantopus mexicanus*	*Himantopus*
Specimen #	AVERAGE	STDEV	55945	23444
M/F			F	M
LoDI	2.733333333	0.398288003	N/A	N/A
w/claw			N/A	N/A
LoDII	9.86	0.563264296	28.07	26.14
w/claw			34.31	N/A
LoDIII	15.215	0.204205779	35.03	34.72
w/claw			43.02	N/A
LoDIV	14.49	0.485661062	29.77	31.12
w/claw	19.57		33.91	N/A
W@Pjoint II	0.97	0.077028133	1.85	1.67
W@Pjoint III	1.39	0.115758369	2.23	2.29
W@Pjoint IV	1.12	0.107082523	2.05	2.08
W@2joint III	1.21	0.134412301	1.78	1.76
W@2joint IV	0.995	0.068556546	1.6	1.71
W@3joint IV	0.8725	0.032015621	1.27	1.33
LoPhI,II	5.4975	0.284414603	15.21	15.04
LoPhII,II	4.88	0.201825007	12.5	11.38
LoPhI,III	6.685	0.067577116	15.73	15.42
LoPhII,III	4.6125	0.168597153	11.2	10.84
LoPhIII,III	4.1275	0.160494029	8.6	7.98
LoPhI,IV	5.0425	0.175380539	12.04	11.73
LoPhII,IV	3.995	0.487066046	8.48	8.11
LoPhIII,IV	3.065	0.288617394	6.13	6.16
LoPhIV,IV	2.93	0.374877758	4.84	5.36
WoPhI,II	0.6125	0.025	1.5	1.44
WoPhII,II	0.6075	0.020615528	1.17	1.05
WoPhI,III	0.885	0.012909944	1.73	1.42
WoPhII,III	0.89	0.057154761	1.55	1.42
WoPhIII,III	0.85	0.042426407	1.28	1.27
WoPhI,IV	0.7025	0.033040379	1.42	1.19
WoPhII,IV	0.7425	0.118145391	1.45	1.35
WoPhIII,IV	0.64	0.045460606	1.14	1.09
WoPhIV,IV	0.61	0.029439203	0.95	0.99
Foot Length	19.165	0.547387736	42.78	43.7
Lotmt	15.5825	0.738077458	106.36	116.78
Lott	36.08333333	1.259219335	115.96	117.77
LoFem	23.1775	0.262726093	32.43	34.26
Wotmt@prox	4.025	0.061373175	6.17	6.35
Wotmt@cond	3.6625	0.041932485	5.41	5.5
Wott@prox	4.446666667	0.316596483	9.21	7.66
Wott@mid	1.763333333	0.096090235	2.67	2.88
Wott@cond	3.583333333	0.141539158	5.21	5.37
Wofem@cond	4.235	0.092556289	7.14	7.08

Name	*Himantopus*	*Himantopus*	*Himantopus mexic*	*Himantopus mexic*	*Calidris alpina*
Specimen #	55940	14655	AVERAGE	STDEV	33027
M/F	F	M			F
LoDI	N/A	N/A			N/A
w/claw	N/A	N/A			N/A
LoDII	28.63	27.53	27.5925	1.067407295	15.75
w/claw	N/A	N/A			N/A
LoDIII	36.94	36.27	35.74	1.043296059	19.33
w/claw	N/A	N/A			N/A
LoDIV	31.98	32.37	31.31	1.151839109	16.56
w/claw	N/A	N/A			N/A
W@Pjoint II	1.63	1.64	1.6975	0.103077641	1.06
W@Pjoint III	2.35	2.04	2.2275	0.134257216	1.39
W@Pjoint IV	1.98	1.55	1.915	0.24691429	1.18
W@2joint III	1.78	1.9	1.805	0.064031242	1.05
W@2joint IV	1.6	1.54	1.6125	0.070887234	0.94
W@3joint IV	1.24	1.27	1.2775	0.037749172	0.74
LoPhI,II	16.33	16.04	15.655	0.627189498	8.71
LoPhII,II	12.5	12.13	12.1275	0.527975694	7.18
LoPhI,III	16.67	15.48	15.825	0.57910851	8.32
LoPhII,III	12.31	12.23	11.645	0.737224525	5.81
LoPhIII,III	8.48	8.54	8.4	0.284253408	4.54
LoPhI,IV	12.67	12.41	12.2125	0.412664109	5.96
LoPhII,IV	8.43	8.53	8.3875	0.189450961	4.38
LoPhIII,IV	6.39	6.44	6.28	0.157691682	3.69
LoPhIV,IV	5.14	5.71	5.2625	0.366640151	3.04
WoPhI,II	1.51	1.39	1.46	0.055976185	0.75
WoPhII,II	0.98	1.04	1.06	0.079582243	0.63
WoPhI,III	1.69	1.52	1.59	0.145373083	0.86
WoPhII,III	1.43	1.51	1.4775	0.062915287	0.77
WoPhIII,III	1.21	1.25	1.2525	0.030956959	0.67
WoPhI,IV	1.31	1.27	1.2975	0.095699181	0.7
WoPhII,IV	1.33	1.38	1.3775	0.052519838	0.73
WoPhIII,IV	1.06	1.17	1.115	0.049328829	0.63
WoPhIV,IV	0.87	0.98	0.9475	0.054390563	0.55
Foot Length	46.88	45.02	44.595	1.779241411	23.7
Lotmt	105.54	113.96	110.66	5.569224961	27.64
Lott	110.77	120.46	116.24	4.088544973	43.15
LoFem	33.53	34.73	33.7375	1.001777587	22.93
Wotmt@prox	6.14	6.13	6.1975	0.103077641	3.65
Wotmt@cond	5.51	5.63	5.5125	0.090323493	3.22
Wott@prox	7.82	8.04	8.1825	0.70248962	4
Wott@mid	2.79	2.8	2.785	0.08660254	1.51
Wott@cond	5.15	5.42	5.2875	0.128160056	3.28
Wofem@cond	7.41	7.57	7.3	0.230217289	4.27

Name	*Calidris alpina*	*Calidris alpina*	*Calidris alpina*	*Calidris alpina*	*Numenius america*
Specimen #	33928	48038	AVERAGE	STDEV	55938
M/F	M	F			M
LoDI	3.3	N/A			9.56
w/claw	N/A	N/A			N/A
LoDII	17.29	15.59	16.21	0.938722536	29.54
w/claw	N/A	N/A			N/A
LoDIII	20.2	18.9	19.47666667	0.662293993	36.37
w/claw	N/A	N/A			N/A
LoDIV	18.24	17.17	17.32333333	0.850431263	33.82
w/claw	N/A	N/A			N/A
W@Pjoint II	1.22	1.06	1.113333333	0.092376043	2.77
W@Pjoint III	1.38	1.28	1.35	0.060827625	2.36
W@Pjoint IV	1.22	1.14	1.18	0.04	2.99
W@2joint III	1.15	1.02	1.073333333	0.068068593	2.3
W@2joint IV	0.99	0.92	0.95	0.036055513	2.51
W@3joint IV	0.83	0.79	0.786666667	0.045092498	1.99
LoPhI,II	9.38	8.88	8.99	0.348281495	17.75
LoPhII,II	7.82	7.15	7.383333333	0.378461799	12.57
LoPhI,III	8.64	8.36	8.44	0.174355958	16.69
LoPhII,III	6.64	5.85	6.1	0.46808119	11.93
LoPhIII,III	4.9	4.81	4.75	0.18734994	9.01
LoPhI,IV	6.41	6.06	6.143333333	0.236290781	13.69
LoPhII,IV	4.75	4.53	4.553333333	0.186100331	7.94
LoPhIII,IV	3.46	3.7	3.616666667	0.135769412	6.45
LoPhIV,IV	3.69	3.4	3.376666667	0.325627599	6.24
WoPhI,II	0.78	0.72	0.75	0.03	1.8
WoPhII,II	0.61	0.59	0.61	0.02	1.48
WoPhI,III	0.85	0.82	0.843333333	0.02081666	2.02
WoPhII,III	0.76	0.76	0.763333333	0.005773503	1.89
WoPhIII,III	0.73	0.64	0.68	0.045825757	1.6
WoPhI,IV	0.74	0.71	0.716666667	0.02081666	1.75
WoPhII,IV	0.7	0.65	0.693333333	0.040414519	1.75
WoPhIII,IV	0.65	0.59	0.623333333	0.030550505	1.6
WoPhIV,IV	0.54	0.52	0.536666667	0.015275252	1.25
Foot Length	24.94	24.85	24.49666667	0.691399547	47.45
Lotmt	27.12	27.82	27.52666667	0.36350149	81.39
Lott	42.54	43.52	43.07	0.494873721	99.47
LoFem	23.8	22.03	22.92	0.885042372	53.25
Wotmt@prox	3.83	3.61	3.696666667	0.117189306	10.52
Wotmt@cond	3.26	3.01	3.163333333	0.134288247	8.72
Wott@prox	4.34	4.31	4.216666667	0.188237439	11.37
Wott@mid	1.54	1.27	1.44	0.147986486	4.73
Wott@cond	3.34	3.06	3.226666667	0.147422296	9.15
Wofem@cond	4.24	4.04	4.183333333	0.125033329	10.57

Name	*Numenius americanus*	*Numenius americai*	*Numenius americai*	*Numenius america*
Specimen #	16247	35400	15801	AVERAGE
M/F	F	F	F	
LoDI	9.51	N/A	9.37	9.48
w/claw	N/A	N/A	N/A	
LoDII	28.54	27.71	27.21	28.25
w/claw	N/A	N/A	33.69	
LoDIII	34.35	33.95	35.08	34.9375
w/claw	N/A	N/A	40.36	
LoDIV	30.9	32.18	33.06	32.49
w/claw	N/A	N/A	N/A	
W@Pjoint II	2.51	2.45	2.72	2.6125
W@Pjoint III	3.56	3.16	3.4	3.12
W@Pjoint IV	2.73	2.86	2.89	2.8675
W@2joint III	2.52	2.47	2.7	2.4975
W@2joint IV	2.31	2.08	2.31	2.3025
W@3joint IV	1.95	1.89	1.96	1.9475
LoPhI,II	16.55	16.93	16.61	16.96
LoPhII,II	12.24	11.49	12.06	12.09
LoPhI,III	15.44	16.1	15.23	15.865
LoPhII,III	11.35	11.04	11.62	11.485
LoPhIII,III	8.49	7.97	8.88	8.5875
LoPhI,IV	12.1	12.81	12.32	12.73
LoPhII,IV	7.9	8.43	7.67	7.985
LoPhIII,IV	5.95	6.4	6.73	6.3825
LoPhIV,IV	5.86	5.62	5.56	5.82
WoPhI,II	1.82	1.77	1.82	1.8025
WoPhII,II	1.57	1.41	1.54	1.5
WoPhI,III	2.03	1.97	2.12	2.035
WoPhII,III	1.86	1.84	1.88	1.8675
WoPhIII,III	1.62	1.59	1.62	1.6075
WoPhI,IV	1.7	1.71	1.85	1.7525
WoPhII,IV	1.78	1.7	1.92	1.7875
WoPhIII,IV	1.75	1.52	1.7	1.6425
WoPhIV,IV	1.39	1.29	1.35	1.32
Foot Length	45.16	45.32	44.87	45.7
Lotmt	78.12	85.64	84.06	82.3025
Lott	94.4	105.85	102.99	100.6775
LoFem	51.16	54.85	54.12	53.345
Wotmt@prox	9.87	10.48	10.78	10.4125
Wotmt@cond	8.69	8.99	9.34	8.935
Wott@prox	10.4	10.88	11.96	11.1525
Wott@mid	4.45	4.52	4.62	4.58
Wott@cond	8.18	8.8	9.34	8.8675
Wofem@cond	9.99	10.62	10.87	10.5125

Name	*Numenius america*	*Charadrius vocifer*	*Charadrius vo*	*Charadrius vo*	*Charadrius vo*
Specimen #	STDEV	14680	15505	11348	15666
M/F		F	M	M	F
LoDI	0.098488578	N/A	N/A	N/A	N/A
w/claw		N/A	N/A	N/A	N/A
LoDII	1.020032679	14.25	13.82	14.82	13.95
w/claw		N/A	N/A	19.09	17.96
LoDIII	1.063433903	20.29	20.17	20.44	18.87
w/claw		N/A	N/A	27	23.97
LoDIV	1.254060073	17.81	17.55	18.36	17.81
w/claw		N/A	N/A	21.48	20.38
W@Pjoint II	0.156284996	1.2	1.17	1.36	1.38
W@Pjoint III	0.532666249	1.48	1.58	1.83	1.69
W@Pjoint IV	0.107199192	1.38	1.27	1.57	1.75
W@2joint III	0.164595464	1.36	1.34	1.5	1.39
W@2joint IV	0.175760253	1.26	1.16	1.36	1.47
W@3joint IV	0.041932485	1.14	1.13	1.14	1.32
LoPhI,II	0.552449093	7.64	7.6	7.7	7.72
LoPhII,II	0.452327315	6.31	6.33	6.37	5.84
LoPhI,III	0.663249576	8.26	8.41	8.16	8.5
LoPhII,III	0.379692858	6.6	6.81	7.43	6.69
LoPhIII,III	0.467216937	5.48	5.49	5.62	4.9
LoPhI,IV	0.705454936	5.8	6.03	6.38	6.32
LoPhII,IV	0.319635209	4.56	4.49	5.18	4.93
LoPhIII,IV	0.322838969	4.11	3.83	4.34	4.13
LoPhIV,IV	0.308544972	3.51	3.75	3.92	3.65
WoPhI,II	0.023629078	0.74	0.74	0.86	1.08
WoPhII,II	0.070710678	0.65	0.62	0.69	0.85
WoPhI,III	0.06244998	1.12	0.95	1.19	1.14
WoPhII,III	0.022173558	0.92	0.88	0.97	1.03
WoPhIII,III	0.015	0.77	0.83	0.93	0.98
WoPhI,IV	0.068495742	0.77	0.74	0.93	0.88
WoPhII,IV	0.094295634	0.82	0.74	0.98	0.83
WoPhIII,IV	0.102753751	0.77	0.72	0.56	0.79
WoPhIV,IV	0.062182527	0.61	0.66	0.71	0.85
Foot Length	1.1814398	27.03	26.55	25.75	27.69
Lotmt	3.294119761	36.99	36.59	36.66	38.2
Lott	4.931783822	51.45	50.7	51.11	53.19
LoFem	1.59675713	27.6	26.83	26.76	28.51
Wotmt@prox	0.385346165	4.6	4.43	4.98	4.91
Wotmt@cond	0.301827765	3.76	3.83	3.8	4.25
Wott@prox	0.668300082	5.91	5.05	5.57	6.22
Wott@mid	0.121928941	1.92	1.94	2.22	2.1
Wott@cond	0.50999183	4.06	4.09	4.35	4.2
Wofem@cond	0.372234245	5.37	5.09	5.19	5.49

Name	*Charadrius vocif*	*Charadrius vocif*	*Calidris minutilla*	*Calidris minutilla*
Specimen #	AVERAGE	STDEV	24073	46521
M/F			F	M
LoDI			2.3	2.68
w/claw			N/A	N/A
LoDII	14.21	0.444747119	12.11	11.46
w/claw	18.525		15.47	N/A
LoDIII	19.9425	0.723481168	14.5	14.93
w/claw	25.485		18.37	N/A
LoDIV	17.8825	0.341113373	13.67	12.36
w/claw	20.93		N/A	N/A
W@Pjoint II	1.2775	0.107819293	0.81	0.78
W@Pjoint III	1.645	0.150222058	1.13	0.97
W@Pjoint IV	1.4925	0.211719154	0.98	0.85
W@2joint III	1.3975	0.071355915	0.83	0.72
W@2joint IV	1.3125	0.133010025	0.78	0.73
W@3joint IV	1.1825	0.091787799	0.62	0.63
LoPhI,II	7.665	0.055075705	7.45	6.64
LoPhII,II	6.2125	0.249582986	5.24	4.82
LoPhI,III	8.3325	0.151739909	6.2	6.01
LoPhII,III	6.8825	0.375	5.19	5.08
LoPhIII,III	5.3725	0.321390209	3.67	3.84
LoPhI,IV	6.1325	0.269242765	5.08	4.51
LoPhII,IV	4.79	0.323831232	3.71	3.46
LoPhIII,IV	4.1025	0.209344214	2.74	2.91
LoPhIV,IV	3.7075	0.172506039	2.51	2.63
WoPhI,II	0.855	0.160312195	0.55	0.56
WoPhII,II	0.7025	0.102428837	0.45	0.44
WoPhI,III	1.1	0.104243305	0.63	0.63
WoPhII,III	0.95	0.064807407	0.57	0.6
WoPhIII,III	0.8775	0.095	0.52	0.51
WoPhI,IV	0.83	0.089814624	0.55	0.61
WoPhII,IV	0.8425	0.100124922	0.58	0.54
WoPhIII,IV	0.71	0.104243305	0.58	0.52
WoPhIV,IV	0.7075	0.103400516	0.4	0.45
Foot Length	26.755	0.816884325	18.04	18.54
Lotmt	37.11	0.747306274	19.17	18.34
Lott	51.6125	1.095456526	32.01	29.3
LoFem	27.425	0.817333061	17.09	16.12
Wotmt@prox	4.73	0.259358182	2.62	2.59
Wotmt@cond	3.91	0.228473193	2.34	2.43
Wott@prox	5.6875	0.501090478	3.2	3.06
Wott@mid	2.045	0.141774469	1.12	1.05
Wott@cond	4.175	0.131275791	2.28	2.32
Wofem@cond	5.285	0.179164729	3.03	2.9

Name	*Calidris minutilla*	*Calidris minutilla*	*Calidris minutilla*	*Calidris minutilla*
Specimen #	11478	49893	AVERAGE	STDEV
M/F	F	M		
LoDI	2.35	2.69	2.505	0.208885934
w/claw	4.5	N/A		
LoDII	11.69	12.03	11.8225	0.302586076
w/claw	15.18	N/A	15.325	
LoDIII	14.8	14.31	14.635	0.281720902
w/claw	19.17	N/A	18.77	
LoDIV	13.1	13.07	13.05	0.536469943
w/claw	14.93	N/A		
W@Pjoint II	0.71	0.9	0.8	0.078740079
W@Pjoint III	1.03	0.85	0.995	0.117046999
W@Pjoint IV	0.85	N/A	0.893333333	0.075055535
W@2joint III	0.78	0.75	0.77	0.046904158
W@2joint IV	0.7	0.67	0.72	0.046904158
W@3joint IV	0.62	0.58	0.6125	0.022173558
LoPhI,II	7.05	6.53	6.9175	0.419632776
LoPhII,II	5.36	5.5	5.23	0.293257566
LoPhI,III	6.01	6.12	6.085	0.092556289
LoPhII,III	5.49	4.57	5.0825	0.383090503
LoPhIII,III	3.91	3.62	3.76	0.137355985
LoPhI,IV	4.73	4.57	4.7225	0.255783111
LoPhII,IV	3.7	3.48	3.5875	0.135984068
LoPhIII,IV	2.49	2.75	2.7225	0.173469498
LoPhIV,IV	2.25	2.27	2.415	0.185741756
WoPhI,II	0.55	0.51	0.5425	0.022173558
WoPhII,II	0.42	0.38	0.4225	0.030956959
WoPhI,III	0.79	0.55	0.65	0.100664459
WoPhII,III	0.6	0.52	0.5725	0.037749172
WoPhIII,III	0.46	0.49	0.495	0.026457513
WoPhI,IV	0.54	0.5	0.55	0.045460606
WoPhII,IV	0.52	0.48	0.53	0.04163332
WoPhIII,IV	0.46	0.42	0.495	0.07
WoPhIV,IV	0.37	0.39	0.4025	0.034034296
Foot Length	17.71	18.93	18.304	0.538547429
Lotmt	18.75	18.57	18.7075	0.351034186
Lott	30.75	30.57	30.6575	1.10879439
LoFem	16.12	16.42	16.4375	0.457411194
Wotmt@prox	2.77	2.48	2.615	0.119582607
Wotmt@cond	2.57	2.4	2.435	0.097467943
Wott@prox	3.07	2.73	3.015	0.200416234
Wott@mid	1	1.14	1.0775	0.06448514
Wott@cond	2.37	2.16	2.2825	0.089582364
Wofem@cond	2.71	2.85	2.8725	0.132256065

Name	*Arenaria interpres*	*Arenaria interpre*	*Arenaria interpres*	*Arenaria interpr*	*Arenaria interpre*
Specimen #	32303	30602	38932	30599	AVERAGE
M/F	F	M	M	F	
LoDI	3.32	N/A	4.49	3.83	3.88
w/claw	7.44	N/A	N/A	N/A	7.44
LoDII	14.78	15.48	15.47	14.08	14.9525
w/claw	17.52	N/A	N/A	N/A	17.52
LoDIII	17.9	19.61	20.92	19.8	19.5575
w/claw	26.84	N/A	N/A	N/A	26.84
LoDIV	16.23	16.93	17.92	16.41	16.8725
w/claw	21.25	N/A	N/A	N/A	21.25
W@Pjoint II	1.47	1.32	1.41	1.39	1.3975
W@Pjoint III	1.8	1.71	1.77	1.71	1.7475
W@Pjoint IV	1.59	1.52	1.53	1.46	1.525
W@2joint III	1.63	1.44	1.4	1.46	1.4825
W@2joint IV	1.63	1.28	1.32	1.29	1.38
W@3joint IV	1.54	1.2	1.15	1.19	1.27
LoPhI,II	8.05	8.9	8.68	8.08	8.4275
LoPhII,II	6.77	7.03	7.13	6.41	6.835
LoPhI,III	8.42	9.25	8.8	8.61	8.77
LoPhII,III	6.03	6.5	6.77	6.5	6.45
LoPhIII,III	4.34	5.32	5.69	5.36	5.1775
LoPhI,IV	6.11	6.5	6.34	6.39	6.335
LoPhII,IV	3.9	4.52	4.43	4.09	4.235
LoPhIII,IV	2.96	3.3	3.56	3.31	3.2825
LoPhIV,IV	3.6*	4.56	3.93	3.53	4.006666667
WoPhI,II	0.95	1.01	0.92	0.94	0.955
WoPhII,II	0.8	0.85	0.77	0.84	0.815
WoPhI,III	1.02	1.13	0.92	1.12	1.0475
WoPhII,III	1.02	1.1	0.91	1.02	1.0125
WoPhIII,III	0.96	0.98	0.81	0.92	0.9175
WoPhI,IV	0.9	0.95	0.85	0.94	0.91
WoPhII,IV	0.95	0.93	0.83	0.92	0.9075
WoPhIII,IV	1	0.85	0.78	0.82	0.8625
WoPhIV,IV	0.99	0.84	0.69	0.84	0.84
Foot Length	23.63	25.04	26	24.87	24.885
Lotmt	27.65	28.12	27.37	27.56	27.675
Lott	47.31	45.88	46.07	45.54	46.2
LoFem	29.53	28.36	28.25	28.99	28.7825
Wotmt@prox	5.14	5.03	4.41	5.03	4.9025
Wotmt@cond	4.65	4.48	4.47	4.44	4.51
Wott@prox	5.88	5.24	4.57	5.82	5.3775
Wott@mid	2	2.27	1.95	2.05	2.0675
Wott@cond	4.37	4.34	4.24	4.45	4.35
Wofem@cond	5.13	5.27	5.11	5.38	5.2225

Name	*Arenaria interpres*	*Meleagris gallopavo*	*Meleagris gall*	*Meleagris gall*	*Meleagris gall*
Specimen #	STDEV	85904	88095	88096	88097
M/F		M	M	M	M
LoDI	0.586600375	20.46	19.67	19.51	21.15
w/claw		N/A	N/A	N/A	N/A
LoDII	0.667601428	50.31	49.55	49.44	52.92
w/claw		N/A	N/A	N/A	N/A
LoDIII	1.247033146	74.07	72.09	71.7	77.72
w/claw		N/A	N/A	N/A	N/A
LoDIV	0.75878741	58.49	55.54	55.31	62.76
w/claw		N/A	N/A	N/A	N/A
W@Pjoint II	0.061846584	7.6	6.38	5.94	6.58
W@Pjoint III	0.045	9.22	8.98	4.51	9.57
W@Pjoint IV	0.053229065	6.93	7	7.13	7.44
W@2joint III	0.101447852	7.14	7.18	7.4	7.78
W@2joint IV	0.167531092	6.35	6.07	6.04	6.21
W@3joint IV	0.181291662	5.35	5.57	5.61	5.75
LoPhI,II	0.42828145	30.7	30	29.79	32.47
LoPhII,II	0.321403174	21.9	20.93	20.92	23.13
LoPhI,III	0.355621522	33.56	32.79	32.22	35.64
LoPhII,III	0.30757113	24.45	24.02	23.87	25.47
LoPhIII,III	0.582430253	19.7	18.37	18.84	20.51
LoPhI,IV	0.164215306	24.55	22.62	23.14	24.18
LoPhII,IV	0.29011492	14.21	13.76	13.76	15.34
LoPhIII,IV	0.246356787	11.83	10.99	11.59	13.4
LoPhIV,IV	0.519262297	13.78	12.87	12.8	14.9
WoPhI,II	0.038729833	4.58	4.95	4.06	4.97
WoPhII,II	0.036968455	4.3	4.69	3.87	4.77
WoPhI,III	0.098446263	6.44	6.55	6.08	6.63
WoPhII,III	0.07804913	5.27	5.69	4.98	5.59
WoPhIII,III	0.075883683	4.6	5.09	4.45	5.18
WoPhI,IV	0.045460606	4.64	5.2	4.6	5.08
WoPhII,IV	0.053150729	4.72	5.08	4.73	5.01
WoPhIII,IV	0.096046864	4.52	4.85	4.55	4.78
WoPhIV,IV	0.122474487	3.75	4.14	4.05	4.38
Foot Length	0.973396117	100.54	97.74	99.06	104.96
Lotmt	0.318799833	165.67	164.66	159	176.26
Lott	0.771794446	228.4	229.79	227.31	231.66
LoFem	0.595503988	142.28	145.16	139.57	149.02
Wotmt@prox	0.332402868	23.47	24.42	24.61	25.37
Wotmt@cond	0.09486833	23.59	24.12	22.19	23.59
Wott@prox	0.610812301	32.59	32.38	32.13	35.71
Wott@mid	0.14103782	13.41	16.02	12.58	15.96
Wott@cond	0.086794777	21.52	21.64	22.08	22.83
Wofem@cond	0.126852933	30.14	32.75	30.51	32.38

Name	*Meleagris gall*	*Meleagris gall*	*Colinus virginianus*	*Colinus virginianu*
Specimen #	AVERAGE	STDEV	19628	22997
M/F			F	M
LoDI	20.1975	0.758743479	6.38	7.13
w/claw			N/A	N/A
LoDII	50.555	1.623422311	17.41	17.81
w/claw			21.58	24.35
LoDIII	73.895	2.753016527	25.36	27.48
w/claw			N/A	N/A
LoDIV	58.025	3.472890247	18.84	19.98
w/claw			23.9	24.21
W@Pjoint II	6.625	0.702827622	1.61	1.64
W@Pjoint III	8.07	2.385665526	2.38	2.32
W@Pjoint IV	7.125	0.225757983	2.08	1.77
W@2joint III	7.375	0.293200728	1.9	1.86
W@2joint IV	6.1675	0.142448821	1.69	1.73
W@3joint IV	5.57	0.165730705	1.49	1.44
LoPhI,II	30.74	1.217182539	9.82	9.67
LoPhII,II	21.72	1.046358766	7.93	8.5
LoPhI,III	33.5525	1.496069851	10.14	11
LoPhII,III	24.4525	0.721497286	8.19	9.58
LoPhIII,III	19.355	0.946660798	7.6	8.07
LoPhI,IV	23.6225	0.896079424	6.37	7.45
LoPhII,IV	14.2675	0.745804934	4.92	4.72
LoPhIII,IV	11.9525	1.02763077	3.87	4.25
LoPhIV,IV	13.5875	0.982288993	5	5.27
WoPhI,II	4.64	0.426223728	1.1	1.18
WoPhII,II	4.4075	0.412987086	1.01	1.04
WoPhI,III	6.425	0.242830531	1.62	1.69
WoPhII,III	5.3825	0.322632402	1.34	1.34
WoPhIII,III	4.83	0.359351267	1.17	1.23
WoPhI,IV	4.88	0.304630924	1.25	1.26
WoPhII,IV	4.885	0.186993761	1.34	1.26
WoPhIII,IV	4.675	0.164620776	1.22	1.2
WoPhIV,IV	4.08	0.260384331	1.07	1
Foot Length	100.575	3.139102844	32.28	33.67
Lotmt	166.3975	7.200464684	31.4	32.62
Lott	229.29	1.877888886	54.33	56.73
LoFem	144.0075	4.046771347	41.09	42.73
Wotmt@prox	24.4675	0.781467636	5.7	5.41
Wotmt@cond	23.3725	0.826977428	5.38	5.63
Wott@prox	33.2025	1.68220837	7.72	7.53
Wott@mid	14.4925	1.762221609	3.09	3.42
Wott@cond	22.0175	0.592754868	5.27	5.18
Wofem@cond	31.445	1.310788567	6.8	6.99

Name	*Colinus virginianus*	*Colinus virginianu*	*Colinus virginianus*	*Colinus virginianus*
Specimen #	85971	12808	AVERAGE	STDEV
M/F	F	M		
LoDI	6.97	6.42	6.725	0.381269808
w/claw	N/A	N/A		
LoDII	18	17.43	17.6625	0.290674503
w/claw	N/A	N/A		
LoDIII	28.26	26.63	26.9325	1.241809835
w/claw	N/A	N/A		
LoDIV	22.04	20.97	20.4575	1.36763482
w/claw	N/A	N/A		
W@Pjoint II	1.81	1.91	1.7425	0.142214627
W@Pjoint III	2.44	2.55	2.4225	0.098107084
W@Pjoint IV	1.95	1.84	1.91	0.13540064
W@2joint III	1.93	1.96	1.9125	0.042720019
W@2joint IV	1.67	1.76	1.7125	0.040311289
W@3joint IV	1.38	1.41	1.43	0.046904158
LoPhI,II	10.1	9.72	9.8275	0.192072035
LoPhII,II	8.37	8.02	8.205	0.273313007
LoPhI,III	10.84	10.67	10.6625	0.373485832
LoPhII,III	9.56	9.09	9.105	0.650666325
LoPhIII,III	8.19	8.09	7.9875	0.263612721
LoPhI,IV	7.27	6.93	7.005	0.475078941
LoPhII,IV	5.05	4.99	4.92	0.143527001
LoPhIII,IV	4.66	4.44	4.305	0.334912924
LoPhIV,IV	5.34	5.25	5.215	0.148436294
WoPhI,II	1.27	1.23	1.195	0.073257537
WoPhII,II	1.11	1.12	1.07	0.053541261
WoPhI,III	1.64	1.61	1.64	0.035590261
WoPhII,III	1.46	1.41	1.3875	0.0585235
WoPhIII,III	1.21	1.16	1.1925	0.033040379
WoPhI,IV	1.3	1.25	1.265	0.023804761
WoPhII,IV	1.3	1.21	1.2775	0.055602758
WoPhIII,IV	1.16	1.16	1.185	0.03
WoPhIV,IV	0.97	0.89	0.9825	0.074554231
Foot Length	34.73	33.35	33.5075	1.008707919
Lotmt	32.84	33.2	32.515	0.780832889
Lott	54.89	56.19	55.535	1.114315934
LoFem	42.68	43.83	42.5825	1.127693073
Wotmt@prox	5.63	5.77	5.6275	0.155857841
Wotmt@cond	5.76	5.73	5.625	0.172530191
Wott@prox	7.41	7.54	7.55	0.12780193
Wott@mid	3.54	3.58	3.4075	0.222317341
Wott@cond	5.27	5.31	5.2575	0.055
Wofem@cond	7.04	7.19	7.005	0.160934769

Name	*Geococcyx californianus*	*Geococcyx ca*	*Geococcyx ca*	*Geococcyx ca*	*Geococcyx ca*	*Geococcyx ca*
Specimen #	91058	22621	20429	20422	AVERAGE	STDEV
M/F	M	M	?	?		
LoDI	13.66	13.25	11.96	12.02	12.7225	0.86256884
w/claw	20.8	N/A	N/A	N/A	20.8	
LoDII	22.53	22.48	20.93	20.52	21.615	1.04142531
w/claw	31.33	N/A	N/A	N/A	31.33	
LoDIII	32.94	33.67	31.39	30.75	32.1875	1.34987345
w/claw	42.22	N/A	N/A	N/A	42.22	
LoDIV	25.79	24.51	22.44	22.53	23.8175	1.62536919
w/claw	32.57	N/A	N/A	N/A	32.57	
W@Pjoint II	2.9	2.7	2.43	2.62	2.6625	0.19465782
W@Pjoint III	3.7	3.55	3.14	3.36	3.4375	0.24226363
W@Pjoint IV	3.07	2.3	2.18	2.25	2.45	0.41625313
W@2joint III	3.2	2.91	2.63	2.76	2.875	0.24501701
W@2joint IV	2.23	1.77	1.77	1.74	1.8775	0.23542515
W@3joint IV	1.89	1.66	1.45	1.62	1.655	0.18119971
LoPhI,II	13.38	13.15	12.84	11.92	12.8225	0.64106032
LoPhII,II	9.82	10.24	9.13	9.43	9.655	0.48155997
LoPhI,III	13.92	13.91	13.37	12.4	13.4	0.7144695
LoPhII,III	11.8	12.05	10.48	10.57	11.225	0.81553663
LoPhIII,III	10.52	9.95	9.23	9.06	9.69	0.67453688
LoPhI,IV	10.02	9.23	8.39	8.36	9	0.79056942
LoPhII,IV	7.2	6.62	6.4	5.71	6.4825	0.6157042
LoPhIII,IV	5.02	5.06	4.85	4.68	4.9025	0.17404501
LoPhIV,IV	4.48	5.03	4.42	4.45	4.595	0.29103264
WoPhI,II	1.96	2.05	1.86	1.87	1.935	0.08888194
WoPhII,II	1.65	1.75	1.5	1.51	1.6025	0.11982626
WoPhI,III	2.54	2.76	2.41	2.46	2.5425	0.15456929
WoPhII,III	2.27	2.3	2.07	2.21	2.2125	0.10210289
WoPhIII,III	2	2.04	1.84	1.91	1.9475	0.08995369
WoPhI,IV	1.83	1.82	1.64	1.66	1.7375	0.10144785
WoPhII,IV	1.7	1.62	1.45	1.54	1.5775	0.10719919
WoPhIII,IV	1.48	1.42	1.31	1.41	1.405	0.07047458
WoPhIV,IV	1.26	1.26	1.15	1.18	1.2125	0.05619905
Foot Length	41.14	40.08	37.43	36.55	38.8	2.16436288
Lotmt	69.17	67.79	65.83	61.21	66	3.47495803
Lott	91.82	90.57	87.7	N/A	90.03	2.11241568
LoFem	59.51	58.24	52.28	52.86	55.7225	3.68454769
Wotmt@prox	8.67	8.6	8.24	8.12	8.4075	0.26874709
Wotmt@cond	9.11	8.9	7.46	8.34	8.4525	0.73717366
Wott@prox	11.63	11.9	10.78	N/A	11.4366667	0.58449408
Wott@mid	4.47	4.73	3.94	N/A	4.38	0.40261644
Wott@cond	7.72	7.69	7.15	7.4	7.49	0.26870058
Wofem@cond	10.94	10.87	9.63	9.95	10.3475	0.65748891

Name	*Colaptes auratus*	*Colaptes auratus*	*Dryocopus pileatus*	*Dryocopus pileatus*
Specimen #	AVERAGE	STDEV	19705	23158
M/F			F	F
LoDI	7.96	0.234236348	9.95	10.36
w/claw	13.35		15.54	N/A
LoDII	15.475	0.555127613	15.58	17.04
w/claw	21.045		24.71	N/A
LoDIII	21.5375	0.493448748	23.83	25.24
w/claw	28.375		29.52	N/A
LoDIV	17.8025	0.29635283	19.4	20.43
w/claw	21.86		27.98	N/A
W@Pjoint II	1.5825	0.207585324	2.09	1.99
W@Pjoint III	2.1675	0.143845982	2.59	2.81
W@Pjoint IV	1.8875	0.102753751	2.41	2.4
W@2joint III	1.695	0.19807406	2.18	2.15
W@2joint IV	1.7025	0.166808273	2.4	2.38
W@3joint IV	1.4475	0.042720019	1.99	1.8
LoPhI,II	7.5175	0.483209754	7.13	7.24
LoPhII,II	8.525	0.293655127	10.3	10.86
LoPhI,III	6.6925	0.07804913	6.77	7.4
LoPhII,III	8.0625	0.228673712	8.9	8.97
LoPhIII,III	8.41	0.079582243	10.58	10.96
LoPhI,IV	6.0375	0.094295634	6.12	6.77
LoPhII,IV	4.835	0.214864298	5.61	5.59
LoPhIII,IV	4.2675	0.280995255	4.91	5.01
LoPhIV,IV	4.9875	0.292161485	5.71	5.99
WoPhI,II	1.0175	0.060207973	1.61	1.61
WoPhII,II	0.9075	0.078475049	1.18	1.27
WoPhI,III	1.5825	0.255	1.95	2.04
WoPhII,III	1.2175	0.073654599	1.61	1.76
WoPhIII,III	1.06	0.051639778	1.27	1.45
WoPhI,IV	1.29	0.104562581	1.47	1.64
WoPhII,IV	1.4075	0.127638813	1.72	1.9
WoPhIII,IV	1.24	0.159791531	1.63	1.62
WoPhIV,IV	1.055	0.116761866	1.34	1.44
Foot Length	24.445	0.435545635	28.79	30.94
Lotmt	30.285	1.244521327	34.49	35.39
Lott	42.9225	1.339337523	48.58	49.9
LoFem	31.1425	0.892650548	38.57	39.5
Wotmt@prox	5.5325	0.456973741	6.95	7.79
Wotmt@cond	5.2475	0.133010025	6.78	6.84
Wott@prox	5.955	0.627614531	7.52	9.02
Wott@mid	2.8775	0.495471156	4.54	5.04
Wott@cond	4.85	0.260128174	6.26	6.76
Wofem@cond	6.2975	0.285	8.39	9

Name	*Dryocopus pileatus*	*Dryocopus pileatus*	*Dryocopus pileatus*	*Dryocopus pileatus*
Specimen #	11212	96265	AVERAGE	STDEV
M/F	M	M		
LoDI	10.18	11.47	10.49	0.674536878
w/claw	N/A	20.02	17.78	
LoDII	18.34	19.39	17.5875	1.647733292
w/claw	N/A	31.89	28.3	
LoDIII	26.31	27.78	25.79	1.670788237
w/claw	N/A	41.01	35.265	
LoDIV	22.15	22.92	21.225	1.601176651
w/claw	N/A	36.51	32.245	
W@Pjoint II	1.64	2.45	2.0425	0.333204142
W@Pjoint III	2.71	3.07	2.795	0.204205779
W@Pjoint IV	2.48	2.72	2.5025	0.149303941
W@2joint III	2.1	2.42	2.2125	0.142214627
W@2joint IV	2.27	2.54	2.3975	0.110867789
W@3joint IV	2.09	2.08	1.99	0.134412301
LoPhI,II	7.79	8.55	7.6775	0.649377907
LoPhII,II	11.42	12.04	11.155	0.746435976
LoPhI,III	7.44	7.43	7.26	0.327108545
LoPhII,III	9.33	9.82	9.255	0.421149221
LoPhIII,III	11.99	13.11	11.66	1.135458791
LoPhI,IV	6.77	7.31	6.7425	0.486852134
LoPhII,IV	5.22	6	5.605	0.318590646
LoPhIII,IV	5.41	6.09	5.355	0.535505991
LoPhIV,IV	6.99	7.62	6.5775	0.885941119
WoPhI,II	1.73	1.65	1.65	0.056568542
WoPhII,II	1.28	1.35	1.27	0.069761498
WoPhI,III	2.17	2.04	2.05	0.090553851
WoPhII,III	1.72	1.77	1.715	0.073257537
WoPhIII,III	1.37	1.39	1.37	0.074833148
WoPhI,IV	1.54	1.66	1.5775	0.088835053
WoPhII,IV	1.96	2.02	1.9	0.129614814
WoPhIII,IV	1.56	1.66	1.6175	0.041932485
WoPhIV,IV	1.34	1.47	1.3975	0.06751543
Foot Length	31.4	32.62	30.9375	1.5975476
Lotmt	36.21	36.99	35.77	1.074678246
Lott	50.96	49.93	49.8425	0.975307644
LoFem	40.28	4.59	30.735	17.44401043
Wotmt@prox	7.57	7.36	7.4175	0.357712641
Wotmt@cond	7.13	7.18	6.9825	0.201721756
Wott@prox	7.05	N/A	7.863333333	1.028899088
Wott@mid	3.42	4.49	4.3725	0.681829646
Wott@cond	6.53	6.91	6.615	0.28360771
Wofem@cond	8.79	8.91	8.7725	0.269118933

Specimen #	13265	79890	17276	13267	AVERAGE
M/F	F	M	F	M	
LoDI	11.48	11.98	17.71	11.01	13.045
w/claw	20.92	N/A	N/A	N/A	20.92
LoDII	12.82	13.68	13.08	12.3	12.97
w/claw	18.33	N/A	N/A	N/A	18.33
LoDIII	19.11	20.2	19.08	20.19	19.645
w/claw	23.01	N/A	N/A	N/A	23.01
LoDIV	13.41	15.51	15.36	16.02	15.075
w/claw	21.16	N/A	N/A	N/A	21.16
W@Pjoint II	1.93	1.51	1.45	1.65	1.635
W@Pjoint III	1.88	1.64	1.68	1.98	1.795
W@Pjoint IV	1.87	1.24	1.21	1.57	1.4725
W@2joint III	1.75	1.48	1.48	1.92	1.6575
W@2joint IV	1.74	1.15	1.2	1.46	1.3875
W@3joint IV	1.21	1.13	1.11	1.3	1.1875
LoPhI,II	6.77	7.11	6.53	6.51	6.73
LoPhII,II	7.33	7.06	6.96	6.83	7.045
LoPhI,III	6.09	6.61	6.37	6.86	6.4825
LoPhII,III	6.62	6.88	6.31	6.51	6.58
LoPhIII,III	7.6	7.75	7.51	7.17	7.5075
LoPhI,IV	3.75	4.02	4.21	4.53	4.1275
LoPhII,IV	2.75	3.72	3.77	3.93	3.5425
LoPhIII,IV	3.22	4.07	3.86	3.7	3.7125
LoPhIV,IV	3.94	4.76	4.78	5.37	4.7125
WoPhI,II	1.14	1.11	1.08	1.25	1.145
WoPhII,II	0.95	0.92	0.95	1.11	0.9825
WoPhI,III	1.15	1.25	1.22	1.28	1.225
WoPhII,III	1.4	1.18	1.15	1.2	1.2325
WoPhIII,III	1.17	1.02	0.95	1.04	1.045
WoPhI,IV	1.13	0.97	1.01	1.2	1.0775
WoPhII,IV	1.16	0.95	0.94	1.01	1.015
WoPhIII,IV	0.91	0.86	0.91	0.97	0.9125
WoPhIV,IV	1.06	0.85	0.88	0.89	0.92
Foot Length	21.88	23.71	23.45	22.4	22.86
Lotmt	33.25	34.05	35.57	35.74	34.6525
Lott	45.89	47.81	50.42	51.03	48.7875
LoFem	30.15	29.56	31.12	31.25	30.52
Wotmt@prox	4.87	5.03	4.73	5.15	4.945
Wotmt@cond	3.38	3.43	3.5	3.78	3.5225
Wott@prox	6.13	5.32	6.65	N/A	6.033333333
Wott@mid	2.33	2.07	2.29	2.2	2.2225
Wott@cond	4.57	4.74	4.58	4.73	4.655
Wofem@cond	5.7	5.82	5.52	5.8	5.71

Name	*Cyanocitta chris*	*Corvus brachyrhynchos*	*Corvus brach*	*Corvus brach*	*Corvus brach*
Specimen #	STDEV	15149	14664	22261	13248
M/F		F	F	M	M
LoDI	3.135118286	20.84	21.78	21.58	21.59
w/claw		33.46	N/A	N/A	32.05
LoDII	0.573759532	22.29	24.02	23.66	23.19
w/claw		31.08	N/A	N/A	33.04
LoDIII	0.635216499	32.86	37.01	34.61	34.71
w/claw		44.07	N/A	N/A	44.4
LoDIV	1.145382032	24.46	27.61	25.69	26.05
w/claw		32.01	N/A	N/A	34.63
W@Pjoint II	0.213775583	3.23	3.16	2.85	3.47
W@Pjoint III	0.161967075	3.67	3.32	3.32	4.4
W@Pjoint IV	0.311167158	2.82	2.77	2.7	3.1
W@2joint III	0.21639085	3.21	2.94	2.85	3.57
W@2joint IV	0.271462091	2.7	2.54	2.6	2.81
W@3joint IV	0.086554414	2.51	2.17	2.32	2.83
LoPhI,II	0.279523404	12.31	12.09	12.22	12.74
LoPhII,II	0.212053452	12.19	12.96	12.36	11.92
LoPhI,III	0.329380732	11.18	13.27	11.44	12.59
LoPhII,III	0.237627159	9.91	12.27	10.96	11.79
LoPhIII,III	0.245814971	11.87	13.93	13.41	13.64
LoPhI,IV	0.328062494	7.4	7.61	7.66	6.92
LoPhII,IV	0.535871564	6.05	6.51	6.59	6.59
LoPhIII,IV	0.361605218	6.45	6.87	7	6.03
LoPhIV,IV	0.587615237	7.42	8.42	7.35	7.37
WoPhI,II	0.074161985	2.36	2.45	2.39	2.85
WoPhII,II	0.08616844	2.14	2.15	2.18	2.45
WoPhI,III	0.055677644	2.34	2.43	2.37	2.48
WoPhII,III	0.113541476	2.18	2.2	2.22	2.59
WoPhIII,III	0.091833182	2.17	1.92	2.11	2.7
WoPhI,IV	0.106262254	2.33	2.32	2.1	2.32
WoPhII,IV	0.101488916	2.24	1.94	1.96	2.29
WoPhIII,IV	0.045	1.95	1.88	1.79	2.44
WoPhIV,IV	0.09486833	2.1	1.86	1.9	2.55
Foot Length	0.8646001	40.27	42.07	41.85	40.34
Lotmt	1.20477868	59.27	60.41	58.8	61.05
Lott	2.383615951	86.88	86.72	85.8	88.97
LoFem	0.806515137	54.15	53.32	53.03	53.39
Wotmt@prox	0.183575598	9.94	9.7	9.93	9.9
Wotmt@cond	0.178582381	6.65	7.06	6.93	7.23
Wott@prox	0.67024871	11.43	11.29	11.34	11.8
Wott@mid	0.115289491	4.97	4.74	4.76	4.79
Wott@cond	0.092556289	8.9	8.9	8.6	9.16
Wofem@cond	0.137113092	11.08	10.7	10.72	10.99

Name	*Corvus brachy*	*Corvus brachy*	*Cardinalis cardinalis*	*Cardinalis ca*	*Cardinalis carc*
Specimen #	AVERAGE	STDEV	56009	56008	19590
M/F			M	M	F
LoDI	21.4475	0.415321161	8.79	8.37	8.55
w/claw	32.755		N/A	N/A	12.32
LoDII	23.29	0.748286932	9.44	9.85	9.82
w/claw	32.06		N/A	12.41	12.38
LoDIII	34.7975	1.702143257	13.08	16.69	15.69
w/claw	44.235		N/A	21.23	19.82
LoDIV	25.9525	1.297853998	12	12.01	11.21
w/claw	33.32		N/A	14.11	14.62
W@Pjoint II	3.1775	0.255522341	1	0.93	0.93
W@Pjoint III	3.6775	0.509141434	1.28	1.19	1.29
W@Pjoint IV	2.8475	0.175380539	1.06	0.92	0.94
W@2joint III	3.1425	0.32345788	1.26	1.15	1.15
W@2joint IV	2.6625	0.118427193	0.95	0.87	0.96
W@3joint IV	2.4575	0.284648907	0.82	0.73	0.77
LoPhI,II	12.34	0.281543366	4.72	4.94	5.07
LoPhII,II	12.3575	0.440634013	5.47	5.47	5.3
LoPhI,III	12.12	0.981393567	5.12	5.49	5.29
LoPhII,III	11.2325	1.034484574	5.03	5.09	4.92
LoPhIII,III	13.2125	0.919941121	5.94	6.01	6.14
LoPhI,IV	7.3975	0.33767588	3.26	3.24	3.5
LoPhII,IV	6.435	0.259422435	2.89	2.76	2.56
LoPhIII,IV	6.5875	0.439573657	2.81	2.73	2.59
LoPhIV,IV	7.64	0.520832667	3.36	3.18	3.22
WoPhI,II	2.5125	0.228089895	0.71	0.72	0.66
WoPhII,II	2.23	0.147648231	0.84	0.57	0.6
WoPhI,III	2.405	0.06244998	0.92	0.85	0.79
WoPhII,III	2.2975	0.195682566	0.87	0.84	0.82
WoPhIII,III	2.225	0.334115748	0.88	0.73	0.65
WoPhI,IV	2.2675	0.111766125	0.72	0.61	0.79
WoPhII,IV	2.1075	0.183189337	0.61	0.62	0.63
WoPhIII,IV	2.015	0.290803485	0.68	0.63	0.71
WoPhIV,IV	2.1025	0.316267292	0.64	0.66	0.59
Foot Length	41.1325	0.960151898	16.41	18	17.14
Lotmt	59.8825	1.030901709	25.65	24.52	24.84
Lott	87.0925	1.33908862	36.27	34.51	35.85
LoFem	53.4725	0.477798772	22.09	21.54	21.92
Wotmt@prox	9.8675	0.112952792	3.6	3.72	3.66
Wotmt@cond	6.9675	0.24472774	2.52	2.59	2.51
Wott@prox	11.465	0.2307235	4.34	4.85	4.33
Wott@mid	4.815	0.105356538	1.52	1.81	1.43
Wott@cond	8.89	0.228910463	3.01	3.25	3.28
Wofem@cond	10.8725	0.191376592	3.96	3.97	3.82

Name	*Cardinalis card*	*Cardinalis card*	*Cardinalis card*	*Passer domesticus*	*Passer domesticus*
Specimen #	16848	AVERAGE	STDEV	17843	49779
M/F	F			M	M
LoDI	9.36	8.7675	0.430842198	7.2	7.65
w/claw	N/A	12.32		13.11	11.33
LoDII	9.85	9.74	0.200499377	8.03	8.32
w/claw	N/A	12.395		11.92	11.25
LoDIII	16.66	15.53	1.698096974	13.42	13.63
w/claw	N/A	20.525		16.3	14.82
LoDIV	11.73	11.7375	0.37482218	8.58	9.26
w/claw	N/A	14.365		12.95	12.52
W@Pjoint II	0.93	0.9475	0.035	1.06	0.83
W@Pjoint III	1.35	1.2775	0.066017674	1.32	1.15
W@Pjoint IV	0.84	0.94	0.090921211	1.13	0.84
W@2joint III	1.15	1.1775	0.055	1.24	0.97
W@2joint IV	0.86	0.91	0.05228129	0.85	0.87
W@3joint IV	0.65	0.7425	0.071821538	1.05	0.76
LoPhI,II	4.87	4.9	0.145830952	2.9	4.47
LoPhII,II	5.09	5.3325	0.180439279	4.58	4.87
LoPhI,III	5.39	5.3225	0.157770931	4.12	4.97
LoPhII,III	5.1	5.035	0.082663978	4.62	4.79
LoPhIII,III	6.17	6.065	0.108474267	4.83	5.54
LoPhI,IV	3.22	3.305	0.131021627	2.16	2.63
LoPhII,IV	2.75	2.74	0.135892114	2.78	2.33
LoPhIII,IV	2.65	2.695	0.095742711	2.7	2.58
LoPhIV,IV	3.11	3.2175	0.105316982	2.36	2.48
WoPhI,II	0.73	0.705	0.031091264	0.79	0.62
WoPhII,II	0.61	0.655	0.124498996	0.77	0.57
WoPhI,III	0.82	0.845	0.055677644	1.19	0.9
WoPhII,III	0.81	0.835	0.026457513	0.89	0.74
WoPhIII,III	0.74	0.75	0.095568475	0.85	0.61
WoPhI,IV	0.69	0.7025	0.074554231	N/A	0.7
WoPhII,IV	0.67	0.6325	0.026299556	0.65	0.66
WoPhIII,IV	0.68	0.675	0.033166248	0.76	0.64
WoPhIV,IV	0.62	0.6275	0.029860788	0.8	0.59
Foot Length	N/A	17.18333333	0.795885251	12.64	14.31
Lotmt	24.5	24.8775	0.538044298	19.35	19.05
Lott	35.88	35.6275	0.769171632	28.82	27.63
LoFem	21.82	21.8425	0.23041629	18.19	17.68
Wotmt@prox	3.54	3.63	0.077459667	2.9	2.8
Wotmt@cond	2.42	2.51	0.069761498	2.31	2.19
Wott@prox	4.5	4.505	0.242830531	3.22	4.11
Wott@mid	1.46	1.555	0.174068952	1.6	1.24
Wott@cond	3.11	3.1625	0.125797456	2.47	2.54
Wofem@cond	3.81	3.89	0.086794777	3.16	3.27

Name	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*
Specimen #	49763	48762	AVERAGE	STDEV
M/F	M	F		
LoDI	7.78	7.29	7.48	0.278926514
w/claw	12.69	N/A	12.37666667	
LoDII	7.97	9.13	8.3625	0.534002185
w/claw	N/A	N/A	11.585	
LoDIII	14.55	15.08	14.17	0.780299088
w/claw	N/A	N/A	15.56	
LoDIV	N/A	9.69	9.176666667	0.559672523
w/claw	N/A	N/A	12.735	
W@Pjoint II	0.84	0.86	0.8975	0.109048919
W@Pjoint III	1.05	1.14	1.165	0.112694277
W@Pjoint IV	0.84	0.85	0.915	0.143410832
W@2joint III	0.82	0.96	0.9975	0.175570499
W@2joint IV	0.73	0.76	0.8025	0.068007353
W@3joint IV	0.67	0.69	0.7925	0.175949803
LoPhI,II	4.53	4.33	4.0575	0.776203367
LoPhII,II	4.89	4.8	4.785	0.142009389
LoPhI,III	4.88	4.83	4.7	0.39098167
LoPhII,III	4.83	5	4.81	0.155991453
LoPhIII,III	5.41	5.25	5.2575	0.308693483
LoPhI,IV	2.93	2.4	2.53	0.328532089
LoPhII,IV	2.5	2.27	2.47	0.228473193
LoPhIII,IV	2.76	2.38	2.605	0.167630546
LoPhIV,IV	2.82	2.64	2.575	0.199582898
WoPhI,II	0.59	0.63	0.6575	0.089953692
WoPhII,II	0.54	0.53	0.6025	0.112952792
WoPhI,III	0.68	0.77	0.885	0.222485955
WoPhII,III	0.66	0.67	0.74	0.106144556
WoPhIII,III	0.59	0.6	0.6625	0.125266383
WoPhI,IV	0.58	0.67	0.65	0.06244998
WoPhII,IV	0.54	0.6	0.6125	0.055
WoPhIII,IV	0.54	0.59	0.6325	0.094295634
WoPhIV,IV	0.35	0.5	0.56	0.188148877
Foot Length	N/A	N/A	13.475	1.180868325
Lotmt	19.32	18.51	19.0575	0.389133653
Lott	28.74	27.31	28.125	0.768223058
LoFem	18.56	18.07	18.125	0.362629287
Wotmt@prox	2.75	2.85	2.825	0.064549722
Wotmt@cond	2.15	2.13	2.195	0.080622577
Wott@prox	3.8	3.62	3.6875	0.371606871
Wott@mid	1.2	1.21	1.3125	0.192418814
Wott@cond	2.61	2.74	2.59	0.115181017
Wofem@cond	3.23	3.31	3.2425	0.063966137

Name	*Turdus migratorius*	*Turdus migrator*	*Turdus migrato*	*Turdus migrat*	*Turdus migratoriu*
Specimen #	19866	22416	22417	16501	AVERAGE
M/F	M	F	F	M	
LoDI	9.58	9.09	10.39	9.96	9.755
w/claw	15	14.61	15.95	18.48	16.01
LoDII	11.58	12.21	13.27	12.13	12.2975
w/claw	15.28	16.46	N/A	17.36	16.36666667
LoDIII	19.52	20.23	20.76	19.15	19.915
w/claw	23.58	24.49	25.81	25.91	24.9475
LoDIV	12.76	13.24	14.29	13.56	13.4625
w/claw	16.09	16.01	17.08	18.49	16.9175
W@Pjoint II	1.18	1.35	1.52	0.98	1.2575
W@Pjoint III	1.7	1.69	1.66	1.55	1.65
W@Pjoint IV	1.51	1.27	1.53	1.23	1.385
W@2joint III	1.67	1.55	1.6	1.38	1.55
W@2joint IV	1.37	1.23	1.5	1.19	1.3225
W@3joint IV	1.15	1.06	1.22	1.14	1.1425
LoPhI,II	5.61	6.39	6.42	6.4	6.205
LoPhII,II	6.28	6.26	6.35	5.91	6.2
LoPhI,III	6.18	6.95	7.14	6.6	6.7175
LoPhII,III	7.49	6.72	7.34	6.84	7.0975
LoPhIII,III	7.5	7.17	7.53	7.26	7.365
LoPhI,IV	2.92	3.62	4.23	3.83	3.65
LoPhII,IV	3.45	3.82	4.74	3.56	3.8925
LoPhIII,IV	2.65	3.48	3.65	3.85	3.4075
LoPhIV,IV	2.64	3.71	3.75	3.84	3.485
WoPhI,II	1.24	0.95	1.12	0.71	1.005
WoPhII,II	0.69	0.75	0.82	0.6	0.715
WoPhI,III	1.16	1.07	1.26	0.98	1.1175
WoPhII,III	1.1	0.9	1.18	0.9	1.02
WoPhIII,III	0.92	0.85	1.01	0.71	0.8725
WoPhI,IV	1.31	1	1.14	0.94	1.0975
WoPhII,IV	1.15	0.85	0.94	0.88	0.955
WoPhIII,IV	0.92	0.8	1.16	0.71	0.8975
WoPhIV,IV	0.86	0.71	0.88	0.85	0.825
Foot Length	22.96	23.13	21.78	21.43	22.325
Lotmt	32.96	32.83	34.12	33.39	33.325
Lott	45.1	45.33	46.13	45.37	45.4825
LoFem	26.3	27.17	27.36	27.49	27.08
Wotmt@prox	4.31	4.26	4.36	3.96	4.2225
Wotmt@cond	3.44	3.6	4.68	3.46	3.795
Wott@prox	5.32	5.37	5.48	5.4	5.3925
Wott@mid	1.71	2.01	2.06	1.85	1.9075
Wott@cond	4.15	3.88	4.11	3.69	3.9575
Wofem@cond	4.73	4.65	4.77	4.62	4.6925

Name	*Turdus migratoriu*	*Zenaida macroura*	*Zenaida macro*	*Zenaida macro*	*Zenaida macro*
Specimen #	STDEV	22716	11653	15533	22394
M/F		M	F	F	M
LoDI	0.553202796	9.56	8.16	9.37	9.65
w/claw		15.14	N/A	N/A	N/A
LoDII	0.706228245	13.91	12.33	12.92	13.17
w/claw		19.47	N/A	N/A	N/A
LoDIII	0.719837945	19.58	16.63	18.51	18.52
w/claw		N/A	N/A	N/A	N/A
LoDIV	0.642203239	13.4	12.66	14.32	13.09
w/claw		18.07	N/A	N/A	N/A
W@Pjoint II	0.231282655	1.44	1.51	1.26	1.52
W@Pjoint III	0.068799225	1.57	1.55	1.36	1.58
W@Pjoint IV	0.156950098	1.38	1.41	1.27	1.36
W@2joint III	0.123558353	1.31	1.39	1.17	1.33
W@2joint IV	0.141273966	1.17	1.21	1.14	1.19
W@3joint IV	0.065510813	1.13	1.4	1.03	1.1
LoPhI,II	0.396862697	8	7.21	7.83	8
LoPhII,II	0.197146308	6.83	5.43	5.62	5.84
LoPhI,III	0.422403835	7.54	6.89	7.86	7.46
LoPhII,III	0.374911101	6.56	5.84	6.01	6.45
LoPhIII,III	0.177482393	6.17	5.47	5.54	6.14
LoPhI,IV	0.548513142	5.54	4.2	4.91	4.81
LoPhII,IV	0.585910972	3.33	3.18	3.51	3.41
LoPhIII,IV	0.52715431	2.86	3.13	3.02	3.07
LoPhIV,IV	0.565950528	4.34	3.47	3.61	3.97
WoPhI,II	0.229855027	1.06	0.95	0.94	1.1
WoPhII,II	0.093273791	0.84	0.77	0.77	0.81
WoPhI,III	0.120104121	1.18	1.03	1.09	1.01
WoPhII,III	0.142361043	1.08	0.99	0.99	1.03
WoPhIII,III	0.126589889	0.83	0.91	0.77	0.79
WoPhI,IV	0.164595464	0.97	1.04	0.93	1
WoPhII,IV	0.135277493	1.02	1.06	0.96	1.03
WoPhIII,IV	0.195	0.98	0.94	0.91	0.97
WoPhIV,IV	0.077674535	0.77	0.73	0.78	0.73
Foot Length	0.84642385	23.68	21.64	22.5	21.91
Lotmt	0.581520994	20.64	19.26	20.99	21.25
Lott	0.447762958	37.25	35.14	37.04	37.91
LoFem	0.53634566	28.53	26.83	27.89	28.91
Wotmt@prox	0.179698822	4.71	4.47	4.69	4.69
Wotmt@cond	0.594278274	4.51	4.3	4.55	4.51
Wott@prox	0.067019898	4.67	4.69	5.04	5.27
Wott@mid	0.159243001	2.62	2.37	2.46	2.35
Wott@cond	0.214378948	4.18	4.1	4.21	4.36
Wofem@cond	0.06946222	4.88	4.36	4.56	4.64

Name	*Zenaida macroura*	*Zenaida macroura*	*Columba livia*	*Columba livia*	*Columba livia*
Specimen #	AVERAGE	STDEV	84415	84400	84401
M/F			M	F	F
LoDI	9.185	0.600354062	13.35	12.21	11.19
w/claw	15.14		N/A	17.71	15.89
LoDII	13.0825	0.654490896	21.89	18.46	17.89
w/claw	19.47		29.69	25.04	25.72
LoDIII	18.31	1.227382038	31.15	26.16	25.03
w/claw			39.36	33.16	32.95
LoDIV	13.3675	0.703769612	23.29	19.37	18.21
w/claw	18.07		30.15	25.46	25.25
W@Pjoint II	1.4325	0.120381339	2.77	2.48	2.25
W@Pjoint III	1.515	0.1040833	3.23	2.72	2.55
W@Pjoint IV	1.355	0.060277138	2.76	2.19	2.14
W@2joint III	1.3	0.093094934	2.77	2.47	2.28
W@2joint IV	1.1775	0.029860788	2.54	2.02	1.99
W@3joint IV	1.165	0.162172747	2.34	1.97	1.84
LoPhI,II	7.76	0.375322084	12.55	10.9	10.28
LoPhII,II	5.93	0.622949971	10.34	8.04	8.45
LoPhI,III	7.4375	0.403846093	12.86	11.35	10.63
LoPhII,III	6.215	0.344915449	11.16	9.51	9.18
LoPhIII,III	5.83	0.376563408	10.08	8.9	8.28
LoPhI,IV	4.865	0.54860429	8.29	7.06	6.58
LoPhII,IV	3.3575	0.139373599	6.02	4.86	4.27
LoPhIII,IV	3.02	0.115758369	5.23	3.58	4.03
LoPhIV,IV	3.8475	0.390074779	7.07	5.89	5.66
WoPhI,II	1.0125	0.079739158	1.86	1.55	1.56
WoPhII,II	0.7975	0.034034296	1.52	1.21	1.29
WoPhI,III	1.0775	0.076321688	2.09	1.71	1.67
WoPhII,III	1.0225	0.042720019	2.07	1.53	1.64
WoPhIII,III	0.825	0.061913919	1.77	1.27	1.45
WoPhI,IV	0.985	0.046547467	2	1.5	1.65
WoPhII,IV	1.0175	0.041932485	1.95	1.57	1.82
WoPhIII,IV	0.95	0.031622777	1.97	1.55	1.71
WoPhIV,IV	0.7525	0.026299556	1.72	1.24	1.35
Foot Length	22.4325	0.905883547	39.75	34.38	29.09
Lotmt	20.535	0.885983446	36.2	32.62	30.58
Lott	36.835	1.189243457	65.54	59.3	54.72
LoFem	28.04	0.909871786	48.16	43.25	40.46
Wotmt@prox	4.64	0.113724814	8.37	7.7	6.97
Wotmt@cond	4.4675	0.113247517	8.3	7.02	6.55
Wott@prox	4.9175	0.289985632	9.5	8.57	8.12
Wott@mid	2.45	0.123017614	3.95	3.95	3.57
Wott@cond	4.2125	0.108742816	7.85	7.11	6.51
Wofem@cond	4.61	0.215096877	9.18	7.79	8.11

Name	*Columba livia*	*Columba livia*	*Columba livia*	*Gavia pacifica*	*Gavia pacifica*
Specimen #	84410	AVERAGE	STDEV	80175	30572
M/F	M			?	F
LoDI	11.34	12.0225	0.992685751	N/A	11.75
w/claw	16.38	16.66		N/A	N/A
LoDII	19.12	19.34	1.772737995	N/A	65.46
w/claw	26.03	26.62		N/A	N/A
LoDIII	27.4	27.435	2.659078788	78.33	76.6
w/claw	33.03	34.625		N/A	N/A
LoDIV	20.71	20.395	2.183659009	82.05	84
w/claw	26.53	26.8475		N/A	N/A
W@Pjoint II	2.58	2.52	0.216487105	N/A	3.51
W@Pjoint III	2.73	2.8075	0.293527398	3.88	4.3
W@Pjoint IV	2.58	2.4175	0.301371863	3.6	4.28
W@2joint III	2.58	2.525	0.205020324	3.17	3.36
W@2joint IV	2.39	2.235	0.27282473	3.36	4.27
W@3joint IV	2.23	2.095	0.230144882	3.2	3.6
LoPhI,II	10.82	11.1375	0.981100572	42.98	42.74
LoPhII,II	9.17	9	1.008067458	N/A	24.09
LoPhI,III	11.38	11.555	0.936536171	36.82	35.99
LoPhII,III	9.27	9.78	0.930483745	22.74	23.39
LoPhIII,III	8.82	9.02	0.758419409	20.16	20.67
LoPhI,IV	7.61	7.385	0.735594997	30.3	30.65
LoPhII,IV	5.05	5.05	0.726957128	18.43	18.11
LoPhIII,IV	4.51	4.3375	0.705850551	16.99	17.01
LoPhIV,IV	6.45	6.2675	0.629517011	18.95	19.83
WoPhI,II	1.65	1.655	0.143874946	2.65	2.94
WoPhII,II	1.37	1.3475	0.132256065	N/A	2.3
WoPhI,III	1.83	1.825	0.189296945	3.11	3.25
WoPhII,III	1.69	1.7325	0.234716141	3.5	2.95
WoPhIII,III	1.37	1.465	0.216256021	2.81	3.05
WoPhI,IV	1.87	1.755	0.223084438	2.91	3.14
WoPhII,IV	1.85	1.7975	0.161529151	2.69	2.77
WoPhIII,IV	1.9	1.7825	0.189978069	2.41	2.46
WoPhIV,IV	1.45	1.44	0.205426386	2.29	2.51
Foot Length	32.94	34.04	4.413320745	93.81	97.52
Lotmt	33.44	33.21	2.327946162	71.94	73.82
Lott	61.16	60.18	4.482410066	112.85	117.6
LoFem	44.1	43.9925	3.183785744	43.09	44.29
Wotmt@prox	8.04	7.77	0.599388577	12.19	12.17
Wotmt@cond	7.52	7.3475	0.748392722	8.66	9.7
Wott@prox	9.03	8.805	0.593885511	9.94	9.18
Wott@mid	4.14	3.9025	0.23907809	7.42	9.01
Wott@cond	7.57	7.26	0.585718931	12.15	12.23
Wofem@cond	8.53	8.4025	0.600409582	14.57	14.56

Name	*Gavia pacifica*	*Gavia pacifica*	*Gavia pacifica*	*Anas discors*	*Anas discors*
Specimen #	30573	AVERAGE	STDEV	98160	13307
M/F	F			F	M
LoDI	N/A	11.75		6.91	6.21
w/claw	N/A			N/A	N/A
LoDII	64.43	64.945	0.728319985	23.61	25.1
w/claw	N/A			N/A	N/A
LoDIII	76.88	77.27	0.928601098	31.3	32.97
w/claw	N/A			N/A	N/A
LoDIV	83.75	83.26666667	1.061052936	29.78	32.18
w/claw	N/A			N/A	N/A
W@Pjoint II	3.35	3.43	0.113137085	1.75	1.99
W@Pjoint III	4.31	4.163333333	0.245424802	2.48	2.73
W@Pjoint IV	3.76	3.88	0.355527777	1.95	2.28
W@2joint III	3.62	3.383333333	0.225905585	1.9	2.05
W@2joint IV	3.7	3.776666667	0.459818805	1.54	1.74
W@3joint IV	3.75	3.516666667	0.284312035	1.31	1.5
LoPhI,II	42.38	42.7	0.301993377	13.61	14.39
LoPhII,II	23.02	23.555	0.756604256	9.91	10.85
LoPhI,III	35.65	36.15333333	0.601858234	14.42	15.28
LoPhII,III	22.51	22.88	0.456398948	9.43	10.45
LoPhIII,III	19.66	20.16333333	0.505008251	7.74	8.86
LoPhI,IV	31.16	30.70333333	0.432473506	11.34	11.85
LoPhII,IV	18.16	18.23333333	0.172143351	7.17	8.62
LoPhIII,IV	16.09	16.69666667	0.525483904	5.15	6.82
LoPhIV,IV	19.26	19.34666667	0.446355613	6.07	7.13
WoPhI,II	3.23	2.94	0.29	1.29	1.38
WoPhII,II	2.34	2.32	0.028284271	1.05	1.27
WoPhI,III	3.36	3.24	0.125299641	1.8	1.77
WoPhII,III	3.01	3.153333333	0.301717307	1.47	1.59
WoPhIII,III	2.89	2.916666667	0.122202019	1.24	1.36
WoPhI,IV	3.18	3.076666667	0.14571662	1.24	1.33
WoPhII,IV	2.67	2.71	0.052915026	1.11	1.25
WoPhIII,IV	2.55	2.473333333	0.070945989	0.91	1.11
WoPhIV,IV	2.19	2.33	0.163707055	0.75	0.99
Foot Length	93.19	94.84	2.34155931	37.76	38.34
Lotmt	72.78	72.84666667	0.941771381	29.09	30.77
Lott	118.01	116.1533333	2.868106228	53.77	56.33
LoFem	42.94	43.44	0.739932429	33.89	35
Wotmt@prox	12.4	12.25333333	0.127410099	5.63	6.37
Wotmt@cond	9.27	9.21	0.522589705	5.3	6.38
Wott@prox	11.47	10.19666667	1.166376154	5.6	7.55
Wott@mid	9.85	8.76	1.234139376	2.74	3.83
Wott@cond	11.91	12.09666667	0.16653328	5.27	5.94
Wofem@cond	14.55	14.56	0.01	6.74	7.97

Name	*Anas discors*	*Anas discors*	*Anas discors*	*Anas discors*	*Ardea alba*	*Ardea alba*
Specimen #	17239	14236	AVERAGE	STDEV	24320	89895
M/F	M	F			F	F
LoDI	6.81	7.13	6.765	0.39340395	39.44	36.91
w/claw	N/A	N/A			N/A	N/A
LoDII	25.54	24.65	24.725	0.82738544	67.66	65
w/claw	N/A	N/A			N/A	N/A
LoDIII	34.81	32.91	32.9975	1.43469799	98.32	92.79
w/claw	N/A	N/A			N/A	N/A
LoDIV	34.04	32.22	32.055	1.74725499	81.49	79.69
w/claw	N/A	N/A			N/A	N/A
W@Pjoint II	1.91	1.96	1.9025	0.10688779	3.76	3.54
W@Pjoint III	2.7	2.55	2.615	0.11958261	4.28	4.38
W@Pjoint IV	2.14	2.05	2.105	0.140119	4.38	4.28
W@2joint III	1.96	1.89	1.95	0.07348469	3.45	3.22
W@2joint IV	1.73	1.62	1.6575	0.09535023	3.57	3.25
W@3joint IV	1.38	1.32	1.3775	0.08732125	2.91	2.79
LoPhI,II	14.73	14.02	14.1875	0.48196646	38.97	38.38
LoPhII,II	11.03	10.71	10.625	0.49433457	28.58	27.51
LoPhI,III	15.53	15.05	15.07	0.47560488	34.7	34.31
LoPhII,III	11.13	10.73	10.435	0.72578693	37.54	36.15
LoPhIII,III	8.91	8.67	8.545	0.54653454	26.33	25.01
LoPhI,IV	12.4	12.21	11.95	0.46626173	28.26	26.25
LoPhII,IV	8.7	8.44	8.2325	0.71662984	22.66	21.75
LoPhIII,IV	6.93	6.08	6.245	0.82180695	18.73	18.76
LoPhIV,IV	7.04	6.87	6.7775	0.4838302	16.03	15.41
WoPhI,II	1.38	1.53	1.395	0.09949874	2.87	2.81
WoPhII,II	1.17	1.31	1.2	0.11604597	2.23	2.26
WoPhI,III	1.82	1.77	1.79	0.0244949	2.9	2.87
WoPhII,III	1.6	1.58	1.56	0.06055301	2.65	2.68
WoPhIII,III	1.4	1.34	1.335	0.06806859	2.05	2.11
WoPhI,IV	1.35	1.31	1.3075	0.04787136	2.78	2.86
WoPhII,IV	1.26	1.24	1.215	0.07047458	2.56	2.61
WoPhIII,IV	1.1	1.11	1.0575	0.09844626	2.24	2.26
WoPhIV,IV	0.94	0.95	0.9075	0.10719919	1.76	1.96
Foot Length	43.53	40.31	39.985	2.60315834	111.08	104.73
Lotmt	30.99	30.69	30.385	0.87260147	150.06	149.51
Lott	55.65	54.21	54.99	1.2011106	201.32	188.73
LoFem	35.56	34.51	34.74	0.71072733	78	75.18
Wotmt@prox	6	6.02	6.005	0.3022692	11.77	11.85
Wotmt@cond	6.12	6.22	6.005	0.48204426	13.36	13.19
Wott@prox	7.39	7.58	7.03	0.9569744	12.83	12.92
Wott@mid	3.72	3.47	3.44	0.49037401	5.86	6.04
Wott@cond	5.67	5.75	5.6575	0.28206087	10.85	11.38
Wofem@cond	7.63	7.25	7.3975	0.52784941	10.26	12.59

Name	*Ardea alba*	*Ardea alba*	*Ardea alba*	*Ardea alba*	*Calidris alba*	*Calidris alba*
Specimen #	21230	55619	AVERAGE	STDEV	32312	32304
M/F	M	M			F	F
LoDI	38.54	40.47	38.84	1.5090615	N/A	N/A
w/claw	N/A	N/A			N/A	N/A
LoDII	67.61	71.25	67.88	2.5672683	11.4	11.11
w/claw	N/A	N/A			N/A	N/A
LoDIII	95.07	98.93	96.2775	2.8768197	15.06	13.67
w/claw	N/A	N/A			N/A	N/A
LoDIV	85.77	86.79	83.435	3.391966	14.17	12.5
w/claw	N/A	N/A			N/A	N/A
W@Pjoint II	3.58	4.16	3.76	0.2833137	1.15	1.12
W@Pjoint III	4.24	4.77	4.4175	0.2422636	1.42	1.43
W@Pjoint IV	4.25	4.56	4.3675	0.1398511	1.23	1.23
W@2joint III	3.16	3.67	3.375	0.2330236	1.15	1.17
W@2joint IV	3.41	3.74	3.4925	0.2104559	1.03	1.04
W@3joint IV	2.74	3.11	2.8875	0.1645955	0.88	0.9
LoPhI,II	39.19	40.64	39.295	0.9596701	6.73	6.16
LoPhII,II	29.29	31.79	29.2925	1.8186511	4.67	5.05
LoPhI,III	35.62	35.8	35.1075	0.7174666	6.79	5.94
LoPhII,III	37.39	38.57	37.4125	0.9917115	4.78	4.64
LoPhIII,III	24.64	28.08	26.015	1.5560741	3.49	3.73
LoPhI,IV	28.25	29.26	28.005	1.2622863	5.17	4.67
LoPhII,IV	23.11	23.97	22.8725	0.9248558	3.61	3.1
LoPhIII,IV	18.76	20.12	19.0925	0.685146	2.77	2.64
LoPhIV,IV	16.76	17.33	16.3825	0.8387044	2.62	2.55
WoPhI,II	3.1	3.18	2.99	0.1779513	0.69	0.67
WoPhII,II	2.38	2.42	2.3225	0.0917878	0.59	0.61
WoPhI,III	3.19	3.27	3.0575	0.2022169	0.76	0.79
WoPhII,III	2.86	3.02	2.8025	0.1721191	0.72	0.75
WoPhIII,III	2.27	2.34	2.1925	0.1352467	0.71	0.7
WoPhI,IV	2.97	3.1	2.9275	0.1388944	0.73	0.62
WoPhII,IV	2.73	2.92	2.705	0.1601041	0.65	0.64
WoPhIII,IV	2.46	2.58	2.385	0.1636052	0.66	0.62
WoPhIV,IV	2.02	2.02	1.94	0.1232883	0.56	0.54
Foot Length	107.64	110.03	108.37	2.8214772	N/A	17.64
Lotmt	165.12	168.74	158.3575	10.010902	28.35	25.32
Lott	221.08	226.06	209.2975	17.382666	42.59	40.5
LoFem	82.28	82.36	79.455	3.5029654	24.09	22.58
Wotmt@prox	12.51	13.23	12.34	0.6797058	3.88	3.77
Wotmt@cond	13.96	14.15	13.665	0.4622049	3.81	3.49
Wott@prox	14.81	14.72	13.82	1.0924285	4.4	4.38
Wott@mid	6.76	6.95	6.4025	0.5333151	1.68	1.59
Wott@cond	11.15	11.76	11.285	0.3838837	3.45	3.07
Wofem@cond	13.54	13.45	12.46	1.5278962	4.35	4.24

Name	*Calidris alba*	*Calidris alba*	*Calidris alba*	*Calidris alba*	*Lecucophaeus pipixcan*
Specimen #	32311	32309	AVERAGE	STDEV	19183
M/F	M	M			M
LoDI	N/A	N/A			2.97
w/claw	N/A	N/A			N/A
LoDII	10.78	11.02	11.0775	0.25617377	25.37
w/claw	N/A	N/A			N/A
LoDIII	14.04	13.08	13.9625	0.83163995	33.03
w/claw	N/A	N/A			N/A
LoDIV	13.75	11.33	12.9375	1.2851297	30.99
w/claw	N/A	N/A			N/A
W@Pjoint II	1.18	1.12	1.1425	0.02872281	1.79
W@Pjoint III	1.44	1.3	1.3975	0.06551081	2.2
W@Pjoint IV	1.31	1.18	1.2375	0.05377422	1.75
W@2joint III	1.23	1.2	1.1875	0.035	1.95
W@2joint IV	1.07	0.89	1.0075	0.0801561	1.55
W@3joint IV	0.9	0.8	0.87	0.04760952	1.26
LoPhI,II	5.89	6.24	6.255	0.3502856	13.52
LoPhII,II	4.89	5.02	4.9075	0.17289207	11.43
LoPhI,III	6.28	5.74	6.1875	0.45937457	15.76
LoPhII,III	4.37	4.54	4.5825	0.17250604	10.01
LoPhIII,III	3.39	3.7	3.5775	0.16439282	8.55
LoPhI,IV	4.89	4.48	4.8025	0.2968024	11.4
LoPhII,IV	3.54	3.4	3.4125	0.22588714	7.31
LoPhIII,IV	2.87	2.56	2.71	0.13735599	6.94
LoPhIV,IV	2.45	2.27	2.4725	0.15195942	6.29
WoPhI,II	0.8	0.66	0.705	0.06454972	1.13
WoPhII,II	0.66	0.57	0.6075	0.0386221	1.04
WoPhI,III	0.82	0.72	0.7725	0.04272002	1.54
WoPhII,III	0.79	0.74	0.75	0.0294392	1.31
WoPhIII,III	0.76	0.72	0.7225	0.02629956	1.23
WoPhI,IV	0.77	0.63	0.6875	0.07410578	1.26
WoPhII,IV	0.75	0.7	0.685	0.05066228	1.35
WoPhIII,IV	0.65	0.63	0.64	0.01825742	1.09
WoPhIV,IV	0.6	0.55	0.5625	0.02629956	0.98
Foot Length	17.36	15.78	16.9266667	1.00286257	41.72
Lotmt	25.06	25.37	26.025	1.55594559	45.43
Lott	39.43	39.81	40.5825	1.40971333	68.63
LoFem	21.74	22.29	22.675	1.00560098	36.11
Wotmt@prox	3.77	3.65	3.7675	0.09394147	6.84
Wotmt@cond	3.62	3.52	3.61	0.14445299	6.53
Wott@prox	4.22	4.21	4.3025	0.10144785	6.88
Wott@mid	1.49	1.47	1.5575	0.09708244	3.01
Wott@cond	3.25	3.18	3.2375	0.15986974	5.89
Wofem@cond	4.2	4.12	4.2275	0.09569918	6.92

Name	*Lecucophaeus*	*Lecucophaeus*	*Lecucophaeus*	*Lecucophaeus*	*Lecucophaeus*
Specimen #	89215	85826	14624	AVERAGE	STDEV
M/F	M	F	F		
LoDI	N/A	N/A	3.64	3.305	0.473761543
w/claw	N/A	N/A	N/A		
LoDII	23.55	23.53	23.63	24.02	0.90103644
w/claw	N/A	N/A	N/A		
LoDIII	30.77	30.88	30.21	31.2225	1.240198237
w/claw	N/A	N/A	N/A		
LoDIV	29.79	29.38	29.9	30.015	0.687434845
w/claw	N/A	N/A	N/A		
W@Pjoint II	1.58	1.65	1.64	1.665	0.088881944
W@Pjoint III	2.15	2.21	2.12	2.17	0.042426407
W@Pjoint IV	1.61	1.61	1.8	1.6925	0.097425185
W@2joint III	1.78	1.82	1.83	1.845	0.073257537
W@2joint IV	1.32	1.49	1.39	1.4375	0.102428837
W@3joint IV	1.17	1.19	1.13	1.1875	0.054390563
LoPhI,II	12.62	12.71	12.7	12.8875	0.423585883
LoPhII,II	11.31	11.19	11.4	11.3325	0.107819293
LoPhI,III	14.64	13.97	14.35	14.68	0.770497675
LoPhII,III	9.61	9.14	9.38	9.535	0.370270172
LoPhIII,III	7.77	7.69	7.2	7.8025	0.55841293
LoPhI,IV	10.41	10.28	10.34	10.6075	0.530997489
LoPhII,IV	7.42	6.88	7.73	7.335	0.35161532
LoPhIII,IV	6.69	6.65	6.88	6.79	0.141656862
LoPhIV,IV	6.11	5.89	6.19	6.12	0.170098011
WoPhI,II	1.26	1.18	1.23	1.2	0.057154761
WoPhII,II	1.1	0.97	1.11	1.055	0.064549722
WoPhI,III	1.68	1.41	1.43	1.515	0.12396236
WoPhII,III	1.49	1.31	1.31	1.355	0.09
WoPhIII,III	1.27	1.1	1.34	1.235	0.10082989
WoPhI,IV	1.31	1.19	1.32	1.27	0.059441848
WoPhII,IV	1.39	1.34	1.18	1.315	0.092556289
WoPhIII,IV	1.12	0.95	1.01	1.0425	0.077190241
WoPhIV,IV	1.02	0.89	0.97	0.965	0.054467115
Foot Length	38.19	36.7	38.14	38.6875	2.136467099
Lotmt	45	41.57	43.23	43.8075	1.769602121
Lott	66.77	64.15	65.14	66.1725	1.962385878
LoFem	N/A	32.91	33.75	34.25666667	1.659076048
Wotmt@prox	6.81	6.7	6.67	6.755	0.082663978
Wotmt@cond	6.16	5.68	6.06	6.1075	0.34941618
Wott@prox	6.44	6.39	6.78	6.6225	0.243909136
Wott@mid	2.78	2.32	2.84	2.7375	0.294886984
Wott@cond	5.91	5.66	5.73	5.7975	0.122031417
Wofem@cond	6.83	4.35	6.49	6.1475	1.212555841

Name	*Cepphus columba*	*Cepphus colum*	*Cepphus columl*	*Cepphus colum*	*Cepphus colun*
Specimen #	30533	60534	82987	85956	AVERAGE
M/F	F	F	?	F	
LoDI	N/A	N/A	N/A	N/A	
w/claw	N/A	N/A	N/A	N/A	
LoDII	28.94	27.87	26.07	27.43	27.5775
w/claw	N/A	N/A	N/A	N/A	
LoDIII	38.3	37.19	36.88	38.48	37.7125
w/claw	N/A	N/A	N/A	N/A	
LoDIV	38.86	37.68	37.48	39.62	38.41
w/claw	N/A	N/A	N/A	N/A	
W@Pjoint II	2.21	2.32	2.22	2.58	2.3325
W@Pjoint III	2.65	2.7	2.55	2.6	2.625
W@Pjoint IV	2.16	2.34	2.24	2.6	2.335
W@2joint III	2.21	2.38	2.3	2.51	2.35
W@2joint IV	1.78	1.92	1.96	2.25	1.9775
W@3joint IV	1.62	1.66	1.6	1.76	1.66
LoPhI,II	15.51	15.44	14.3	14.9	15.0375
LoPhII,II	13.92	12.97	12.61	13.18	13.17
LoPhI,III	16.07	16.71	15.77	16.77	16.33
LoPhII,III	12.38	12.03	11.85	12.08	12.085
LoPhIII,III	11.57	10.39	10.66	10.92	10.885
LoPhI,IV	12.81	13.05	12.55	13.28	12.9225
LoPhII,IV	9	9.1	9.16	9.37	9.1575
LoPhIII,IV	9.39	8.5	8.69	8.97	8.8875
LoPhIV,IV	10.64	8.75	9.05	9.07	9.3775
WoPhI,II	1.68	1.76	1.5	1.75	1.6725
WoPhII,II	1.44	1.53	1.29	1.53	1.4475
WoPhI,III	2.05	2.07	1.78	2.16	2.015
WoPhII,III	1.87	1.91	1.74	1.95	1.8675
WoPhIII,III	1.61	1.62	1.41	1.6	1.56
WoPhI,IV	1.58	1.7	1.37	1.71	1.59
WoPhII,IV	1.45	1.49	1.31	1.64	1.4725
WoPhIII,IV	1.4	1.35	1.11	1.46	1.33
WoPhIV,IV	1.19	1.19	1.01	1.22	1.1525
Foot Length	46.95	45.27	45.07	45.18	45.6175
Lotmt	35.52	34.91	34.56	34.29	34.82
Lott	70.66	65.94	66.27	65.85	67.18
LoFem	40.31	38	41.1	40.24	39.9125
Wotmt@prox	7.17	7.17	7.07	7.41	7.205
Wotmt@cond	6.82	7.14	6.29	6.62	6.7175
Wott@prox	7.48	7.72	6.78	8.32	7.575
Wott@mid	4.74	4.68	3	4.83	4.3125
Wott@cond	6.37	6.54	6.04	6.57	6.38
Wofem@cond	7.92	7.84	7.61	7.99	7.84

Name	*Cepphus colun*	*Porzana carolina*	*Porzana carol*	*Porzana caro*	*Porzana carol*
Specimen #	STDEV	98235	?	82394	82391
M/F		F	F	M	M
LoDI		10.09	9.79	10.43	9.7
w/claw		N/A	N/A	N/A	N/A
LoDII	1.188314633	26.26	24.9	26.96	26.1
w/claw		N/A	N/A	N/A	N/A
LoDIII	0.795880016	32.76	32.29	34.68	33.64
w/claw		N/A	N/A	N/A	N/A
LoDIV	1.010676341	28.06	27.91	29.83	29.43
w/claw		N/A	N/A	N/A	N/A
W@Pjoint II	0.1723127	1.26	1.29	1.46	1.4
W@Pjoint III	0.064549722	1.44	1.6	1.83	1.71
W@Pjoint IV	0.191398363	1.41	1.5	1.49	1.66
W@2joint III	0.127279221	1.27	1.23	1.4	1.35
W@2joint IV	0.197378655	1.18	1.22	1.37	1.31
W@3joint IV	0.071180522	1.09	1.17	1.19	1.18
LoPhI,II	0.562161009	15.41	14.22	15.22	14.78
LoPhII,II	0.552630075	11.49	10.83	12.23	11.71
LoPhI,III	0.489625707	14.39	13.78	14.29	13.68
LoPhII,III	0.220075745	9.8	10.01	10.99	10.58
LoPhIII,III	0.505338171	9.35	8.74	10.1	9.44
LoPhI,IV	0.31383382	10.87	10.26	10.95	10.55
LoPhII,IV	0.156284996	6.69	6.65	6.99	7.26
LoPhIII,IV	0.386641522	4.9	5.45	5.77	6.1
LoPhIV,IV	0.854297957	6.3	6.1	7.04	6.47
WoPhI,II	0.120381339	1.14	1.05	1.17	1.16
WoPhII,II	0.113247517	0.78	0.81	0.88	0.91
WoPhI,III	0.163808832	1.2	1.23	1.26	1.17
WoPhII,III	0.091058589	0.99	1.08	1.09	1.05
WoPhIII,III	0.10033278	0.81	0.83	0.88	0.88
WoPhI,IV	0.158113883	1.12	1.09	1.14	1.09
WoPhII,IV	0.13573872	0.97	0.97	1.07	1.01
WoPhIII,IV	0.15340578	0.79	0.86	0.95	0.93
WoPhIV,IV	0.096046864	0.68	0.72	0.75	0.75
Foot Length	0.892090242	36.94	38.45	40.12	39.34
Lotmt	0.531224999	33.35	31.36	34.37	34.1
Lott	2.327015256	51.96	50.18	53.63	53.24
LoFem	1.333301041	34.88	33.88	34.8	34.64
Wotmt@prox	0.144568323	4.25	4.21	4.57	4.46
Wotmt@cond	0.356499182	4.51	4.16	4.8	4.87
Wott@prox	0.636945838	5.28	5.48	5.48	5.54
Wott@mid	0.877168741	2.39	2.02	2.26	2.13
Wott@cond	0.243173463	4	4.05	4.28	4.25
Wofem@cond	0.165126214	4.91	4.98	5.34	5.22

Name	*Porzana carol*	*Porzana carol*	*Molothrus ate*	*Molothrus ate*	*Molothrus ater*
Specimen #	AVERAGE	STDEV	35240	15327	22549
M/F			M	F	M
LoDI	10.0025	0.33018934	10.57	9.39	10.4
w/claw			N/A	N/A	N/A
LoDII	26.055	0.855784241	11.74	11.73	12.76
w/claw			N/A	N/A	N/A
LoDIII	33.3425	1.052690996	17.21	16.43	18.72
w/claw			N/A	N/A	N/A
LoDIV	28.8075	0.965621561	13.1	12.57	14.53
w/claw			N/A	N/A	N/A
W@Pjoint II	1.3525	0.093585968	1.15	1.13	1.4
W@Pjoint III	1.645	0.16583124	1.26	1.24	1.46
W@Pjoint IV	1.515	0.104721854	1.17	1.19	1.27
W@2joint III	1.3125	0.076757193	1.18	1.16	1.18
W@2joint IV	1.27	0.086023253	1.16	1.15	1.2
W@3joint IV	1.1575	0.045734742	1.13	0.99	1.13
LoPhI,II	14.9075	0.528858834	5.78	5.4	6
LoPhII,II	11.565	0.579971264	5.96	6.7	6.76
LoPhI,III	14.035	0.356884669	5.68	5.33	5.86
LoPhII,III	10.345	0.541756403	5.41	5.34	6.01
LoPhIII,III	9.4075	0.556619259	6.12	5.29	6.85
LoPhI,IV	10.6575	0.316372671	3.59	2.79	3.25
LoPhII,IV	6.8975	0.285350661	2.85	2.79	3.27
LoPhIII,IV	5.555	0.510979452	2.82	2.99	3.51
LoPhIV,IV	6.4775	0.404341028	3.84	3.94	4.5
WoPhI,II	1.13	0.054772256	0.82	0.72	0.85
WoPhII,II	0.845	0.060277138	0.78	0.71	0.79
WoPhI,III	1.215	0.038729833	0.85	0.76	0.89
WoPhII,III	1.0525	0.045	0.83	0.77	0.86
WoPhIII,III	0.85	0.035590261	0.78	0.66	0.83
WoPhI,IV	1.11	0.024494897	0.87	0.88	0.87
WoPhII,IV	1.005	0.047258156	0.76	0.79	0.88
WoPhIII,IV	0.8825	0.072743843	0.81	0.73	0.84
WoPhIV,IV	0.725	0.033166248	0.83	0.75	0.77
Foot Length	38.7125	1.364487083	N/A	18.49	21.04
Lotmt	33.295	1.360257329	26.25	24.33	26.59
Lott	52.2525	1.55493569	35.81	33.37	36.72
LoFem	34.55	0.457675285	22.22	20.51	22.97
Wotmt@prox	4.3725	0.171342736	2.95	3.4	3.67
Wotmt@cond	4.585	0.323367696	4.27	2.5	2.76
Wott@prox	5.445	0.113578167	4.29	3.96	4.41
Wott@mid	2.2	0.160208198	1.93	1.44	1.67
Wott@cond	4.145	0.140593978	3.27	3.25	3.38
Wofem@cond	5.1125	0.201556444	3.88	3.66	3.95

Name	*Molothrus ater*	*Molothrus ate*	*Molothrus ate*	*Sitta canadensis*	*Sitta canadensis*
Specimen #	35241	AVERAGE	STDEV	23549	23540
M/F				F	F
LoDI	9.2	9.89	0.69488608	8.63	8.14
w/claw	N/A			N/A	N/A
LoDII	11.18	11.8525	0.65915982	7.1	6.92
w/claw	N/A			N/A	N/A
LoDIII	16.43	17.1975	1.07954852	11.92	11.11
w/claw	N/A			N/A	N/A
LoDIV	12.62	13.205	0.91507741	8.68	8.99
w/claw	N/A			N/A	N/A
W@Pjoint II	1.11	1.1975	0.13598407	0.69	0.64
W@Pjoint III	1.22	1.295	0.11120552	0.88	0.77
W@Pjoint IV	1.11	1.185	0.06608076	0.68	0.61
W@2joint III	1.05	1.1425	0.06238322	0.78	0.72
W@2joint IV	1.12	1.1575	0.03304038	0.71	0.62
W@3joint IV	0.92	1.0425	0.105	0.63	0.59
LoPhI,II	5.47	5.6625	0.27909079	3.36	3.31
LoPhII,II	5.71	6.2825	0.52728076	3.74	3.82
LoPhI,III	5.3	5.5425	0.27305372	3.86	3.34
LoPhII,III	5.13	5.4725	0.37756898	3.78	3.63
LoPhIII,III	6	6.065	0.63877487	4.28	4.71
LoPhI,IV	3.22	3.2125	0.32785922	2.54	2.33
LoPhII,IV	2.59	2.875	0.28583212	1.89	1.87
LoPhIII,IV	2.81	3.0325	0.32887434	2.58	2.19
LoPhIV,IV	4	4.07	0.29416549	3.01	3.1
WoPhI,II	0.83	0.805	0.05802298	0.49	0.39
WoPhII,II	0.65	0.7325	0.06551081	0.38	0.3
WoPhI,III	0.87	0.8425	0.05737305	0.5	0.48
WoPhII,III	0.78	0.81	0.04242641	0.48	0.43
WoPhIII,III	0.7	0.7425	0.07675719	0.43	0.37
WoPhI,IV	0.79	0.8525	0.04193249	0.49	N/A
WoPhII,IV	0.8	0.8075	0.05123475	0.45	0.39
WoPhIII,IV	0.73	0.7775	0.05619905	0.46	0.35
WoPhIV,IV	0.65	0.75	0.07483315	0.38	0.34
Foot Length	18.51	19.3466667	1.46650378	13.55	12.19
Lotmt	23.51	25.17	1.48817562	15.42	15.93
Lott	31.75	34.4125	2.26960165	20.32	21.07
LoFem	19.88	21.395	1.44218584	12.18	12.6
Wotmt@prox	3.2	3.305	0.30512293	2.08	2.05
Wotmt@cond	2.61	3.035	0.83020078	1.63	1.53
Wott@prox	4.13	4.1975	0.19551215	2.84	2.35
Wott@mid	1.43	1.6175	0.23599082	0.81	0.81
Wott@cond	3	3.225	0.16051999	1.9	1.88
Wofem@cond	3.35	3.71	0.26993826	2.43	2.49

Name	*Sitta canadensi*	*Sitta canadensis*	*Sitta canadensis*	*Sitta canadensis*	*Corvus corax*
Specimen #	23546	23545	AVERAGE	STDEV	17234
M/F	M	M			M
LoDI	8.1	8.34	8.3025	0.242263631	24.89
w/claw	N/A	N/A			N/A
LoDII	6.81	6.66	6.8725	0.18536001	30.64
w/claw	N/A	N/A			N/A
LoDIII	11.55	10.79	11.3425	0.495269287	41.75
w/claw	N/A	N/A			N/A
LoDIV	8.29	9.04	8.75	0.345543051	32.41
w/claw	N/A	N/A			N/A
W@Pjoint II	0.69	0.69	0.6775	0.025	3.73
W@Pjoint III	0.86	0.82	0.8325	0.048562674	4.38
W@Pjoint IV	0.7	0.66	0.6625	0.038622101	3.66
W@2joint III	0.8	0.8	0.775	0.037859389	3.99
W@2joint IV	0.69	0.7	0.68	0.040824829	3.18
W@3joint IV	0.64	0.63	0.6225	0.022173558	2.98
LoPhI,II	3.18	3.11	3.24	0.115181017	14.78
LoPhII,II	3.81	3.46	3.7075	0.168794747	16.72
LoPhI,III	3.22	3.54	3.49	0.279761803	13.9
LoPhII,III	3.71	3.7	3.705	0.061373175	13.85
LoPhIII,III	4.33	4.43	4.4375	0.192072035	16.38
LoPhI,IV	1.96	2.58	2.3525	0.283710533	9.2
LoPhII,IV	1.87	1.85	1.87	0.016329932	8
LoPhIII,IV	2.11	2.1	2.245	0.226936114	8.47
LoPhIV,IV	3.13	3.1	3.085	0.051961524	10.19
WoPhI,II	0.53	0.49	0.475	0.059721576	3.09
WoPhII,II	0.37	0.39	0.36	0.040824829	2.73
WoPhI,III	0.55	0.62	0.5375	0.062383224	2.93
WoPhII,III	0.49	0.52	0.48	0.037416574	2.98
WoPhIII,III	0.43	0.45	0.42	0.034641016	2.67
WoPhI,IV	0.54	0.47	0.5	0.036055513	2.89
WoPhII,IV	0.48	0.46	0.445	0.038729833	2.77
WoPhIII,IV	0.45	0.43	0.4225	0.049916597	2.52
WoPhIV,IV	0.39	0.4	0.3775	0.026299556	2.47
Foot Length	13.33	12.57	12.91	0.637704216	50.5
Lotmt	15.86	16.03	15.81	0.269196335	70.13
Lott	20.32	20.66	20.5925	0.356405668	112.73
LoFem	12.11	12.51	12.35	0.241246762	67.05
Wotmt@prox	2.24	2.09	2.115	0.085049005	12.23
Wotmt@cond	1.69	1.56	1.6025	0.071821538	8.85
Wott@prox	2.52	2.59	2.575	0.203387971	15.12
Wott@mid	0.86	0.89	0.8425	0.039475731	7.48
Wott@cond	1.97	1.91	1.915	0.038729833	11.92
Wofem@cond	2.54	2.48	2.485	0.045092498	14.08

Name	*Corvus corax*	*Corvus corax*	*Corvus corax*	*Corvus corax*	*Corvus corax*
Specimen #	17229	23081	17228	AVERAGE	STDEV
M/F	F	F	M		
LoDI	24.91	24.3	25.85	24.9875	0.640852297
w/claw	N/A	N/A	N/A		
LoDII	29.24	28.14	30.4	29.605	1.152200793
w/claw	N/A	N/A	N/A		
LoDIII	41.25	40.08	43.55	41.6575	1.442760664
w/claw	N/A	N/A	N/A		
LoDIV	31.78	30.83	32.33	31.8375	0.727707588
w/claw	N/A	N/A	N/A		
W@Pjoint II	4.12	3.88	3.96	3.9225	0.162557682
W@Pjoint III	4.33	4.14	4.44	4.3225	0.129711218
W@Pjoint IV	3.46	3.33	3.74	3.5475	0.186793112
W@2joint III	3.84	3.83	3.92	3.895	0.075055535
W@2joint IV	3.37	3.1	3.39	3.26	0.142594998
W@3joint IV	3.03	2.78	3.04	2.9575	0.121209186
LoPhI,II	14.74	14.29	15.46	14.8175	0.48251943
LoPhII,II	15.88	15.32	16.3	16.055	0.598080262
LoPhI,III	13.59	13.9	14.24	13.9075	0.265502668
LoPhII,III	13.17	13.26	14.32	13.65	0.538949596
LoPhIII,III	16.05	15.61	16.39	16.1075	0.367366756
LoPhI,IV	8.36	9.17	9.02	8.9375	0.392969464
LoPhII,IV	7.64	7.57	8.24	7.8625	0.314364438
LoPhIII,IV	8.33	7.65	8.62	8.2675	0.428359273
LoPhIV,IV	9.82	9.18	9.63	9.705	0.420198366
WoPhI,II	3.12	2.83	3.18	3.055	0.154596248
WoPhII,II	2.59	2.5	2.8	2.655	0.135277493
WoPhI,III	2.96	2.89	3	2.945	0.046547467
WoPhII,III	2.99	2.73	3.07	2.9425	0.147280911
WoPhIII,III	2.64	2.52	2.77	2.65	0.102956301
WoPhI,IV	3.07	2.85	3.07	2.97	0.116619038
WoPhII,IV	2.84	2.56	2.9	2.7675	0.148183445
WoPhIII,IV	2.52	2.2	2.62	2.465	0.182847842
WoPhIV,IV	2.45	2.22	2.62	2.44	0.165126214
Foot Length	48.09	47.83	49.08	48.875	1.209807147
Lotmt	64.91	66.35	69.14	67.6325	2.419839871
Lott	105.88	108.61	112.9	110.03	3.404203284
LoFem	65.24	65.08	65.71	65.77	0.894240833
Wotmt@prox	12.11	11.63	12.43	12.1	0.34
Wotmt@cond	8.88	8.51	8.84	8.77	0.174164673
Wott@prox	14.61	14.7	15.5	14.9825	0.41039615
Wott@mid	6.3	6.44	7.75	6.9925	0.729446137
Wott@cond	11.36	10.78	11.46	11.38	0.468472696
Wofem@cond	13.4	13	13.76	13.56	0.465331423

Subzero Storage:

Name	*Meleagris gallopovo*	*Meleagris gallopovo*	*Meleagris gallopovo*	*Meleagris gallopovo*
No	N/A	N/A	AVERAGE	STDEV
LoDI	21.48	19.49	20.485	1.407142495
w/claw	32.96	25.94	29.45	
LoDII	45.17	49.55	47.36	3.097127702
w/claw	62.92	63.57	63.245	
LoDIII	70.47	75.07	72.77	3.252691193
w/claw	86.85	91.46	89.155	
LoDIV	51.37	53.44	52.405	1.463711037
w/claw	63.25	67.76	65.505	
W@Pjoint II	10.45	9.62	10.035	0.586898628
W@Pjoint III	11.88	10.88	11.38	0.707106781
W@Pjoint IV	11.43	7.66	9.545	2.665792565
W@2joint III	10.38	9.56	9.97	0.579827561
W@2joint IV	9.34	7.91	8.625	1.011162697
W@3joint IV	8.02	7.46	7.74	0.395979797
LoPI,II	17.04	15.84	16.44	0.848528137
LoPII,II	10.32	17.74	14.03	5.246732316
LoPI,III	10.19	21.07	15.63	7.693321779
LoPII,III	6.6	17.93	12.265	8.011519831
LoPIII,III	7.8	17.26	12.53	6.68923015
LoPI,IV	8	3.93	5.965	2.877924599
LoPII,IV	9.72	11.22	10.47	1.060660172
LoPIII,IV	7.02	8.52	7.77	1.060660172
LoPIV,IV	5.07	19.89	12.48	10.4793225
WoTII	5.07	10.09	7.58	3.549676042
WoTIII	9.25	13.12	11.185	2.736503243
WoTIV	7.26	11.05	9.155	2.679934701
FLw/hal	N/A	N/A	N/A	0
FLw/out hal	74.33	81.17	77.75	4.836610383
Lotmt	148.08	128	138.04	14.19870417
Wotmt@prox	N/A	22.38	22.38	0
Wotmt@cond	23.27	24.68	23.975	0.997020561

Name	*Colaptes auritus*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*
No	N/A	N/A	N/A	N/A	N/A
LoDI	7.7	6.42	9.17	8.38	7.83
w/claw	11.66	12.24	14.52	12.83	12.16
LoDII	11.18	7.22	9.71	9.09	8.1
w/claw	18.28	10.3	12.83	12.96	11.48
LoDIII	16.95	10.35	15.82	15.05	13.23
w/claw	25.11	15.38	18.81	19.6	17.15
LoDIV	17.48	8.54	10.26	10.17	8.7
w/claw	23.91	10.52	12.37	12.82	11.18
W@Pjoint II	2.21	1.31	1.35	1.19	1.16
W@Pjoint III	2.87	1.49	1.56	1.36	1.52
W@Pjoint IV	2.99	1.59	N/A	N/A	N/A
W@2joint III	2.95	1.27	1.44	1.26	1.26
W@2joint IV	2.75	1.41	1.15	1.2	1.15
W@3joint IV	2.84	1.24	1.26	1.26	1.16
LoPI,II	5.81	1.48	1.38	1.79	2.2
LoPII,II	3.7	4.03	5.51	5.28	4.85
LoPI,III	N/A	2.15	1.83	1.78	1.34
LoPII,III	4.83	3.28	3.17	4.44	3.14
LoPIII,III	5.35	6.07	7.52	7	6.1
LoPI,IV	3.76	N/A	N/A	N/A	N/A
LoPII,IV	3.12	2.39	2.69	2.02	2.07
LoPIII,IV	3.61	1.52	1.96	1.84	2.16
LoPIV,IV	3.01	2.6	4.28	3.81	3.06
WoTII	1.5	1.15	1.33	1.29	N/A
WoTIII	1.94	1.7	1.25	1.38	N/A
WoTIV	2.44	1.18	1.33	1.18	N/A
FLw/hal	28.6	23.15	25.66	25.14	N/A
FLw/out hal	23.51	15.54	16.36	14.93	N/A
Lotmt	34.25	20.23	21.78	21.19	N/A
Wotmt@prox	N/A	2.91	2.28	2.83	N/A
Wotmt@cond	6.74	3.06	3.33	3.69	N/A

Name	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*	*Turdus migratorius*
No	N/A	N/A	AVERAGE	STDEV	N/A
LoDI	8.89	8.14	8.138333333	1.088057903	11.08
w/claw	13.03	13.23	13.00166667		15.48
LoDII	9.31	8.56	8.665	0.906305688	11.02
w/claw	11.56	11.86	11.83166667		14.06
LoDIII	14.61	15.18	14.04	2.004255473	16.12
w/claw	18.98	19.63	18.25833333		21.38
LoDIV	9.42	8.79	9.313333333	3.163758314	9.72
w/claw	12.49	11.91	11.88166667		12.13
W@Pjoint II	1.32	1.26	1.265	0.07609205	1.91
W@Pjoint III	1.38	1.49	1.466666667	0.079414524	2.46
W@Pjoint IV	N/A	N/A	1.59	0	2.2
W@2joint III	1.3	1.27	1.3	0.070142712	2.4
W@2joint IV	1.14	1.17	1.203333333	0.103473024	2.04
W@3joint IV	1.15	1.15	1.203333333	0.055377492	1.75
LoPI,II	1.95	2.15	1.825	0.340631766	2.78
LoPII,II	5.71	5.08	5.076666667	0.596176708	4.52
LoPI,III	1.48	1.13	1.618333333	0.371128908	2.53
LoPII,III	3.02	2.27	3.22	0.699056507	4.23
LoPIII,III	6.91	6.06	6.61	0.620386976	6.05
LoPI,IV	N/A	N/A	N/A	0	2.38
LoPII,IV	2.42	2.4	2.331666667	0.248951133	2.57
LoPIII,IV	1.86	1.77	1.851666667	0.211510441	2.56
LoPIV,IV	4.04	2.98	3.461666667	0.67250031	3.08
WoTII	1.15	1.15	1.214	0.088769364	1.38
WoTIII	1.15	1.45	1.386	0.210309296	1.34
WoTIV	1.19	1.22	1.22	0.06363961	1.44
FLw/hal	21.19	24.22	23.872	1.777658572	N/A
FLw/out hal	15.69	16.71	15.846	0.701377217	18.77
Lotmt	22.14	22.02	21.472	0.784773853	32.8
Wotmt@prox	3.33	2.32	2.734	0.439579344	4.76
Wotmt@cond	3	3.18	3.252	0.275445094	4.5

Name	*Gavia pacifica*	*Lecucophaeus pipixcan*	*Chepphus columba*	*Sitta canadensis*	*Aechmorphorus occidentalis*
No	N/A	N/A	N/A	N/A	N/A
LoDI	12.27	6.19	N/A	10.49	19.51
w/claw	N/A	N/A	N/A	18.17	N/A
LoDII	69.23	22.01	35.77	6.17	59.6
w/claw	74.56	27.23	39.77	9	N/A
LoDIII	85.99	30.2	46.62	12.98	62.49
w/claw	N/A	36.93	50.71	15.75	N/A
LoDIV	91.39	30.2	42.74	8.61	69.01
w/claw	N/A	34.63	45.8	12.39	76.14
W@Pjoint II	7.06	1.82	3.1	1.17	5.35
W@Pjoint III	6.2	2.81	3.65	1.31	6.4
W@Pjoint IV	N/A	2.21	2.7	N/A	5.34
W@2joint III	6.18	2.82	3.42	1.46	6
W@2joint IV	5.09	2.2	2.64	1.12	5.75
W@3joint IV	4.42	1.84	2.53	1.05	4.86
LoPI,II	27.23	6.28	17.78	1.2	22.59
LoPII,II	30.88	12.32	12.61	5.34	25.58
LoPI,III	27.88	13.03	14.8	2.41	17.81
LoPII,III	24.37	7.01	10.25	1.84	16.47
LoPIII,III	31.7	8.88	14.69	6.23	18.36
LoPI,IV	24.78	10.77	9.2	0.87	26.15
LoPII,IV	15.23	7.24	9.62	1.61	13.3
LoPIII,IV	16.88	7.09	8.75	1.61	9.8
LoPIV,IV	24.04	5.58	10.32	4.86	17.57
WoTII	4.81	1.76	2.22	1.27	3.12
WoTIII	6.44	2.54	3.71	1.25	3.03
WoTIV	4.2	2.14	2.34	1.14	5.01
FLw/hal	N/A	N/A	N/A	25.4	N/A
FLw/out hal	102.8	38.36	46.25	15.6	84.12
Lotmt	84.44	48.2	45.1	22.3	77.12
Wotmt@prox	14.78	5.43	7.96	1.81	12.73
Wotmt@cond	10.25	6.13	7.44	3.75	10.74

Name	*Aechmorphorus occidentalis*	*Aechmorphorus occidentalis*	*Aechmorphorus occidentalis*	*Corvus corax*	*Anas discors*
No	N/A	AVERAGE	STDEV	N/A	N/A
LoDI	14.6	17.055	3.471894296	28.33	7.8
w/claw	N/A			42.18	9.59
LoDII	55.98	57.79	2.559726548	28.55	24.38
w/claw	60.17	60.17		38.46	30.69
LoDIII	60.98	61.735	1.06773124	42.56	38.91
w/claw	67.43	67.43		57.06	46.42
LoDIV	69.26	69.135	0.176776695	33.18	32.11
w/claw	79.44	77.79		39.75	37.98
W@Pjoint II	3.39	4.37	1.385929291	6.53	2.62
W@Pjoint III	5.84	6.12	0.395979797	6.98	2.69
W@Pjoint IV	4.65	4.995	0.487903679	N/A	2.86
W@2joint III	3.63	4.815	1.675843071	6.42	2.46
W@2joint IV	4.43	5.09	0.933380951	6.2	2.29
W@3joint IV	4.14	4.5	0.509116882	6.02	1.84
LoPI,II	20.31	21.45	1.612203461	5.06	9.23
LoPII,II	22.9	24.24	1.895046174	16.13	10.66
LoPI,III	14.38	16.095	2.425376259	6.92	10.96
LoPII,III	18.23	17.35	1.244507935	5.79	8.51
LoPIII,III	16.71	17.535	1.166726189	20.03	14.05
LoPI,IV	22.33	24.24	2.701147904	N/A	8.72
LoPII,IV	14.31	13.805	0.714177849	8.25	8.62
LoPIII,IV	9.03	9.415	0.544472222	5.97	5.77
LoPIV,IV	12.62	15.095	3.500178567	12.12	7.54
WoTII	5.33	4.225	1.562705986	7.53	3.19
WoTIII	5.6	4.315	1.817264428	7.19	3.58
WoTIV	5.77	5.39	0.537401154	7.23	3.02
FLw/hal	N/A	N/A	0	75.42	N/A
FLw/out hal	78.92	81.52	3.676955262	48.9	42.44
Lotmt	80.09	78.605	2.10010714	81	35.62
Wotmt@prox	13.55	13.14	0.579827561	16.21	7.4
Wotmt@cond	9.63	10.185	0.784888527	13.23	6.31

Name	*Anas discors*	*Anas discors*	*Anas discors*	*Molothrus ater*	*Ardea alba*	*Calidris alba*	*Porzana carolina*
No	N/A	AVERAGE	STDEV	N/A	N/A	N/A	N/A
LoDI	6.14	6.97	1.17379726	10.33	40.04	N/A	10.47
w/claw	9.41	9.5		16.65	49.74	N/A	13.97
LoDII	25.27	24.825	0.62932504	11.38	60.58	10.52	27.86
w/claw	31.81	31.25		13.39	71.65	14.64	33.42
LoDIII	37.46	38.185	1.02530483	16.23	85.88	13.59	36.98
w/claw	45.45	45.935		19.5	95.45	17.35	45.41
LoDIV	37.32	34.715	3.68402633	14.44	74.61	11.78	30.95
w/claw	41.51	39.745		17.14	81.74	14.97	35.33
W@Pjoint II	2.44	2.53	0.12727922	1.5	6.05	1.68	2.28
W@Pjoint III	2.96	2.825	0.19091883	1.69	6.75	2.04	2.38
W@Pjoint IV	2.36	2.61	0.35355339	N/A	6.35	1.6	2.16
W@2joint III	2.39	2.425	0.04949747	1.62	5.71	1.92	1.88
W@2joint IV	2.22	2.255	0.04949747	1.45	5.48	1.35	1.93
W@3joint IV	1.91	1.875	0.04949747	1.29	4.33	1.2	1.65
LoPI,II	9.43	9.33	0.14142136	1.97	22.61	3.37	12.24
LoPII,II	10.81	10.735	0.10606602	4.42	18.61	3.02	9.34
LoPI,III	8.77	9.865	1.54856385	N/A	20.13	1.99	10.38
LoPII,III	4.98	6.745	2.49608694	5.01	24.4	1.83	8.63
LoPIII,III	10.37	12.21	2.60215295	8.24	14.43	1.85	7.95
LoPI,IV	6.34	7.53	1.68291414	N/A	14.99	2.96	6.58
LoPII,IV	6.09	7.355	1.78898016	2.31	12.9	1.14	4.85
LoPIII,IV	5.37	5.57	0.28284271	2.3	11.3	1.26	3.66
LoPIV,IV	7.26	7.4	0.1979899	5.25	6.4	1.37	4.87
WoTII	2.14	2.665	0.74246212	1.4	5.04	1.17	1.88
WoTIII	3.25	3.415	0.23334524	1.52	5.35	1.18	2.08
WoTIV	1.85	2.435	0.82731493	1.52	3.97	1.14	1.66
FLw/hal	N/A	N/A	0	29.87	110.03	N/A	52.38
FLw/out hal	40.86	41.65	1.11722871	18.37	92.22	18.14	41.36
Lotmt	31.83	33.725	2.6799347	32.63	147.11	26.06	34.93
Wotmt@prox	7.16	7.28	0.16970563	3.61	14.14	3.6	4.8
Wotmt@cond	6.81	6.56	0.35355339	3.9	17	4.23	5.53

Ethanol Specimens:

Name	*Cardinalis cardinalis*	*Anas discors*	*Zenaida macroura*	*Molothrus ater*	*Molothrus ater*	*Molothrus ater*
No	87491	47915	40398	48687	38843	AVERAGE
LoDI	10.18	7.99	10.06	10.52	10.48	10.5
w/claw	15.44	11.03	13.18	15.68	17.33	16.505
LoDII	9.27	25.92	14.8	12.66	11.78	12.22
w/claw	13.19	32.35	24.05	17.17	13.44	15.305
LoDIII	16.7	34.81	20.68	15.81	15.41	15.61
w/claw	21.84	41.97	24.05	19.78	19.43	19.605
LoDIV	11.52	32.46	13.69	12.86	14.53	13.695
w/claw	14.73	36.1	17.89	17.39	16.29	16.84
W@Pjoint II	1.55	2.77	2.22	1.53	1.93	1.73
W@Pjoint III	1.85	3.11	2.48	1.8	2.26	2.03
W@Pjoint IV	N/A	2.49	N/A	N/A	N/A	N/A
W@2joint III	1.76	3.39	2.19	1.4	1.98	1.69
W@2joint IV	1.33	2.67	2.17	1.75	1.79	1.77
W@3joint IV	1.27	2.46	1.76	1.58	1.65	1.615
LoPI,II	2.53	6.72	2.76	2.38	1.79	2.085
LoPII,II	5.73	11.52	8.64	7.68	8.19	7.935
LoPI,III	2.56	7.86	5.58	2.43	1.14	1.785
LoPII,III	2.94	5.38	5.75	2.87	3.41	3.14
LoPIII,III	7.06	11.95	6.24	8.68	9.12	8.9
LoPI,IV	1.8	7.35	1.22	1.64	1.43	1.535
LoPII,IV	2.71	5.37	2.27	2.15	1.99	2.07
LoPIII,IV	1.88	5.3	2.96	2.13	2.78	2.455
LoPIV,IV	4.27	8.45	6.3	4.95	5.93	5.44
WoTII	1.6	2.53	2.54	1.37	1.62	1.495
WoTIII	1.43	3.49	2.49	1.71	1.96	1.835
WoTIV	1.32	2.13	2.29	1.63	1.61	1.62
FLw/hal	28.22	N/A	N/A	N/A	N/A	N/A
FLw/out hal	17.15	41.73	24.31	20.36	19.71	20.035
Lotmt	31.09	34.26	27.52	28.48	29.88	29.18
Wotmt@prox	3.79	7.6	4.96	4.01	3.54	3.775
Wotmt@cond	4.25	6.9	6.04	4.84	4.87	4.855

Name	*Molothrus ater*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*	*Passer domesticus*
No	STDEV	46202	46198	46200	46192
LoDI	0.02828427	8.94	8.27	8.1	8.32
w/claw		13.5	13.83	13.26	13.21
LoDII	0.62225397	8.16	9.15	8.43	8.6
w/claw		11.52	13.23	11.49	12.59
LoDIII	0.28284271	14.03	14.52	13.57	14.24
w/claw		19.26	19.25	18.29	19.32
LoDIV	1.18086832	8.92	9.61	7.68	9.22
w/claw		12.31	13.42	10.35	12.8
W@Pjoint II	0.28284271	1.43	1.24	1.38	1.37
W@Pjoint III	0.32526912	1.74	1.7	1.64	1.78
W@Pjoint IV	0	N/A	N/A	N/A	N/A
W@2joint III	0.41012193	1.59	1.47	1.6	1.56
W@2joint IV	0.02828427	1.54	1.4	1.48	1.43
W@3joint IV	0.04949747	1.31	1.27	1.26	1.34
LoPI,II	0.417193	1.87	1.95	1.7	1.81
LoPII,II	0.36062446	5.87	5.26	4.51	5.15
LoPI,III	0.91216775	2.1	0.7	N/A	0.95
LoPII,III	0.38183766	3.05	2.25	2.61	2.68
LoPIII,III	0.31112698	7.03	6	6.41	6.79
LoPI,IV	0.14849242	0.73	1.16	1.01	N/A
LoPII,IV	0.11313708	1.9	2.08	1.62	2.49
LoPIII,IV	0.45961941	1.75	1.94	1.4	2
LoPIV,IV	0.69296465	4.06	3.42	3.32	3.27
WoTII	0.1767767	1.2	1.09	1.18	1.27
WoTIII	0.1767767	1.5	1.52	1.43	1.67
WoTIV	0.01414214	1.34	1.4	1.22	1.37
FLw/hal	0	26.36	23.65	N/A	25.52
FLw/out hal	0.45961941	17.22	16.21	13.44	16.8
Lotmt	0.98994949	19.54	19.48	20.58	18.83
Wotmt@prox	0.33234019	2.38	3.1	3.01	3.19
Wotmt@cond	0.0212132	1.36	3.33	3.17	3.45

Name	*Passer domesticus*	*Passer domesticus*	*Charadrius vociferus*	*Charadrius vociferus*	*Charadrius vociferus*
No	AVERAGE	STDEV	47937	48525	47936
LoDI	8.4075	0.367276009	N/A	N/A	N/A
w/claw	13.45		N/A	N/A	N/A
LoDII	8.585	0.417971291	13.97	14.32	12.37
w/claw	12.2075		18.34	17.49	16.67
LoDIII	14.09	0.400582909	20.57	20.96	19.8
w/claw	19.03		25.73	26.32	25.48
LoDIV	8.8575	0.834281128	16.07	16.91	16.96
w/claw	12.22		21.45	20.19	21.02
W@Pjoint II	1.355	0.081034972	1.86	1.77	2.01
W@Pjoint III	1.715	0.059721576	2.48	2.34	2.63
W@Pjoint IV	N/A	0	2.05	2.1	2.01
W@2joint III	1.555	0.059160798	2.06	1.9	2.11
W@2joint IV	1.4625	0.061305247	1.9	1.66	1.84
W@3joint IV	1.295	0.036968455	1.77	1.31	1.66
LoPI,II	1.8325	0.105316982	4.81	4.2	3.8
LoPII,II	5.1975	0.557098136	2.33	2.73	4.08
LoPI,III	1.25	0.746659226	1.46	3.37	3.59
LoPII,III	2.6475	0.327859218	2.56	2.78	3.29
LoPIII,III	6.5575	0.450878772	4.17	2.45	2.05
LoPI,IV	0.966666667	0.21825062	2.58	1.87	N/A
LoPII,IV	2.0225	0.36463452	1.59	1.38	2.21
LoPIII,IV	1.7725	0.270231382	1.13	3.45	2.73
LoPIV,IV	3.5175	0.367003633	2.31	3.81	1.25
WoTII	1.185	0.074161985	1.33	1.5	1.62
WoTIII	1.53	0.100995049	2.62	1.95	2.24
WoTIV	1.3325	0.078898669	1.71	1.3	1.44
FLw/hal	25.17666667	1.387239465	N/A	N/A	N/A
FLw/out hal	15.9175	1.702828529	26.31	24.47	25.32
Lotmt	19.6075	0.723665438	36.73	35.59	N/A
Wotmt@prox	2.92	0.367423461	5.18	5.36	5.16
Wotmt@cond	2.8275	0.98503384	5.01	4.11	5.03

Name	*Charadrius vociferus*	*Charadrius vociferus*	*Turdus migratorius*	*Turdus migratorius*	*Turdus migratorius*
No	AVERAGE	STDEV	49536	149534	49535
LoDI			10.74	12.89	11.08
w/claw			16.74	17.36	17.72
LoDII	13.55333333	1.039631345	12.77	12.08	13.51
w/claw	17.5		16.06	16.74	18.79
LoDIII	20.44333333	0.590282418	21.2	20.64	21.41
w/claw	25.84333333		26.93	28.9	28.01
LoDIV	16.64666667	0.500033332	13.66	12.41	14.19
w/claw	20.88666667		17.64	18.07	18.99
W@Pjoint II	1.88	0.121243557	2.06	1.7	2.07
W@Pjoint III	2.483333333	0.145028733	2.55	2.21	2.61
W@Pjoint IV	2.053333333	0.045092498	N/A	N/A	N/A
W@2joint III	2.023333333	0.109696551	2.22	2.08	2.21
W@2joint IV	1.8	0.12489996	1.65	1.87	2.02
W@3joint IV	1.58	0.240208243	1.57	1.48	1.64
LoPI,II	4.27	0.508625599	4.08	2.29	2.15
LoPII,II	3.046666667	0.916969647	7.79	7.34	7.63
LoPI,III	2.806666667	1.171423635	1.25	1.11	1.37
LoPII,III	2.876666667	0.374477414	5.16	5.55	4.66
LoPIII,III	2.89	1.126410227	9.67	9.46	9.97
LoPI,IV	2.225	0.502045815	1.19	1.42	1.58
LoPII,IV	1.726666667	0.431547603	2.27	2.28	2.58
LoPIII,IV	2.436666667	1.187490351	2.75	2.51	2.59
LoPIV,IV	2.456666667	1.286286645	6.31	5.23	5.47
WoTII	1.483333333	0.14571662	1.14	1.32	1.19
WoTIII	2.27	0.336005952	1.47	1.75	1.62
WoTIV	1.483333333	0.208406654	1.29	1.26	1.59
FLw/hal	N/A	0	N/A	34.68	35.57
FLw/out hal	25.36666667	0.920887253	23.97	23.24	24.42
Lotmt	36.16	0.806101731	38.13	35.45	26.06
Wotmt@prox	5.233333333	0.110151411	4.44	4.76	3.6
Wotmt@cond	4.716666667	0.525483904	4.35	4.59	4.23

Name	*Turdus migratorius*	*Turdus migratorius*	*Porzana carolina*	*Calidris alba*	*Calidris alba*
No	AVERAGE	STDEV	47925	38318	38939
LoDI	11.57	1.155724881	10.21	N/A	N/A
w/claw	17.27333333		15.34	N/A	N/A
LoDII	12.78666667	0.715145673	27.04	11.58	12.05
w/claw	17.19666667		35.26	14.64	15.25
LoDIII	21.08333333	0.398036849	37.34	15.22	15.07
w/claw	27.94666667		46.17	19.25	19.21
LoDIV	13.42	0.913947482	30.08	13.06	13.59
w/claw	18.23333333		37.53	15.9	15.89
W@Pjoint II	1.943333333	0.210792157	2	2.07	1.67
W@Pjoint III	2.456666667	0.215715862	2.62	1.83	2.34
W@Pjoint IV	N/A	0	2.06	1.65	1.63
W@2joint III	2.17	0.078102497	1.94	1.52	2
W@2joint IV	1.846666667	0.186100331	1.81	1.46	1.41
W@3joint IV	1.563333333	0.080208063	1.56	1.43	1.37
LoPI,II	2.84	1.076150547	10.05	3.2	2.3
LoPII,II	7.586666667	0.228108161	9.69	2.99	2.97
LoPI,III	1.243333333	0.130128142	7.49	2.9	1.29
LoPII,III	5.123333333	0.44613152	7.72	2.32	2.01
LoPIII,III	9.7	0.256320112	8.51	2.31	2.47
LoPI,IV	1.396666667	0.196044213	6.6	2.8	1.25
LoPII,IV	2.376666667	0.176162803	3.61	1.37	1.79
LoPIII,IV	2.616666667	0.122202019	3.19	1.14	1.37
LoPIV,IV	5.67	0.567097875	4.79	1.65	1.6
WoTII	1.216666667	0.092915732	1.52	1.35	1.18
WoTIII	1.613333333	0.140118997	2.26	1.27	1.25
WoTIV	1.38	0.182482876	1.63	1.26	1.22
FLw/hal	35.125	0.629325035	52.57	N/A	N/A
FLw/out hal	23.87666667	0.595510985	38.88	17.73	17.93
Lotmt	33.21333333	6.338235822	N/A	25.25	24.65
Wotmt@prox	4.266666667	0.599110452	5.2	3.6	3.6
Wotmt@cond	4.39	0.183303028	5.51	3.62	3.98

Name	*Calidris alba*	*Calidris alba*	*Calidris alba*	*Sitta canadensis*	*Sitta canadensis*
No	38.942	AVERAGE	STDEV	45213	37834
LoDI	N/A			10.25	11.26
w/claw	N/A			16.33	16.27
LoDII	12.82	12.15	0.626019169	8.42	7.05
w/claw	16.27	15.38666667		12.66	10.59
LoDIII	16.03	15.44	0.516430053	14.63	12.86
w/claw	20.33	19.59666667		19.92	16.31
LoDIV	14.17	13.60666667	0.555187656	11.16	9.78
w/claw	16.65	16.14666667		16.25	14.87
W@Pjoint II	1.72	1.82	0.217944947	1.15	1.32
W@Pjoint III	1.81	1.993333333	0.300388637	1.55	1.31
W@Pjoint IV	1.63	1.636666667	0.011547005	N/A	N/A
W@2joint III	1.63	1.716666667	0.25146239	1.45	1.55
W@2joint IV	1.57	1.48	0.081853528	1.24	1.18
W@3joint IV	1.49	1.43	0.06	1.19	1.18
LoPI,II	3.87	3.123333333	0.787802852	1.13	1.07
LoPII,II	4.37	3.443333333	0.802579176	4.75	4.81
LoPI,III	1.57	1.92	0.860174401	0.4	0.41
LoPII,III	1.77	2.033333333	0.275741425	4.03	3.43
LoPIII,III	2.73	2.503333333	0.211974841	7.29	7.1
LoPI,IV	1.88	1.976666667	0.779508392	0.31	0.83
LoPII,IV	1.65	1.603333333	0.213853532	1.27	1.34
LoPIII,IV	1.13	1.213333333	0.135769412	1.89	1.73
LoPIV,IV	1.65	1.633333333	0.028867513	5.12	4.48
WoTII	1.23	1.253333333	0.087368949	1.13	1.16
WoTIII	1.49	1.336666667	0.133166562	1.16	1.07
WoTIV	1.13	1.203333333	0.066583281	1.13	1.18
FLw/hal	N/A	N/A	0	27.02	26.61
FLw/out hal	17.5	17.72	0.215174348	15.59	14.44
Lotmt	25.44	25.11333333	0.412350983	20.1	17.05
Wotmt@prox	4.27	3.823333333	0.38682468	2.85	2.72
Wotmt@cond	4.32	3.973333333	0.350047616	3.98	3.36

Name	*Sitta canadensis*	*Sitta canadensis*	*Sitta canadensis*
No	38735	AVERAGE	STDEV
LoDI	11.47	10.99333333	0.6522525
w/claw	17.85	16.81666667	
LoDII	8.8	8.09	0.920489
w/claw	12.46	11.90333333	
LoDIII	13.67	13.72	0.8860587
w/claw	17.89	18.04	
LoDIV	10.69	10.54333333	0.7015934
w/claw	15.33	15.48333333	
W@Pjoint II	1.23	1.233333333	0.085049
W@Pjoint III	1.25	1.37	0.1587451
W@Pjoint IV	1.35	1.35	0
W@2joint III	1.5	1.5	0.05
W@2joint IV	1.2	1.206666667	0.0305505
W@3joint IV	1.18	1.183333333	0.0057735
LoPI,II	1.2	1.133333333	0.0650641
LoPII,II	5.71	5.09	0.5377732
LoPI,III	1.12	0.643333333	0.4128357
LoPII,III	4.43	3.963333333	0.5033223
LoPIII,III	6.93	7.106666667	0.1800926
LoPI,IV	0.66	0.6	0.2651415
LoPII,IV	1.36	1.323333333	0.0472582
LoPIII,IV	2.57	2.063333333	0.4460194
LoPIV,IV	4.94	4.846666667	0.3300505
WoTII	1.17	1.153333333	0.0208167
WoTIII	1.36	1.196666667	0.1484363
WoTIV	0.85	1.053333333	0.1778576
FLw/hal	26.76	26.79666667	0.2074448
FLw/out hal	15.99	15.34	0.8046738
Lotmt	15.88	17.67666667	2.178677
Wotmt@prox	2.5	2.69	0.1769181
Wotmt@cond	3.35	3.563333333	0.3608786

Appendix III

Descriptive Statistics: LoDI, LoDII, LoDIII, LoDIV, W@Pjoint II, ...

Variable	Name	N	N*	Mean	SE Mean	StDev
LoDI	Aechmorphorus occidental	0	5	*	*	*
	Aechmorphorus occidental	2	0	17.06	2.46	3.47
	Anas discors	4	0	6.765	0.197	0.393
	Anas discors (alcohol)	1	0	7.9900	*	*
	Anas discors (skin)	2	0	6.970	0.830	1.174
	Ardea alba	4	0	38.840	0.755	1.509
	Ardea alba (skin)	1	0	40.040	*	*
	Calidris alba	0	4	*	*	*
	Calidris alba (alcohol)	0	3	*	*	*
	Calidris alba (skin)	0	1	*	*	*
	Cepphus columba	0	4	*	*	*
	Chepphus columba (skin)	0	1	*	*	*
	Corvus corax	4	0	24.987	0.320	0.641
	Corvus corax (skin)	1	0	28.330	*	*
	Gavia pacifica	1	2	11.750	*	*
	Gavia pacifica (skin)	1	0	12.270	*	*
	Lecucophaeus pipixcan	2	2	3.305	0.335	0.474
	Lecucophaeus pipixcan (s	1	0	6.1900	*	*
	Meleagris gallopavo	4	0	20.197	0.379	0.759
	Meleagris gallopovo (ski	2	0	20.485	0.995	1.407
	Molothrus ater	4	0	9.890	0.347	0.695
	Molothrus ater (alcohol)	2	0	10.500	0.0200	0.0283
	Molothrus ater (skin)	1	0	10.330	*	*
	Passer domesticus	4	0	7.480	0.139	0.279
	Passer domesticus (alcoh	4	0	8.408	0.184	0.367
	Passer domesticus (skin)	6	0	8.138	0.397	0.973
	Porzana carolina	4	0	10.003	0.165	0.330
	Porzana carolina (alcoho	1	0	10.210	*	*
	Porzana carolina (skin)	1	0	10.470	*	*
	Sitta canadensis	4	0	8.303	0.121	0.242
	Sitta canadensis (alcoho	3	0	10.993	0.377	0.652
	Sitta canadensis (skin)	1	0	10.490	*	*
	Turdus migratorius	4	0	9.755	0.277	0.553
	Turdus migratorius (alco	3	0	11.570	0.667	1.156
	Turdus migratorius (skin	1	0	11.080	*	*
LoDII	Aechmorphorus occidental	5	0	52.24	1.47	3.28
	Aechmorphorus occidental	2	0	57.79	1.81	2.56
	Anas discors	4	0	24.725	0.414	0.827
	Anas discors (alcohol)	1	0	25.920	*	*
	Anas discors (skin)	2	0	24.825	0.445	0.629
	Ardea alba	4	0	67.88	1.28	2.57
	Ardea alba (skin)	1	0	60.580	*	*
	Calidris alba	4	0	11.078	0.128	0.256
	Calidris alba (alcohol)	3	0	12.150	0.361	0.626
	Calidris alba (skin)	1	0	10.520	*	*
	Cepphus columba	4	0	27.578	0.594	1.188
	Chepphus columba (skin)	1	0	35.770	*	*
	Corvus corax	4	0	29.605	0.576	1.152
	Corvus corax (skin)	1	0	28.550	*	*
	Gavia pacifica	2	1	64.945	0.515	0.728
	Gavia pacifica (skin)	1	0	69.230	*	*
	Lecucophaeus pipixcan	4	0	24.020	0.451	0.901
	Lecucophaeus pipixcan (s	1	0	22.010	*	*
	Meleagris gallopavo	4	0	50.555	0.812	1.623
	Meleagris gallopovo (ski	2	0	47.36	2.19	3.10
	Molothrus ater	4	0	11.852	0.330	0.659

	Molothrus ater (alcohol)	2	0	12.220	0.440	0.622
	Molothrus ater (skin)	1	0	11.380	*	*
	Passer domesticus	4	0	8.363	0.267	0.534
	Passer domesticus (alcoh	4	0	8.585	0.209	0.418
	Passer domesticus (skin)	6	0	8.665	0.370	0.906
	Porzana carolina	4	0	26.055	0.428	0.856
	Porzana carolina (alcoho	1	0	27.040	*	*
	Porzana carolina (skin)	1	0	27.860	*	*
	Sitta canadensis	4	0	6.8725	0.0927	0.1854
	Sitta canadensis (alcoho	3	0	8.090	0.531	0.920
	Sitta canadensis (skin)	1	0	6.1700	*	*
	Turdus migratorius	4	0	12.298	0.353	0.706
	Turdus migratorius (alco	3	0	12.787	0.413	0.715
	Turdus migratorius (skin	1	0	11.020	*	*
LoDIII	Aechmorphorus occidental	5	0	59.81	1.46	3.27
	Aechmorphorus occidental	2	0	61.735	0.755	1.068
	Anas discors	4	0	32.998	0.717	1.435
	Anas discors (alcohol)	1	0	34.810	*	*
	Anas discors (skin)	2	0	38.185	0.725	1.025
	Ardea alba	4	0	96.28	1.44	2.88
	Ardea alba (skin)	1	0	85.880	*	*
	Calidris alba	4	0	13.963	0.416	0.832
	Calidris alba (alcohol)	3	0	15.440	0.298	0.516
	Calidris alba (skin)	1	0	13.590	*	*
	Cepphus columba	4	0	37.712	0.398	0.796
	Chepphus columba (skin)	1	0	46.620	*	*
	Corvus corax	4	0	41.657	0.721	1.443
	Corvus corax (skin)	1	0	42.560	*	*
	Gavia pacifica	3	0	77.270	0.536	0.929
	Gavia pacifica (skin)	1	0	85.990	*	*
	Lecucophaeus pipixcan	4	0	31.222	0.620	1.240
	Lecucophaeus pipixcan (s	1	0	30.200	*	*
	Meleagris gallopavo	4	0	73.90	1.38	2.75
	Meleagris gallopovo (ski	2	0	72.77	2.30	3.25
	Molothrus ater	4	0	17.197	0.540	1.080
	Molothrus ater (alcohol)	2	0	15.610	0.200	0.283
	Molothrus ater (skin)	1	0	16.230	*	*
	Passer domesticus	4	0	14.170	0.390	0.780
	Passer domesticus (alcoh	4	0	14.090	0.200	0.401
	Passer domesticus (skin)	6	0	14.040	0.818	2.004
	Porzana carolina	4	0	33.343	0.526	1.053
	Porzana carolina (alcoho	1	0	37.340	*	*
	Porzana carolina (skin)	1	0	36.980	*	*
	Sitta canadensis	4	0	11.342	0.248	0.495
	Sitta canadensis (alcoho	3	0	13.720	0.512	0.886
	Sitta canadensis (skin)	1	0	12.980	*	*
	Turdus migratorius	4	0	19.915	0.360	0.720
	Turdus migratorius (alco	3	0	21.083	0.230	0.398
	Turdus migratorius (skin	1	0	16.120	*	*
LoDIV	Aechmorphorus occidental	5	0	66.61	1.94	4.34
	Aechmorphorus occidental	2	0	69.135	0.125	0.177
	Anas discors	4	0	32.055	0.874	1.747
	Anas discors (alcohol)	1	0	32.460	*	*
	Anas discors (skin)	2	0	34.72	2.60	3.68
	Ardea alba	4	0	83.44	1.70	3.39
	Ardea alba (skin)	1	0	74.610	*	*
	Calidris alba	4	0	12.938	0.643	1.285
	Calidris alba (alcohol)	3	0	13.607	0.321	0.555
	Calidris alba (skin)	1	0	11.780	*	*
	Cepphus columba	4	0	38.410	0.505	1.011
	Chepphus columba (skin)	1	0	42.740	*	*

	Corvus corax	4	0	31.837	0.364	0.728
	Corvus corax (skin)	1	0	33.180	*	*
	Gavia pacifica	3	0	83.267	0.613	1.061
	Gavia pacifica (skin)	1	0	91.390	*	*
	Lecucophaeus pipixcan	4	0	30.015	0.344	0.687
	Lecucophaeus pipixcan (s	1	0	30.200	*	*
	Meleagris gallopavo	4	0	58.02	1.74	3.47
	Meleagris gallopovo (ski	2	0	52.41	1.03	1.46
	Molothrus ater	4	0	13.205	0.458	0.915
	Molothrus ater (alcohol)	2	0	13.695	0.835	1.181
	Molothrus ater (skin)	1	0	14.440	*	*
	Passer domesticus	3	1	9.177	0.323	0.560
	Passer domesticus (alcoh	4	0	8.857	0.417	0.834
	Passer domesticus (skin)	6	0	9.313	0.310	0.760
	Porzana carolina	4	0	28.807	0.483	0.966
	Porzana carolina (alcoho	1	0	30.080	*	*
	Porzana carolina (skin)	1	0	30.950	*	*
	Sitta canadensis	4	0	8.750	0.173	0.346
	Sitta canadensis (alcoho	3	0	10.543	0.405	0.702
	Sitta canadensis (skin)	1	0	8.6100	*	*
	Turdus migratorius	4	0	13.463	0.321	0.642
	Turdus migratorius (alco	3	0	13.420	0.528	0.914
	Turdus migratorius (skin	1	0	9.7200	*	*
W@Pjoint II	Aechmorphorus occidental	5	0	4.578	0.123	0.275
	Aechmorphorus occidental	2	0	4.370	0.980	1.386
	Anas discors	4	0	1.9025	0.0534	0.1069
	Anas discors (alcohol)	1	0	2.7700	*	*
	Anas discors (skin)	2	0	2.5300	0.0900	0.1273
	Ardea alba	4	0	3.760	0.142	0.283
	Ardea alba (skin)	1	0	6.0500	*	*
	Calidris alba	4	0	1.1425	0.0144	0.0287
	Calidris alba (alcohol)	3	0	1.820	0.126	0.218
	Calidris alba (skin)	1	0	1.6800	*	*
	Cepphus columba	4	0	2.3325	0.0862	0.1723
	Chepphus columba (skin)	1	0	3.1000	*	*
	Corvus corax	4	0	3.9225	0.0813	0.1626
	Corvus corax (skin)	1	0	6.5300	*	*
	Gavia pacifica	2	1	3.4300	0.0800	0.1131
	Gavia pacifica (skin)	1	0	7.0600	*	*
	Lecucophaeus pipixcan	4	0	1.6650	0.0444	0.0889
	Lecucophaeus pipixcan (s	1	0	1.8200	*	*
	Meleagris gallopavo	4	0	6.625	0.351	0.703
	Meleagris gallopovo (ski	2	0	10.035	0.415	0.587
	Molothrus ater	4	0	1.1975	0.0680	0.1360
	Molothrus ater (alcohol)	2	0	1.730	0.200	0.283
	Molothrus ater (skin)	1	0	1.5000	*	*
	Passer domesticus	4	0	0.8975	0.0545	0.1090
	Passer domesticus (alcoh	4	0	1.3550	0.0405	0.0810
	Passer domesticus (skin)	6	0	1.2650	0.0311	0.0761
	Porzana carolina	4	0	1.3525	0.0468	0.0936
	Porzana carolina (alcoho	1	0	2.0000	*	*
	Porzana carolina (skin)	1	0	2.2800	*	*
	Sitta canadensis	4	0	0.6775	0.0125	0.0250
	Sitta canadensis (alcoho	3	0	1.2333	0.0491	0.0850
	Sitta canadensis (skin)	1	0	1.1700	*	*
	Turdus migratorius	4	0	1.258	0.116	0.231
	Turdus migratorius (alco	3	0	1.943	0.122	0.211
	Turdus migratorius (skin	1	0	1.9100	*	*
W@Pjoint III	Aechmorphorus occidental	5	0	4.232	0.135	0.301
	Aechmorphorus occidental	2	0	6.120	0.280	0.396
	Anas discors	4	0	2.6150	0.0598	0.1196

	Anas discors (alcohol)	1	0	3.1100	*	*
	Anas discors (skin)	2	0	2.825	0.135	0.191
	Ardea alba	4	0	4.418	0.121	0.242
	Ardea alba (skin)	1	0	6.7500	*	*
	Calidris alba	4	0	1.3975	0.0328	0.0655
	Calidris alba (alcohol)	3	0	1.993	0.173	0.300
	Calidris alba (skin)	1	0	2.0400	*	*
	Cepphus columba	4	0	2.6250	0.0323	0.0645
	Chepphus columba (skin)	1	0	3.6500	*	*
	Corvus corax	4	0	4.3225	0.0649	0.1297
	Corvus corax (skin)	1	0	6.9800	*	*
	Gavia pacifica	3	0	4.163	0.142	0.245
	Gavia pacifica (skin)	1	0	6.2000	*	*
	Lecucophaeus pipixcan	4	0	2.1700	0.0212	0.0424
	Lecucophaeus pipixcan (s	1	0	2.8100	*	*
	Meleagris gallopavo	4	0	8.07	1.19	2.39
	Meleagris gallopovo (ski	2	0	11.380	0.500	0.707
	Molothrus ater	4	0	1.2950	0.0556	0.1112
	Molothrus ater (alcohol)	2	0	2.030	0.230	0.325
	Molothrus ater (skin)	1	0	1.6900	*	*
	Passer domesticus	4	0	1.1650	0.0563	0.1127
	Passer domesticus (alcoh	4	0	1.7150	0.0299	0.0597
	Passer domesticus (skin)	6	0	1.4667	0.0324	0.0794
	Porzana carolina	4	0	1.6450	0.0829	0.1658
	Porzana carolina (alcoho	1	0	2.6200	*	*
	Porzana carolina (skin)	1	0	2.3800	*	*
	Sitta canadensis	4	0	0.8325	0.0243	0.0486
	Sitta canadensis (alcoho	3	0	1.3700	0.0917	0.1587
	Sitta canadensis (skin)	1	0	1.3100	*	*
	Turdus migratorius	4	0	1.6500	0.0344	0.0688
	Turdus migratorius (alco	3	0	2.457	0.125	0.216
	Turdus migratorius (skin	1	0	2.4600	*	*
W@Pjoint IV	Aechmorphorus occidental	5	0	4.542	0.166	0.372
	Aechmorphorus occidental	2	0	4.995	0.345	0.488
	Anas discors	4	0	2.1050	0.0701	0.1401
	Anas discors (alcohol)	1	0	2.4900	*	*
	Anas discors (skin)	2	0	2.610	0.250	0.354
	Ardea alba	4	0	4.3675	0.0699	0.1399
	Ardea alba (skin)	1	0	6.3500	*	*
	Calidris alba	4	0	1.2375	0.0269	0.0538
	Calidris alba (alcohol)	3	0	1.6367	0.00667	0.0115
	Calidris alba (skin)	1	0	1.6000	*	*
	Cepphus columba	4	0	2.3350	0.0957	0.1914
	Chepphus columba (skin)	1	0	2.7000	*	*
	Corvus corax	4	0	3.5475	0.0934	0.1868
	Corvus corax (skin)	0	1	*	*	*
	Gavia pacifica	3	0	3.880	0.205	0.356
	Gavia pacifica (skin)	0	1	*	*	*
	Lecucophaeus pipixcan	4	0	1.6925	0.0487	0.0974
	Lecucophaeus pipixcan (s	1	0	2.2100	*	*
	Meleagris gallopavo	4	0	7.125	0.113	0.226
	Meleagris gallopovo (ski	2	0	9.54	1.88	2.67
	Molothrus ater	4	0	1.1850	0.0330	0.0661
	Molothrus ater (alcohol)	0	2	*	*	*
	Molothrus ater (skin)	0	1	*	*	*
	Passer domesticus	4	0	0.9150	0.0717	0.1434
	Passer domesticus (alcoh	0	4	*	*	*
	Passer domesticus (skin)	1	5	1.5900	*	*
	Porzana carolina	4	0	1.5150	0.0524	0.1047
	Porzana carolina (alcoho	1	0	2.0600	*	*
	Porzana carolina (skin)	1	0	2.1600	*	*
	Sitta canadensis	4	0	0.6625	0.0193	0.0386

	Sitta canadensis (alcoho	1	2	1.3500	*	*
	Sitta canadensis (skin)	0	1	*	*	*
	Turdus migratorius	4	0	1.3850	0.0785	0.1570
	Turdus migratorius (alco	0	3	*	*	*
	Turdus migratorius (skin	1	0	2.2000	*	*
W@2joint III	Aechmorphorus occidental	5	0	4.820	0.141	0.316
	Aechmorphorus occidental	2	0	4.81	1.18	1.68
	Anas discors	4	0	1.9500	0.0367	0.0735
	Anas discors (alcohol)	1	0	3.3900	*	*
	Anas discors (skin)	2	0	2.4250	0.0350	0.0495
	Ardea alba	4	0	3.375	0.117	0.233
	Ardea alba (skin)	1	0	5.7100	*	*
	Calidris alba	4	0	1.1875	0.0175	0.0350
	Calidris alba (alcohol)	3	0	1.717	0.145	0.251
	Calidris alba (skin)	1	0	1.9200	*	*
	Cepphus columba	4	0	2.3500	0.0636	0.1273
	Chepphus columba (skin)	1	0	3.4200	*	*
	Corvus corax	4	0	3.8950	0.0375	0.0751
	Corvus corax (skin)	1	0	6.4200	*	*
	Gavia pacifica	3	0	3.383	0.130	0.226
	Gavia pacifica (skin)	1	0	6.1800	*	*
	Lecucophaeus pipixcan	4	0	1.8450	0.0366	0.0733
	Lecucophaeus pipixcan (s	1	0	2.8200	*	*
	Meleagris gallopavo	4	0	7.375	0.147	0.293
	Meleagris gallopovo (ski	2	0	9.970	0.410	0.580
	Molothrus ater	4	0	1.1425	0.0312	0.0624
	Molothrus ater (alcohol)	2	0	1.690	0.290	0.410
	Molothrus ater (skin)	1	0	1.6200	*	*
	Passer domesticus	4	0	0.9975	0.0878	0.1756
	Passer domesticus (alcoh	4	0	1.5550	0.0296	0.0592
	Passer domesticus (skin)	6	0	1.3000	0.0286	0.0701
	Porzana carolina	4	0	1.3125	0.0384	0.0768
	Porzana carolina (alcoho	1	0	1.9400	*	*
	Porzana carolina (skin)	1	0	1.8800	*	*
	Sitta canadensis	4	0	0.7750	0.0189	0.0379
	Sitta canadensis (alcoho	3	0	1.5000	0.0289	0.0500
	Sitta canadensis (skin)	1	0	1.4600	*	*
	Turdus migratorius	4	0	1.5500	0.0618	0.1236
	Turdus migratorius (alco	3	0	2.1700	0.0451	0.0781
	Turdus migratorius (skin	1	0	2.4000	*	*
W@2joint IV	Aechmorphorus occidental	5	0	4.308	0.123	0.274
	Aechmorphorus occidental	2	0	5.090	0.660	0.933
	Anas discors	4	0	1.6575	0.0477	0.0954
	Anas discors (alcohol)	1	0	2.6700	*	*
	Anas discors (skin)	2	0	2.2550	0.0350	0.0495
	Ardea alba	4	0	3.493	0.105	0.210
	Ardea alba (skin)	1	0	5.4800	*	*
	Calidris alba	4	0	1.0075	0.0401	0.0802
	Calidris alba (alcohol)	3	0	1.4800	0.0473	0.0819
	Calidris alba (skin)	1	0	1.3500	*	*
	Cepphus columba	4	0	1.9775	0.0987	0.1974
	Chepphus columba (skin)	1	0	2.6400	*	*
	Corvus corax	4	0	3.2600	0.0713	0.1426
	Corvus corax (skin)	1	0	6.2000	*	*
	Gavia pacifica	3	0	3.777	0.265	0.460
	Gavia pacifica (skin)	1	0	5.0900	*	*
	Lecucophaeus pipixcan	4	0	1.4375	0.0512	0.1024
	Lecucophaeus pipixcan (s	1	0	2.2000	*	*
	Meleagris gallopavo	4	0	6.1675	0.0712	0.1424
	Meleagris gallopovo (ski	2	0	8.625	0.715	1.011
	Molothrus ater	4	0	1.1575	0.0165	0.0330

	Molothrus ater (alcohol)	2	0	1.7700	0.0200	0.0283
	Molothrus ater (skin)	1	0	1.4500	*	*
	Passer domesticus	4	0	0.8025	0.0340	0.0680
	Passer domesticus (alcoh	4	0	1.4625	0.0307	0.0613
	Passer domesticus (skin)	6	0	1.2033	0.0422	0.1035
	Porzana carolina	4	0	1.2700	0.0430	0.0860
	Porzana carolina (alcoho	1	0	1.8100	*	*
	Porzana carolina (skin)	1	0	1.9300	*	*
	Sitta canadensis	4	0	0.6800	0.0204	0.0408
	Sitta canadensis (alcoho	3	0	1.2067	0.0176	0.0306
	Sitta canadensis (skin)	1	0	1.1200	*	*
	Turdus migratorius	4	0	1.3225	0.0706	0.1413
	Turdus migratorius (alco	3	0	1.847	0.107	0.186
	Turdus migratorius (skin	1	0	2.0400	*	*
W@3joint IV	Aechmorphorus occidental	5	0	4.1300	0.0609	0.1362
	Aechmorphorus occidental	2	0	4.500	0.360	0.509
	Anas discors	4	0	1.3775	0.0437	0.0873
	Anas discors (alcohol)	1	0	2.4600	*	*
	Anas discors (skin)	2	0	1.8750	0.0350	0.0495
	Ardea alba	4	0	2.8875	0.0823	0.1646
	Ardea alba (skin)	1	0	4.3300	*	*
	Calidris alba	4	0	0.8700	0.0238	0.0476
	Calidris alba (alcohol)	3	0	1.4300	0.0346	0.0600
	Calidris alba (skin)	1	0	1.2000	*	*
	Cepphus columba	4	0	1.6600	0.0356	0.0712
	Chepphus columba (skin)	1	0	2.5300	*	*
	Corvus corax	4	0	2.9575	0.0606	0.1212
	Corvus corax (skin)	1	0	6.0200	*	*
	Gavia pacifica	3	0	3.517	0.164	0.284
	Gavia pacifica (skin)	1	0	4.4200	*	*
	Lecucophaeus pipixcan	4	0	1.1875	0.0272	0.0544
	Lecucophaeus pipixcan (s	1	0	1.8400	*	*
	Meleagris gallopavo	4	0	5.5700	0.0829	0.1657
	Meleagris gallopovo (ski	2	0	7.740	0.280	0.396
	Molothrus ater	4	0	1.0425	0.0525	0.1050
	Molothrus ater (alcohol)	2	0	1.6150	0.0350	0.0495
	Molothrus ater (skin)	1	0	1.2900	*	*
	Passer domesticus	4	0	0.7925	0.0880	0.1759
	Passer domesticus (alcoh	4	0	1.2950	0.0185	0.0370
	Passer domesticus (skin)	6	0	1.2033	0.0226	0.0554
	Porzana carolina	4	0	1.1575	0.0229	0.0457
	Porzana carolina (alcoho	1	0	1.5600	*	*
	Porzana carolina (skin)	1	0	1.6500	*	*
	Sitta canadensis	4	0	0.6225	0.0111	0.0222
	Sitta canadensis (alcoho	3	0	1.1833	0.00333	0.00577
	Sitta canadensis (skin)	1	0	1.0500	*	*
	Turdus migratorius	4	0	1.1425	0.0328	0.0655
	Turdus migratorius (alco	3	0	1.5633	0.0463	0.0802
	Turdus migratorius (skin	1	0	1.7500	*	*
LoPhI,II	Aechmorphorus occidental	5	0	29.066	0.582	1.302
	Aechmorphorus occidental	2	0	21.45	1.14	1.61
	Anas discors	4	0	14.188	0.241	0.482
	Anas discors (alcohol)	1	0	6.7200	*	*
	Anas discors (skin)	2	0	9.330	0.100	0.141
	Ardea alba	4	0	39.295	0.480	0.960
	Ardea alba (skin)	1	0	22.610	*	*
	Calidris alba	4	0	6.255	0.175	0.350
	Calidris alba (alcohol)	3	0	3.123	0.455	0.788
	Calidris alba (skin)	1	0	3.3700	*	*
	Cepphus columba	4	0	15.038	0.281	0.562
	Chepphus columba (skin)	1	0	17.780	*	*

	Corvus corax	4	0	14.818	0.241	0.483
	Corvus corax (skin)	1	0	5.0600	*	*
	Gavia pacifica	3	0	42.700	0.174	0.302
	Gavia pacifica (skin)	1	0	27.230	*	*
	Lecucophaeus pipixcan	4	0	12.887	0.212	0.424
	Lecucophaeus pipixcan (s	1	0	6.2800	*	*
	Meleagris gallopavo	4	0	30.740	0.609	1.217
	Meleagris gallopovo (ski	2	0	16.440	0.600	0.849
	Molothrus ater	4	0	5.662	0.140	0.279
	Molothrus ater (alcohol)	2	0	2.085	0.295	0.417
	Molothrus ater (skin)	1	0	1.9700	*	*
	Passer domesticus	4	0	4.057	0.388	0.776
	Passer domesticus (alcoh	4	0	1.8325	0.0527	0.1053
	Passer domesticus (skin)	6	0	1.825	0.139	0.341
	Porzana carolina	4	0	14.908	0.264	0.529
	Porzana carolina (alcoho	1	0	10.050	*	*
	Porzana carolina (skin)	1	0	12.240	*	*
	Sitta canadensis	4	0	3.2400	0.0576	0.1152
	Sitta canadensis (alcoho	3	0	1.1333	0.0376	0.0651
	Sitta canadensis (skin)	1	0	1.2000	*	*
	Turdus migratorius	4	0	6.205	0.198	0.397
	Turdus migratorius (alco	3	0	2.840	0.621	1.076
	Turdus migratorius (skin	1	0	2.7800	*	*
LoPhII,II	Aechmorphorus occidental	5	0	23.75	1.60	3.58
	Aechmorphorus occidental	2	0	24.24	1.34	1.90
	Anas discors	4	0	10.625	0.247	0.494
	Anas discors (alcohol)	1	0	11.520	*	*
	Anas discors (skin)	2	0	10.735	0.0750	0.106
	Ardea alba	4	0	29.292	0.909	1.819
	Ardea alba (skin)	1	0	18.610	*	*
	Calidris alba	4	0	4.9075	0.0864	0.1729
	Calidris alba (alcohol)	3	0	3.443	0.463	0.803
	Calidris alba (skin)	1	0	3.0200	*	*
	Cepphus columba	4	0	13.170	0.276	0.553
	Chepphus columba (skin)	1	0	12.610	*	*
	Corvus corax	4	0	16.055	0.299	0.598
	Corvus corax (skin)	1	0	16.130	*	*
	Gavia pacifica	2	1	23.555	0.535	0.757
	Gavia pacifica (skin)	1	0	30.880	*	*
	Lecucophaeus pipixcan	4	0	11.333	0.0539	0.108
	Lecucophaeus pipixcan (s	1	0	12.320	*	*
	Meleagris gallopavo	4	0	21.720	0.523	1.046
	Meleagris gallopovo (ski	2	0	14.03	3.71	5.25
	Molothrus ater	4	0	6.283	0.264	0.527
	Molothrus ater (alcohol)	2	0	7.935	0.255	0.361
	Molothrus ater (skin)	1	0	4.4200	*	*
	Passer domesticus	4	0	4.7850	0.0710	0.1420
	Passer domesticus (alcoh	4	0	5.197	0.279	0.557
	Passer domesticus (skin)	6	0	5.077	0.243	0.596
	Porzana carolina	4	0	11.565	0.290	0.580
	Porzana carolina (alcoho	1	0	9.6900	*	*
	Porzana carolina (skin)	1	0	9.3400	*	*
	Sitta canadensis	4	0	3.7075	0.0844	0.1688
	Sitta canadensis (alcoho	3	0	5.090	0.310	0.538
	Sitta canadensis (skin)	1	0	5.3400	*	*
	Turdus migratorius	4	0	6.2000	0.0986	0.1971
	Turdus migratorius (alco	3	0	7.587	0.132	0.228
	Turdus migratorius (skin	1	0	4.5200	*	*
LoPhI,III	Aechmorphorus occidental	5	0	24.834	0.545	1.219
	Aechmorphorus occidental	2	0	16.09	1.71	2.43
	Anas discors	4	0	15.070	0.238	0.476

	Anas discors (alcohol)	1	0	7.8600	*	*
	Anas discors (skin)	2	0	9.87	1.10	1.55
	Ardea alba	4	0	35.108	0.359	0.717
	Ardea alba (skin)	1	0	20.130	*	*
	Calidris alba	4	0	6.188	0.230	0.459
	Calidris alba (alcohol)	3	0	1.920	0.497	0.860
	Calidris alba (skin)	1	0	1.9900	*	*
	Cepphus columba	4	0	16.330	0.245	0.490
	Chepphus columba (skin)	1	0	14.800	*	*
	Corvus corax	4	0	13.908	0.133	0.266
	Corvus corax (skin)	1	0	6.9200	*	*
	Gavia pacifica	3	0	36.153	0.347	0.602
	Gavia pacifica (skin)	1	0	27.880	*	*
	Lecucophaeus pipixcan	4	0	14.680	0.385	0.770
	Lecucophaeus pipixcan (s	1	0	13.030	*	*
	Meleagris gallopavo	4	0	33.552	0.748	1.496
	Meleagris gallopovo (ski	2	0	15.63	5.44	7.69
	Molothrus ater	4	0	5.543	0.137	0.273
	Molothrus ater (alcohol)	2	0	1.785	0.645	0.912
	Molothrus ater (skin)	0	1	*	*	*
	Passer domesticus	4	0	4.700	0.195	0.391
	Passer domesticus (alcoh	3	1	1.250	0.431	0.747
	Passer domesticus (skin)	6	0	1.618	0.152	0.371
	Porzana carolina	4	0	14.035	0.178	0.357
	Porzana carolina (alcoho	1	0	7.4900	*	*
	Porzana carolina (skin)	1	0	10.380	*	*
	Sitta canadensis	4	0	3.490	0.140	0.280
	Sitta canadensis (alcoho	3	0	0.643	0.238	0.413
	Sitta canadensis (skin)	1	0	2.4100	*	*
	Turdus migratorius	4	0	6.717	0.211	0.422
	Turdus migratorius (alco	3	0	1.2433	0.0751	0.1301
	Turdus migratorius (skin	1	0	2.5300	*	*
LoPhII,III	Aechmorphorus occidental	5	0	18.532	0.512	1.146
	Aechmorphorus occidental	2	0	17.350	0.880	1.245
	Anas discors	4	0	10.435	0.363	0.726
	Anas discors (alcohol)	1	0	5.3800	*	*
	Anas discors (skin)	2	0	6.75	1.76	2.50
	Ardea alba	4	0	37.413	0.496	0.992
	Ardea alba (skin)	1	0	24.400	*	*
	Calidris alba	4	0	4.5825	0.0863	0.1725
	Calidris alba (alcohol)	3	0	2.033	0.159	0.276
	Calidris alba (skin)	1	0	1.8300	*	*
	Cepphus columba	4	0	12.085	0.110	0.220
	Chepphus columba (skin)	1	0	10.250	*	*
	Corvus corax	4	0	13.650	0.269	0.539
	Corvus corax (skin)	1	0	5.7900	*	*
	Gavia pacifica	3	0	22.880	0.264	0.456
	Gavia pacifica (skin)	1	0	24.370	*	*
	Lecucophaeus pipixcan	4	0	9.535	0.185	0.370
	Lecucophaeus pipixcan (s	1	0	7.0100	*	*
	Meleagris gallopavo	4	0	24.453	0.361	0.721
	Meleagris gallopovo (ski	2	0	12.27	5.66	8.01
	Molothrus ater	4	0	5.472	0.189	0.378
	Molothrus ater (alcohol)	2	0	3.140	0.270	0.382
	Molothrus ater (skin)	1	0	5.0100	*	*
	Passer domesticus	4	0	4.8100	0.0780	0.1560
	Passer domesticus (alcoh	4	0	2.648	0.164	0.328
	Passer domesticus (skin)	6	0	3.220	0.285	0.699
	Porzana carolina	4	0	10.345	0.271	0.542
	Porzana carolina (alcoho	1	0	7.7200	*	*
	Porzana carolina (skin)	1	0	8.6300	*	*
	Sitta canadensis	4	0	3.7050	0.0307	0.0614

	Sitta canadensis (alcoho	3	0	3.963	0.291	0.503
	Sitta canadensis (skin)	1	0	1.8400	*	*
	Turdus migratorius	4	0	7.098	0.187	0.375
	Turdus migratorius (alco	3	0	5.123	0.258	0.446
	Turdus migratorius (skin	1	0	4.2300	*	*
LoPhIII,III	Aechmorphorus occidental	5	0	17.362	0.748	1.672
	Aechmorphorus occidental	2	0	17.535	0.825	1.167
	Anas discors	4	0	8.545	0.273	0.547
	Anas discors (alcohol)	1	0	11.950	*	*
	Anas discors (skin)	2	0	12.21	1.84	2.60
	Ardea alba	4	0	26.015	0.778	1.556
	Ardea alba (skin)	1	0	14.430	*	*
	Calidris alba	4	0	3.5775	0.0822	0.1644
	Calidris alba (alcohol)	3	0	2.503	0.122	0.212
	Calidris alba (skin)	1	0	1.8500	*	*
	Cepphus columba	4	0	10.885	0.253	0.505
	Chepphus columba (skin)	1	0	14.690	*	*
	Corvus corax	4	0	16.108	0.184	0.367
	Corvus corax (skin)	1	0	20.030	*	*
	Gavia pacifica	3	0	20.163	0.292	0.505
	Gavia pacifica (skin)	1	0	31.700	*	*
	Lecucophaeus pipixcan	4	0	7.803	0.279	0.558
	Lecucophaeus pipixcan (s	1	0	8.8800	*	*
	Meleagris gallopavo	4	0	19.355	0.473	0.947
	Meleagris gallopovo (ski	2	0	12.53	4.73	6.69
	Molothrus ater	4	0	6.065	0.319	0.639
	Molothrus ater (alcohol)	2	0	8.900	0.220	0.311
	Molothrus ater (skin)	1	0	8.2400	*	*
	Passer domesticus	4	0	5.258	0.154	0.309
	Passer domesticus (alcoh	4	0	6.558	0.225	0.451
	Passer domesticus (skin)	6	0	6.610	0.253	0.620
	Porzana carolina	4	0	9.407	0.278	0.557
	Porzana carolina (alcoho	1	0	8.5100	*	*
	Porzana carolina (skin)	1	0	7.9500	*	*
	Sitta canadensis	4	0	4.4375	0.0960	0.1921
	Sitta canadensis (alcoho	3	0	7.107	0.104	0.180
	Sitta canadensis (skin)	1	0	6.2300	*	*
	Turdus migratorius	4	0	7.3650	0.0887	0.1775
	Turdus migratorius (alco	3	0	9.700	0.148	0.256
	Turdus migratorius (skin	1	0	6.0500	*	*
LoPhI,IV	Aechmorphorus occidental	5	0	25.526	0.514	1.149
	Aechmorphorus occidental	2	0	24.24	1.91	2.70
	Anas discors	4	0	11.950	0.233	0.466
	Anas discors (alcohol)	1	0	7.3500	*	*
	Anas discors (skin)	2	0	7.53	1.19	1.68
	Ardea alba	4	0	28.005	0.631	1.262
	Ardea alba (skin)	1	0	14.990	*	*
	Calidris alba	4	0	4.803	0.148	0.297
	Calidris alba (alcohol)	3	0	1.977	0.450	0.780
	Calidris alba (skin)	1	0	2.9600	*	*
	Cepphus columba	4	0	12.922	0.157	0.314
	Chepphus columba (skin)	1	0	9.2000	*	*
	Corvus corax	4	0	8.938	0.196	0.393
	Corvus corax (skin)	0	1	*	*	*
	Gavia pacifica	3	0	30.703	0.250	0.432
	Gavia pacifica (skin)	1	0	24.780	*	*
	Lecucophaeus pipixcan	4	0	10.608	0.265	0.531
	Lecucophaeus pipixcan (s	1	0	10.770	*	*
	Meleagris gallopavo	4	0	23.623	0.448	0.896
	Meleagris gallopovo (ski	2	0	5.96	2.03	2.88
	Molothrus ater	4	0	3.212	0.164	0.328

	Molothrus ater (alcohol)	2	0	1.535	0.105	0.148
	Molothrus ater (skin)	0	1	*	*	*
	Passer domesticus	4	0	2.530	0.164	0.329
	Passer domesticus (alcoh	3	1	0.967	0.126	0.218
	Passer domesticus (skin)	0	6	*	*	*
	Porzana carolina	4	0	10.657	0.158	0.316
	Porzana carolina (alcoho	1	0	6.6000	*	*
	Porzana carolina (skin)	1	0	6.5800	*	*
	Sitta canadensis	4	0	2.353	0.142	0.284
	Sitta canadensis (alcoho	3	0	0.600	0.153	0.265
	Sitta canadensis (skin)	1	0	0.87000	*	*
	Turdus migratorius	4	0	3.650	0.274	0.549
	Turdus migratorius (alco	3	0	1.397	0.113	0.196
	Turdus migratorius (skin	1	0	2.3800	*	*
LoPhII,IV	Aechmorphorus occidental	5	0	13.482	0.466	1.041
	Aechmorphorus occidental	2	0	13.805	0.505	0.714
	Anas discors	4	0	8.232	0.358	0.717
	Anas discors (alcohol)	1	0	5.3700	*	*
	Anas discors (skin)	2	0	7.35	1.26	1.79
	Ardea alba	4	0	22.872	0.462	0.925
	Ardea alba (skin)	1	0	12.900	*	*
	Calidris alba	4	0	3.413	0.113	0.226
	Calidris alba (alcohol)	3	0	1.603	0.123	0.214
	Calidris alba (skin)	1	0	1.1400	*	*
	Cepphus columba	4	0	9.1575	0.0781	0.1563
	Chepphus columba (skin)	1	0	9.6200	*	*
	Corvus corax	4	0	7.863	0.157	0.314
	Corvus corax (skin)	1	0	8.2500	*	*
	Gavia pacifica	3	0	18.233	0.0994	0.172
	Gavia pacifica (skin)	1	0	15.230	*	*
	Lecucophaeus pipixcan	4	0	7.335	0.176	0.352
	Lecucophaeus pipixcan (s	1	0	7.2400	*	*
	Meleagris gallopavo	4	0	14.267	0.373	0.746
	Meleagris gallopovo (ski	2	0	10.470	0.750	1.061
	Molothrus ater	4	0	2.875	0.143	0.286
	Molothrus ater (alcohol)	2	0	2.0700	0.0800	0.1131
	Molothrus ater (skin)	1	0	2.3100	*	*
	Passer domesticus	4	0	2.470	0.114	0.228
	Passer domesticus (alcoh	4	0	2.023	0.182	0.365
	Passer domesticus (skin)	6	0	2.332	0.102	0.249
	Porzana carolina	4	0	6.897	0.143	0.285
	Porzana carolina (alcoho	1	0	3.6100	*	*
	Porzana carolina (skin)	1	0	4.8500	*	*
	Sitta canadensis	4	0	1.8700	0.00816	0.0163
	Sitta canadensis (alcoho	3	0	1.3233	0.0273	0.0473
	Sitta canadensis (skin)	1	0	1.6100	*	*
	Turdus migratorius	4	0	3.893	0.293	0.586
	Turdus migratorius (alco	3	0	2.377	0.102	0.176
	Turdus migratorius (skin	1	0	2.5700	*	*
LoPhIII,IV	Aechmorphorus occidental	5	0	13.024	0.512	1.145
	Aechmorphorus occidental	2	0	9.415	0.385	0.544
	Anas discors	4	0	6.245	0.411	0.822
	Anas discors (alcohol)	1	0	5.3000	*	*
	Anas discors (skin)	2	0	5.570	0.200	0.283
	Ardea alba	4	0	19.093	0.343	0.685
	Ardea alba (skin)	1	0	11.300	*	*
	Calidris alba	4	0	2.7100	0.0687	0.1374
	Calidris alba (alcohol)	3	0	1.2133	0.0784	0.1358
	Calidris alba (skin)	1	0	1.2600	*	*
	Cepphus columba	4	0	8.887	0.193	0.387
	Chepphus columba (skin)	1	0	8.7500	*	*

	Corvus corax	4	0	8.268	0.214	0.428
	Corvus corax (skin)	1	0	5.9700	*	*
	Gavia pacifica	3	0	16.697	0.303	0.525
	Gavia pacifica (skin)	1	0	16.880	*	*
	Lecucophaeus pipixcan	4	0	6.7900	0.0708	0.1417
	Lecucophaeus pipixcan (s	1	0	7.0900	*	*
	Meleagris gallopavo	4	0	11.952	0.514	1.028
	Meleagris gallopovo (ski	2	0	7.770	0.750	1.061
	Molothrus ater	4	0	3.033	0.164	0.329
	Molothrus ater (alcohol)	2	0	2.455	0.325	0.460
	Molothrus ater (skin)	1	0	2.3000	*	*
	Passer domesticus	4	0	2.6050	0.0838	0.1676
	Passer domesticus (alcoh	4	0	1.773	0.135	0.270
	Passer domesticus (skin)	6	0	1.8517	0.0863	0.2115
	Porzana carolina	4	0	5.555	0.255	0.511
	Porzana carolina (alcoho	1	0	3.1900	*	*
	Porzana carolina (skin)	1	0	3.6600	*	*
	Sitta canadensis	4	0	2.245	0.113	0.227
	Sitta canadensis (alcoho	3	0	2.063	0.258	0.446
	Sitta canadensis (skin)	1	0	1.6100	*	*
	Turdus migratorius	4	0	3.407	0.264	0.527
	Turdus migratorius (alco	3	0	2.6167	0.0706	0.1222
	Turdus migratorius (skin	1	0	2.5600	*	*
LoPhIV,IV	Aechmorphorus occidental	5	0	16.77	1.01	2.25
	Aechmorphorus occidental	2	0	15.09	2.48	3.50
	Anas discors	4	0	6.777	0.242	0.484
	Anas discors (alcohol)	1	0	8.4500	*	*
	Anas discors (skin)	2	0	7.400	0.140	0.198
	Ardea alba	4	0	16.383	0.419	0.839
	Ardea alba (skin)	1	0	6.4000	*	*
	Calidris alba	4	0	2.4725	0.0760	0.1520
	Calidris alba (alcohol)	3	0	1.6333	0.0167	0.0289
	Calidris alba (skin)	1	0	1.3700	*	*
	Cepphus columba	4	0	9.378	0.427	0.854
	Chepphus columba (skin)	1	0	10.320	*	*
	Corvus corax	4	0	9.705	0.210	0.420
	Corvus corax (skin)	1	0	12.120	*	*
	Gavia pacifica	3	0	19.347	0.258	0.446
	Gavia pacifica (skin)	1	0	24.040	*	*
	Lecucophaeus pipixcan	4	0	6.1200	0.0850	0.1701
	Lecucophaeus pipixcan (s	1	0	5.5800	*	*
	Meleagris gallopavo	4	0	13.588	0.491	0.982
	Meleagris gallopovo (ski	2	0	12.48	7.41	10.48
	Molothrus ater	4	0	4.070	0.147	0.294
	Molothrus ater (alcohol)	2	0	5.440	0.490	0.693
	Molothrus ater (skin)	1	0	5.2500	*	*
	Passer domesticus	4	0	2.5750	0.0998	0.1996
	Passer domesticus (alcoh	4	0	3.517	0.184	0.367
	Passer domesticus (skin)	6	0	3.462	0.275	0.673
	Porzana carolina	4	0	6.477	0.202	0.404
	Porzana carolina (alcoho	1	0	4.7900	*	*
	Porzana carolina (skin)	1	0	4.8700	*	*
	Sitta canadensis	4	0	3.0850	0.0260	0.0520
	Sitta canadensis (alcoho	3	0	4.847	0.191	0.330
	Sitta canadensis (skin)	1	0	4.8600	*	*
	Turdus migratorius	4	0	3.485	0.283	0.566
	Turdus migratorius (alco	3	0	5.670	0.327	0.567
	Turdus migratorius (skin	1	0	3.0800	*	*
Foot Length	Aechmorphorus occidental	5	0	74.21	2.06	4.60
	Aechmorphorus occidental	2	0	81.52	2.60	3.68
	Anas discors	4	0	39.98	1.30	2.60

	Anas discors (alcohol)	1	0	41.730	*	*
	Anas discors (skin)	2	0	41.650	0.790	1.117
	Ardea alba	4	0	108.37	1.41	2.82
	Ardea alba (skin)	1	0	92.220	*	*
	Calidris alba	3	1	16.927	0.579	1.003
	Calidris alba (alcohol)	3	0	17.720	0.124	0.215
	Calidris alba (skin)	1	0	18.140	*	*
	Cepphus columba	4	0	45.618	0.446	0.892
	Chepphus columba (skin)	1	0	46.250	*	*
	Corvus corax	4	0	48.875	0.605	1.210
	Corvus corax (skin)	1	0	48.900	*	*
	Gavia pacifica	3	0	94.84	1.35	2.34
	Gavia pacifica (skin)	1	0	102.80	*	*
	Lecucophaeus pipixcan	4	0	38.69	1.07	2.14
	Lecucophaeus pipixcan (s	1	0	38.360	*	*
	Meleagris gallopavo	4	0	100.58	1.57	3.14
	Meleagris gallopovo (ski	2	0	77.75	3.42	4.84
	Molothrus ater	3	1	19.347	0.847	1.467
	Molothrus ater (alcohol)	2	0	20.035	0.325	0.460
	Molothrus ater (skin)	1	0	18.370	*	*
	Passer domesticus	2	2	13.475	0.835	1.181
	Passer domesticus (alcoh	4	0	15.918	0.851	1.703
	Passer domesticus (skin)	5	1	15.846	0.314	0.701
	Porzana carolina	4	0	38.712	0.682	1.364
	Porzana carolina (alcoho	1	0	38.880	*	*
	Porzana carolina (skin)	1	0	41.360	*	*
	Sitta canadensis	4	0	12.910	0.319	0.638
	Sitta canadensis (alcoho	3	0	15.340	0.465	0.805
	Sitta canadensis (skin)	1	0	15.600	*	*
	Turdus migratorius	4	0	22.325	0.423	0.846
	Turdus migratorius (alco	3	0	23.877	0.344	0.596
	Turdus migratorius (skin	1	0	18.770	*	*
Lotmt	Aechmorphorus occidental	5	0	75.08	2.05	4.59
	Aechmorphorus occidental	2	0	78.61	1.48	2.10
	Anas discors	4	0	30.385	0.436	0.873
	Anas discors (alcohol)	1	0	34.260	*	*
	Anas discors (skin)	2	0	33.72	1.89	2.68
	Ardea alba	4	0	158.36	5.01	10.01
	Ardea alba (skin)	1	0	147.11	*	*
	Calidris alba	4	0	26.025	0.778	1.556
	Calidris alba (alcohol)	3	0	25.113	0.238	0.412
	Calidris alba (skin)	1	0	26.060	*	*
	Cepphus columba	4	0	34.820	0.266	0.531
	Chepphus columba (skin)	1	0	45.100	*	*
	Corvus corax	4	0	67.63	1.21	2.42
	Corvus corax (skin)	1	0	81.000	*	*
	Gavia pacifica	3	0	72.847	0.544	0.942
	Gavia pacifica (skin)	1	0	84.440	*	*
	Lecucophaeus pipixcan	4	0	43.807	0.885	1.770
	Lecucophaeus pipixcan (s	1	0	48.200	*	*
	Meleagris gallopavo	4	0	166.40	3.60	7.20
	Meleagris gallopovo (ski	2	0	138.0	10.0	14.2
	Molothrus ater	4	0	25.170	0.744	1.488
	Molothrus ater (alcohol)	2	0	29.180	0.700	0.990
	Molothrus ater (skin)	1	0	32.630	*	*
	Passer domesticus	4	0	19.058	0.195	0.389
	Passer domesticus (alcoh	4	0	19.607	0.362	0.724
	Passer domesticus (skin)	5	1	21.472	0.351	0.785
	Porzana carolina	4	0	33.295	0.680	1.360
	Porzana carolina (alcoho	0	1	*	*	*
	Porzana carolina (skin)	1	0	34.930	*	*
	Sitta canadensis	4	0	15.810	0.135	0.269

	Sitta canadensis (alcoho	3	0	17.68	1.26	2.18
	Sitta canadensis (skin)	1	0	22.300	*	*
	Turdus migratorius	4	0	33.325	0.291	0.582
	Turdus migratorius (alco	3	0	33.21	3.66	6.34
	Turdus migratorius (skin	1	0	32.800	*	*
Wotmt@prox	Aechmorphorus occidental	5	0	12.276	0.247	0.552
	Aechmorphorus occidental	2	0	13.140	0.410	0.580
	Anas discors	4	0	6.005	0.151	0.302
	Anas discors (alcohol)	1	0	7.6000	*	*
	Anas discors (skin)	2	0	7.280	0.120	0.170
	Ardea alba	4	0	12.340	0.340	0.680
	Ardea alba (skin)	1	0	14.140	*	*
	Calidris alba	4	0	3.7675	0.0470	0.0939
	Calidris alba (alcohol)	3	0	3.823	0.223	0.387
	Calidris alba (skin)	1	0	3.6000	*	*
	Cepphus columba	4	0	7.2050	0.0723	0.1446
	Chepphus columba (skin)	1	0	7.9600	*	*
	Corvus corax	4	0	12.100	0.170	0.340
	Corvus corax (skin)	1	0	16.210	*	*
	Gavia pacifica	3	0	12.253	0.0736	0.127
	Gavia pacifica (skin)	1	0	14.780	*	*
	Lecucophaeus pipixcan	4	0	6.7550	0.0413	0.0827
	Lecucophaeus pipixcan (s	1	0	5.4300	*	*
	Meleagris gallopavo	4	0	24.468	0.391	0.781
	Meleagris gallopovo (ski	1	1	22.380	*	*
	Molothrus ater	4	0	3.305	0.153	0.305
	Molothrus ater (alcohol)	2	0	3.775	0.235	0.332
	Molothrus ater (skin)	1	0	3.6100	*	*
	Passer domesticus	4	0	2.8250	0.0323	0.0645
	Passer domesticus (alcoh	4	0	2.920	0.184	0.367
	Passer domesticus (skin)	5	1	2.734	0.197	0.440
	Porzana carolina	4	0	4.3725	0.0857	0.1713
	Porzana carolina (alcoho	1	0	5.2000	*	*
	Porzana carolina (skin)	1	0	4.8000	*	*
	Sitta canadensis	4	0	2.1150	0.0425	0.0850
	Sitta canadensis (alcoho	3	0	2.690	0.102	0.177
	Sitta canadensis (skin)	1	0	1.8100	*	*
	Turdus migratorius	4	0	4.2225	0.0898	0.1797
	Turdus migratorius (alco	3	0	4.267	0.346	0.599
	Turdus migratorius (skin	1	0	4.7600	*	*
Wotmt@cond	Aechmorphorus occidental	5	0	9.374	0.207	0.464
	Aechmorphorus occidental	2	0	10.185	0.555	0.785
	Anas discors	4	0	6.005	0.241	0.482
	Anas discors (alcohol)	1	0	6.9000	*	*
	Anas discors (skin)	2	0	6.560	0.250	0.354
	Ardea alba	4	0	13.665	0.231	0.462
	Ardea alba (skin)	1	0	17.000	*	*
	Calidris alba	4	0	3.6100	0.0722	0.1445
	Calidris alba (alcohol)	3	0	3.973	0.202	0.350
	Calidris alba (skin)	1	0	4.2300	*	*
	Cepphus columba	4	0	6.718	0.178	0.356
	Chepphus columba (skin)	1	0	7.4400	*	*
	Corvus corax	4	0	8.7700	0.0871	0.1742
	Corvus corax (skin)	1	0	13.230	*	*
	Gavia pacifica	3	0	9.210	0.302	0.523
	Gavia pacifica (skin)	1	0	10.250	*	*
	Lecucophaeus pipixcan	4	0	6.107	0.175	0.349
	Lecucophaeus pipixcan (s	1	0	6.1300	*	*
	Meleagris gallopavo	4	0	23.373	0.413	0.827
	Meleagris gallopovo (ski	2	0	23.975	0.705	0.997
	Molothrus ater	4	0	3.035	0.415	0.830

Molothrus ater (alcohol)	2	0	4.8550	0.0150	0.0212
Molothrus ater (skin)	1	0	3.9000	*	*
Passer domesticus	4	0	2.1950	0.0403	0.0806
Passer domesticus (alcoh	4	0	2.828	0.493	0.985
Passer domesticus (skin)	5	1	3.252	0.123	0.275
Porzana carolina	4	0	4.585	0.162	0.323
Porzana carolina (alcoho	1	0	5.5100	*	*
Porzana carolina (skin)	1	0	5.5300	*	*
Sitta canadensis	4	0	1.6025	0.0359	0.0718
Sitta canadensis (alcoho	3	0	3.563	0.208	0.361
Sitta canadensis (skin)	1	0	3.7500	*	*
Turdus migratorius	4	0	3.795	0.297	0.594
Turdus migratorius (alco	3	0	4.390	0.106	0.183
Turdus migratorius (skin	1	0	4.5000	*	*

General Linear Model: LoDII, LoDIII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	2	Aechmorphorus occidentalis, Aechmorphorus occidentalis (skin)

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	43.972	43.972	43.972	4.42	0.089
Error	5	49.691	49.691	9.938		
Total	6	93.663				

S = 3.15250   R-Sq = 46.95%   R-Sq(adj) = 36.34%

Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	5.294	5.294	5.294	0.60	0.473
Error	5	43.977	43.977	8.795		
Total	6	49.271				

S = 2.96572   R-Sq = 10.74%   R-Sq(adj) = 0.00%

Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	9.14	9.14	9.14	0.61	0.472
Error	5	75.50	75.50	15.10		
Total	6	84.64				

S = 3.88588   R-Sq = 10.80%   R-Sq(adj) = 0.00%

Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.0618	0.0618	0.0618	0.14	0.725
Error	5	2.2231	2.2231	0.4446		
Total	6	2.2849				

S = 0.666795   R-Sq = 2.70%   R-Sq(adj) = 0.00%

Unusual Observations for W@Pjoint II

Obs	W@Pjoint II	Fit	SE Fit	Residual	St Resid
6	5.35000	4.37000	0.47150	0.98000	2.08 R
7	3.39000	4.37000	0.47150	-0.98000	-2.08 R

R denotes an observation with a large standardized residual.

Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	5.0922	5.0922	5.0922	48.94	0.001
Error	5	0.5203	0.5203	0.1041		
Total	6	5.6125				

S = 0.322577   R-Sq = 90.73%   R-Sq(adj) = 88.88%

Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.2932	0.2932	0.2932	1.85	0.232
Error	5	0.7911	0.7911	0.1582		
Total	6	1.0843				

S = 0.397776   R-Sq = 27.04%   R-Sq(adj) = 12.44%

Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.0000	0.0000	0.0000	0.00	0.994
Error	5	3.2071	3.2071	0.6414		
Total	6	3.2071				

S = 0.800881   R-Sq = 0.00%   R-Sq(adj) = 0.00%

Unusual Observations for W@2joint III

Obs	W@2joint III	Fit	SE Fit	Residual	St Resid
6	6.00000	4.81500	0.56631	1.18500	2.09 R
7	3.63000	4.81500	0.56631	-1.18500	-2.09 R

R denotes an observation with a large standardized residual.

Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.8736	0.8736	0.8736	3.73	0.111
Error	5	1.1719	1.1719	0.2344		
Total	6	2.0455				

```
S = 0.484124   R-Sq = 42.71%   R-Sq(adj) = 31.25%


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.19557  0.19557  0.19557  2.93  0.147
Error    5  0.33340  0.33340  0.06668
Total    6  0.52897


S = 0.258225   R-Sq = 36.97%   R-Sq(adj) = 24.37%


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  82.862  82.862  82.862  44.16  0.001
Error    5   9.382   9.382   1.876
Total    6  92.244


S = 1.36983   R-Sq = 89.83%   R-Sq(adj) = 87.79%


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1    0.35    0.35    0.35  0.03  0.866
Error    5   54.96   54.96   10.99
Total    6   55.31


S = 3.31544   R-Sq = 0.63%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhII,II

Obs  LoPhII,II      Fit  SE Fit  Residual  St Resid
  2    17.7400  23.7480  1.4827   -6.0080     -2.03 R

R denotes an observation with a large standardized residual.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  109.10  109.10  109.10  46.12  0.001
Error    5   11.83   11.83    2.37
Total    6  120.93


S = 1.53802   R-Sq = 90.22%   R-Sq(adj) = 88.26%


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   1.996   1.996   1.996  1.47  0.280
Error    5   6.798   6.798   1.360
Total    6   8.794
```

S = 1.16604   R-Sq = 22.70%   R-Sq(adj) = 7.23%

Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.043	0.043	0.043	0.02	0.901
Error	5	12.538	12.538	2.508		
Total	6	12.580				

S = 1.58352   R-Sq = 0.34%   R-Sq(adj) = 0.00%

Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	2.363	2.363	2.363	0.94	0.377
Error	5	12.578	12.578	2.516		
Total	6	14.941				

S = 1.58607   R-Sq = 15.81%   R-Sq(adj) = 0.00%

Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.1490	0.1490	0.1490	0.15	0.711
Error	5	4.8439	4.8439	0.9688		
Total	6	4.9930				

S = 0.984269   R-Sq = 2.99%   R-Sq(adj) = 0.00%

Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	18.607	18.607	18.607	16.80	0.009
Error	5	5.537	5.537	1.107		
Total	6	24.144				

S = 1.05229   R-Sq = 77.07%   R-Sq(adj) = 72.48%

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	4.027	4.027	4.027	0.62	0.467
Error	5	32.481	32.481	6.496		
Total	6	36.508				

S = 2.54875   R-Sq = 11.03%   R-Sq(adj) = 0.00%

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P

Name	1	76.34	76.34	76.34	3.88	0.106
Error	5	98.31	98.31	19.66		
Total	6	174.65				

S = 4.43422   R-Sq = 43.71%   R-Sq(adj) = 32.45%

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	17.71	17.71	17.71	1.00	0.364
Error	5	88.79	88.79	17.76		
Total	6	106.50				

S = 4.21400   R-Sq = 16.63%   R-Sq(adj) = 0.00%

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	1.0664	1.0664	1.0664	3.42	0.123
Error	5	1.5571	1.5571	0.3114		
Total	6	2.6235				

S = 0.558054   R-Sq = 40.65%   R-Sq(adj) = 28.78%

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.9396	0.9396	0.9396	3.18	0.135
Error	5	1.4768	1.4768	0.2954		
Total	6	2.4164				

S = 0.543465   R-Sq = 38.88%   R-Sq(adj) = 26.66%

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	57.790	A
Aechmorphorus occidentalis	5	52.242	A

Means that do not share a letter are significantly different.

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	5.548	2.638	2.103	0.0894

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	57.790	A
Aechmorphorus occidentalis	5	52.242	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	5.548	2.638	2.103	0.0894

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	61.735	A
Aechmorphorus occidentalis	5	59.810	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	1.925	2.481	0.7758	0.4729

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	61.735	A
Aechmorphorus occidentalis	5	59.810	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	1.925	2.481	0.7758	0.4730

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	69.135	A
Aechmorphorus occidentalis	5	66.606	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	2.529	3.251	0.7779	0.4718

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	69.135	A
Aechmorphorus occidentalis	5	66.606	A

Means that do not share a letter are significantly different.

```
Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of            Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)       2.529       3.251   0.7779    0.4718


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                               N   Mean  Grouping
Aechmorphorus occidentalis         5  4.578  A
Aechmorphorus occidentalis (skin)  2  4.370  A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of            Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)     -0.2080      0.5579  -0.3728    0.7246


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                               N   Mean  Grouping
Aechmorphorus occidentalis         5  4.578  A
Aechmorphorus occidentalis (skin)  2  4.370  A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of            Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)     -0.2080      0.5579  -0.3728    0.7246


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     III

Name                               N   Mean  Grouping
Aechmorphorus occidentalis (skin)  2  6.120  A
Aechmorphorus occidentalis         5  4.232    B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of            Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)       1.888      0.2699    6.996    0.0009


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name                               N   Mean  Grouping
Aechmorphorus occidentalis (skin)  2  6.120  A
Aechmorphorus occidentalis         5  4.232    B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	1.888	0.2699	6.996	0.0009

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	4.995	A
Aechmorphorus occidentalis	5	4.542	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.4530	0.3328	1.361	0.2316

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	4.995	A
Aechmorphorus occidentalis	5	4.542	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.4530	0.3328	1.361	0.2316

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	4.820	A
Aechmorphorus occidentalis (skin)	2	4.815	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-0.005000	0.6701	-0.007462	0.9943

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	4.820	A
Aechmorphorus occidentalis (skin)	2	4.815	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-0.005000	0.6701	-0.007462	0.9943

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	5.090	A
Aechmorphorus occidentalis	5	4.308	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.7820	0.4050	1.931	0.1114

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	5.090	A
Aechmorphorus occidentalis	5	4.308	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.7820	0.4050	1.931	0.1114

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	4.500	A
Aechmorphorus occidentalis	5	4.130	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.3700	0.2160	1.713	0.1475

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	4.500	A
Aechmorphorus occidentalis	5	4.130	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.3700	0.2160	1.713	0.1475

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	29.066	A
Aechmorphorus occidentalis (skin)	2	21.450	B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-7.616	1.146	-6.645	0.0012

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	29.066	A
Aechmorphorus occidentalis (skin)	2	21.450	B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-7.616	1.146	-6.645	0.0012

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	24.240	A
Aechmorphorus occidentalis	5	23.748	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.4920	2.774	0.1774	0.8662

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	24.240	A
Aechmorphorus occidentalis	5	23.748	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

```
Aechmorphorus occidentalis (skin)      0.4920       2.774   0.1774    0.8662


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name                               N    Mean  Grouping
Aechmorphorus occidentalis         5  24.834  A
Aechmorphorus occidentalis (skin)  2  16.095    B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of           Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)      -8.739       1.287   -6.791    0.0011


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name                               N    Mean  Grouping
Aechmorphorus occidentalis         5  24.834  A
Aechmorphorus occidentalis (skin)  2  16.095    B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of           Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)      -8.739       1.287   -6.791    0.0011


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     LoPhII,III

Name                               N    Mean  Grouping
Aechmorphorus occidentalis         5  18.532  A
Aechmorphorus occidentalis (skin)  2  17.350  A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of           Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)      -1.182      0.9756   -1.212    0.2798


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name                               N    Mean  Grouping
Aechmorphorus occidentalis         5  18.532  A
Aechmorphorus occidentalis (skin)  2  17.350  A

Means that do not share a letter are significantly different.


Name = Aechmorphorus occidentalis  subtracted from:

                                   Difference       SE of           Adjusted
Name                                 of Means  Difference  T-Value   P-Value
Aechmorphorus occidentalis (skin)      -1.182      0.9756   -1.212    0.2798
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	17.535	A
Aechmorphorus occidentalis	5	17.362	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.1730	1.325	0.1306	0.9012

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	17.535	A
Aechmorphorus occidentalis	5	17.362	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.1730	1.325	0.1306	0.9012

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	25.526	A
Aechmorphorus occidentalis (skin)	2	24.240	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-1.286	1.327	-0.9691	0.3770

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	25.526	A
Aechmorphorus occidentalis (skin)	2	24.240	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-1.286	1.327	-0.9691	0.3770

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	13.805	A
Aechmorphorus occidentalis	5	13.482	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.3230	0.8235	0.3922	0.7111

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	13.805	A
Aechmorphorus occidentalis	5	13.482	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.3230	0.8235	0.3922	0.7111

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	13.024	A
Aechmorphorus occidentalis (skin)	2	9.415	B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-3.609	0.8804	-4.099	0.0094

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	13.024	A
Aechmorphorus occidentalis (skin)	2	9.415	B

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-3.609	0.8804	-4.099	0.0094

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	16.774	A
Aechmorphorus occidentalis (skin)	2	15.095	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-1.679	2.132	-0.7874	0.4667

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Aechmorphorus occidentalis	5	16.774	A
Aechmorphorus occidentalis (skin)	2	15.095	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	-1.679	2.132	-0.7874	0.4667

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	81.520	A
Aechmorphorus occidentalis	5	74.210	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	7.310	3.710	1.970	0.1059

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	81.520	A
Aechmorphorus occidentalis	5	74.210	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	7.310	3.710	1.970	0.1059

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	78.605	A
Aechmorphorus occidentalis	5	75.084	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	3.521	3.526	0.9987	0.3638

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	78.605	A
Aechmorphorus occidentalis	5	75.084	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	3.521	3.526	0.9987	0.3638

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	13.140	A
Aechmorphorus occidentalis	5	12.276	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.8640	0.4669	1.850	0.1235

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	13.140	A
Aechmorphorus occidentalis	5	12.276	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.8640	0.4669	1.850	0.1235

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	10.185	A
Aechmorphorus occidentalis	5	9.374	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.8110	0.4547	1.784	0.1346

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Aechmorphorus occidentalis (skin)	2	10.185	A
Aechmorphorus occidentalis	5	9.374	A

Means that do not share a letter are significantly different.

Name = Aechmorphorus occidentalis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Aechmorphorus occidentalis (skin)	0.8110	0.4547	1.784	0.1346

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	3	Anas discors, Anas discors (alcohol), Anas discors (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.2028	1.2028	0.6014	1.31	0.366
Error	4	1.8421	1.8421	0.4605		
Total	6	3.0449				

S = 0.678620   R-Sq = 39.50%   R-Sq(adj) = 9.25%

Unusual Observations for LoDI

Obs	LoDI	Fit	SE Fit	Residual	St Resid	
7	7.99000	7.99000	0.67862	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.1700	1.1700	0.5850	0.96	0.458
Error	4	2.4498	2.4498	0.6124		
Total	6	3.6198				

S = 0.782584   R-Sq = 32.32%   R-Sq(adj) = 0.00%

Unusual Observations for LoDII

Obs	LoDII	Fit	SE Fit	Residual	St Resid
7	25.9200	25.9200	0.7826	0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	35.886	35.886	17.943	9.93	0.028
Error	4	7.226	7.226	1.807		
Total	6	43.112				

S = 1.34409   R-Sq = 83.24%   R-Sq(adj) = 74.86%

Unusual Observations for LoDIII

Obs	LoDIII	Fit	SE Fit	Residual	St Resid
7	34.8100	34.8100	1.3441	0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	9.633	9.633	4.816	0.85	0.493
Error	4	22.731	22.731	5.683		
Total	6	32.364				

S = 2.38384   R-Sq = 29.76%   R-Sq(adj) = 0.00%

Unusual Observations for LoDIV

Obs	LoDIV	Fit	SE Fit	Residual	St Resid
7	32.4600	32.4600	2.3838	0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.89650	0.89650	0.44825	35.52	0.003
Error	4	0.05048	0.05048	0.01262		
Total	6	0.94697				

S = 0.112333   R-Sq = 94.67%   R-Sq(adj) = 92.00%

```
Unusual Observations for W@Pjoint II

                                                St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  7      2.77000  2.77000  0.11233   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.21362  0.21362  0.10681  5.38  0.073
Error    4  0.07935  0.07935  0.01984
Total    6  0.29297


S = 0.140846   R-Sq = 72.92%   R-Sq(adj) = 59.37%


Unusual Observations for W@Pjoint III

     W@Pjoint                                St
Obs       III      Fit   SE Fit  Residual  Resid
  7   3.11000  3.11000  0.14085   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.38027  0.38027  0.19014  4.14  0.106
Error    4  0.18390  0.18390  0.04598
Total    6  0.56417


S = 0.214418   R-Sq = 67.40%   R-Sq(adj) = 51.11%


Unusual Observations for W@Pjoint IV

                                                St
Obs  W@Pjoint IV      Fit   SE Fit  Residual  Resid
  7      2.49000  2.49000  0.21442   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  1.70884  1.70884  0.85442  183.25  0.000
Error    4  0.01865  0.01865  0.00466
Total    6  1.72749


S = 0.0682825   R-Sq = 98.92%   R-Sq(adj) = 98.38%


Unusual Observations for W@2joint III
```

```
     W@2joint                                 St
Obs       III      Fit   SE Fit  Residual  Resid
  7   3.39000  3.39000  0.06828   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  1.04302  1.04302  0.52151  70.18  0.001
Error    4  0.02973  0.02973  0.00743
Total    6  1.07274


S = 0.0862047   R-Sq = 97.23%   R-Sq(adj) = 95.84%


Unusual Observations for W@2joint IV

                                                 St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  7      2.67000  2.67000  0.08620   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  1.05025  1.05025  0.52512  82.94  0.001
Error    4  0.02532  0.02532  0.00633
Total    6  1.07557


S = 0.0795692   R-Sq = 97.65%   R-Sq(adj) = 96.47%


Unusual Observations for W@3joint IV

                                                 St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  7      2.46000  2.46000  0.07957   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  60.777  60.777  30.389  169.56  0.000
Error    4   0.717   0.717   0.179
Total    6  61.494


S = 0.423342   R-Sq = 98.83%   R-Sq(adj) = 98.25%


Unusual Observations for LoPhI,II

                                            St
Obs  LoPhI,II     Fit  SE Fit  Residual  Resid
  7    6.7200  6.7200  0.4233   -0.0000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.6476	0.6476	0.3238	1.74	0.286
Error	4	0.7443	0.7443	0.1861		
Total	6	1.3920				

S = 0.431379   R-Sq = 46.53%   R-Sq(adj) = 19.79%

Unusual Observations for LoPhII,II

Obs	LoPhII,II	Fit	SE Fit	Residual	St Resid	
7	11.5200	11.5200	0.4314	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	61.816	61.816	30.908	40.18	0.002
Error	4	3.077	3.077	0.769		
Total	6	64.893				

S = 0.877019   R-Sq = 95.26%   R-Sq(adj) = 92.89%

Unusual Observations for LoPhI,III

Obs	LoPhI,III	Fit	SE Fit	Residual	St Resid	
7	7.8600	7.8600	0.8770	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	30.695	30.695	15.348	7.86	0.041
Error	4	7.811	7.811	1.953		
Total	6	38.506				

S = 1.39739   R-Sq = 79.72%   R-Sq(adj) = 69.57%

Unusual Observations for LoPhII,III

Obs	LoPhII,III	Fit	SE Fit	Residual	St Resid	
7	5.3800	5.3800	1.3974	-0.0000	*	X

X denotes an observation whose X value gives it large leverage.

```
Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  21.996  21.996  10.998  5.74  0.067
Error    4   7.667   7.667   1.917
Total    6  29.663


S = 1.38449   R-Sq = 74.15%   R-Sq(adj) = 61.23%


Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  7      11.9500  11.9500  1.3845    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  34.428  34.428  17.214  19.76  0.008
Error    4   3.484   3.484   0.871
Total    6  37.912


S = 0.933327   R-Sq = 90.81%   R-Sq(adj) = 86.21%


Unusual Observations for LoPhI,IV

                                            St
Obs  LoPhI,IV     Fit  SE Fit  Residual  Resid
  7    7.3500  7.3500  0.9333    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2   6.688   6.688   3.344  2.82  0.172
Error    4   4.741   4.741   1.185
Total    6  11.429


S = 1.08871   R-Sq = 58.52%   R-Sq(adj) = 37.78%


Unusual Observations for LoPhII,IV

                                               St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  7    5.37000  5.37000  1.08871   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests
```

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.0518	1.0518	0.5259	1.00	0.445
Error	4	2.1061	2.1061	0.5265		
Total	6	3.1579				

S = 0.725620   R-Sq = 33.31%   R-Sq(adj) = 0.00%

Unusual Observations for LoPhIII,IV

Obs	LoPhIII,IV	Fit	SE Fit	Residual	St Resid	
7	5.30000	5.30000	0.72562	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	2.3563	2.3563	1.1781	6.36	0.057
Error	4	0.7415	0.7415	0.1854		
Total	6	3.0978				

S = 0.430545   R-Sq = 76.06%   R-Sq(adj) = 64.10%

Unusual Observations for LoPhIV,IV

Obs	LoPhIV,IV	Fit	SE Fit	Residual	St Resid	
7	8.45000	8.45000	0.43054	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	4.910	4.910	2.455	0.46	0.664
Error	4	21.578	21.578	5.394		
Total	6	26.488				

S = 2.32258   R-Sq = 18.54%   R-Sq(adj) = 0.00%

Unusual Observations for Foot Length

Obs	Foot Length	Fit	SE Fit	Residual	St Resid	
7	41.7300	41.7300	2.3226	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	21.411	21.411	10.706	4.52	0.094
Error	4	9.466	9.466	2.367		

```
Total    6  30.878


S = 1.53837   R-Sq = 69.34%   R-Sq(adj) = 54.01%


Unusual Observations for Lotmt

                                            St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  7  34.2600  34.2600  1.5384    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  3.3408  3.3408  1.6704  22.06  0.007
Error    4  0.3029  0.3029  0.0757
Total    6  3.6437


S = 0.275182   R-Sq = 91.69%   R-Sq(adj) = 87.53%


Unusual Observations for Wotmt@prox

                                                St
Obs  Wotmt@prox      Fit   SE Fit  Residual  Resid
  7     7.60000  7.60000  0.27518   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.8428  0.8428  0.4214  2.05  0.244
Error    4  0.8221  0.8221  0.2055
Total    6  1.6649


S = 0.453349   R-Sq = 50.62%   R-Sq(adj) = 25.93%


Unusual Observations for Wotmt@cond

                                                St
Obs  Wotmt@cond      Fit   SE Fit  Residual  Resid
  7     6.90000  6.90000  0.45335   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name                    N   Mean  Grouping
Anas discors (alcohol)  1  7.990  A
Anas discors (skin)     2  6.970  A
Anas discors            4  6.765  A

Means that do not share a letter are significantly different.
```

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.2250	0.7587	1.6146	0.5451
Anas discors (skin)	0.2050	0.5877	0.3488	1.0000

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-1.020	0.8311	-1.227	0.8611

Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Anas discors (alcohol)	1	7.990	A
Anas discors (skin)	2	6.970	A
Anas discors	4	6.765	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.2250	0.7587	1.6146	0.3399
Anas discors (skin)	0.2050	0.5877	0.3488	0.9362

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-1.020	0.8311	-1.227	0.5003

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Anas discors (alcohol)	1	25.920	A
Anas discors (skin)	2	24.825	A
Anas discors	4	24.725	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.1950	0.8750	1.3658	0.7313
Anas discors (skin)	0.1000	0.6777	0.1475	1.0000

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-1.095	0.9585	-1.142	0.9510

```
Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                    N    Mean  Grouping
Anas discors (alcohol)  1  25.920  A
Anas discors (skin)     2  24.825  A
Anas discors            4  24.725  A

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of           Adjusted
Name                      of Means  Difference  T-Value   P-Value
Anas discors (alcohol)      1.1950      0.8750   1.3658    0.4373
Anas discors (skin)         0.1000      0.6777   0.1475    0.9881


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Anas discors (skin)      -1.095      0.9585   -1.142    0.5417


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name                    N    Mean  Grouping
Anas discors (skin)     2  38.185  A
Anas discors (alcohol)  1  34.810  A B
Anas discors            4  32.997    B

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of           Adjusted
Name                      of Means  Difference  T-Value   P-Value
Anas discors (alcohol)       1.813       1.503    1.206    0.8827
Anas discors (skin)          5.188       1.164    4.457    0.0336


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Anas discors (skin)       3.375       1.646    2.050    0.3290


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name                    N    Mean  Grouping
Anas discors (skin)     2  38.185  A
Anas discors (alcohol)  1  34.810  A B
Anas discors            4  32.997    B

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of           Adjusted
Name                      of Means  Difference  T-Value   P-Value
Anas discors (alcohol)       1.813       1.503    1.206    0.5104
Anas discors (skin)          5.188       1.164    4.457    0.0242
```

```
Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Anas discors (skin)       3.375       1.646    2.050    0.2160


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name                    N    Mean  Grouping
Anas discors (skin)     2  34.715  A
Anas discors (alcohol)  1  32.460  A
Anas discors            4  32.055  A

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of           Adjusted
Name                      of Means  Difference  T-Value   P-Value
Anas discors (alcohol)      0.4050       2.665   0.1520    1.0000
Anas discors (skin)         2.6600       2.064   1.2885    0.8012


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Anas discors (skin)       2.255       2.920   0.7724     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                    N    Mean  Grouping
Anas discors (skin)     2  34.715  A
Anas discors (alcohol)  1  32.460  A
Anas discors            4  32.055  A

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of           Adjusted
Name                      of Means  Difference  T-Value   P-Value
Anas discors (alcohol)      0.4050       2.665   0.1520    0.9874
Anas discors (skin)         2.6600       2.064   1.2885    0.4717


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Anas discors (skin)       2.255       2.920   0.7724    0.7378


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                    N   Mean  Grouping
Anas discors (alcohol)  1  2.770  A
Anas discors (skin)     2  2.530  A
```

Anas discors	4	1.902	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.8675	0.12559	6.907	0.0069
Anas discors (skin)	0.6275	0.09728	6.450	0.0089

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.2400	0.1376	-1.744	0.4681

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Anas discors (alcohol)	1	2.770	A
Anas discors (skin)	2	2.530	A
Anas discors	4	1.902	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.8675	0.12559	6.907	0.0051
Anas discors (skin)	0.6275	0.09728	6.450	0.0066

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.2400	0.1376	-1.744	0.2971

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Anas discors (alcohol)	1	3.110	A
Anas discors (skin)	2	2.825	A
Anas discors	4	2.615	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.4950	0.1575	3.143	0.1042
Anas discors (skin)	0.2100	0.1220	1.722	0.4807

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.2850	0.1725	-1.652	0.5215

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Anas discors (alcohol)	1	3.110	A
Anas discors (skin)	2	2.825	A
Anas discors	4	2.615	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.4950	0.1575	3.143	0.0730
Anas discors (skin)	0.2100	0.1220	1.722	0.3042

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.2850	0.1725	-1.652	0.3270

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Anas discors (skin)	2	2.610	A
Anas discors (alcohol)	1	2.490	A
Anas discors	4	2.105	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.3850	0.2397	1.606	0.5506
Anas discors (skin)	0.5050	0.1857	2.720	0.1590

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.1200	0.2626	0.4570	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Anas discors (skin)	2	2.610	A
Anas discors (alcohol)	1	2.490	A
Anas discors	4	2.105	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.3850	0.2397	1.606	0.3429
Anas discors (skin)	0.5050	0.1857	2.720	0.1094

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.1200	0.2626	0.4570	0.8942

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Anas discors (alcohol)	1	3.390	A
Anas discors (skin)	2	2.425	B
Anas discors	4	1.950	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.4400	0.07634	18.862	0.0001
Anas discors (skin)	0.4750	0.05913	8.033	0.0039

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.9650	0.08363	-11.54	0.0010

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Anas discors (alcohol)	1	3.390	A
Anas discors (skin)	2	2.425	B
Anas discors	4	1.950	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.4400	0.07634	18.862	0.0001
Anas discors (skin)	0.4750	0.05913	8.033	0.0029

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.9650	0.08363	-11.54	0.0007

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	2.670	A
Anas discors (skin)	2	2.255	A
Anas discors	4	1.658	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.0125	0.09638	10.505	0.0014
Anas discors (skin)	0.5975	0.07466	8.003	0.0040

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.4150	0.1056	-3.931	0.0513

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	2.670	A
Anas discors (skin)	2	2.255	B
Anas discors	4	1.658	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.0125	0.09638	10.505	0.0010
Anas discors (skin)	0.5975	0.07466	8.003	0.0029

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.4150	0.1056	-3.931	0.0367

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	2.460	A
Anas discors (skin)	2	1.875	B
Anas discors	4	1.377	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Difference	SE of	Adjusted

Name	of Means	Difference	T-Value	P-Value
Anas discors (alcohol)	1.0825	0.08896	12.168	0.0008
Anas discors (skin)	0.4975	0.06891	7.220	0.0059

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.5850	0.09745	-6.003	0.0116

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	2.460	A
Anas discors (skin)	2	1.875	B
Anas discors	4	1.377	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.0825	0.08896	12.168	0.0006
Anas discors (skin)	0.4975	0.06891	7.220	0.0043

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.5850	0.09745	-6.003	0.0085

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Anas discors	4	14.188	A
Anas discors (skin)	2	9.330	B
Anas discors (alcohol)	1	6.720	C

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-7.467	0.4733	-15.78	0.0003
Anas discors (skin)	-4.858	0.3666	-13.25	0.0006

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	2.610	0.5185	5.034	0.0219

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping

```
Anas discors            4  14.188  A
Anas discors (skin)     2   9.330    B
Anas discors (alcohol)  1   6.720      C

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of            Adjusted
Name                      of Means  Difference  T-Value    P-Value
Anas discors (alcohol)      -7.467      0.4733   -15.78     0.0002
Anas discors (skin)         -4.858      0.3666   -13.25     0.0004


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value    P-Value
Anas discors (skin)       2.610      0.5185    5.034     0.0159


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name                    N    Mean  Grouping
Anas discors (alcohol)  1  11.520  A
Anas discors (skin)     2  10.735  A
Anas discors            4  10.625  A

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of            Adjusted
Name                      of Means  Difference  T-Value    P-Value
Anas discors (alcohol)      0.8950      0.4823   1.8557     0.4112
Anas discors (skin)         0.1100      0.3736   0.2944     1.0000


Name = Anas discors (alcohol)  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value    P-Value
Anas discors (skin)     -0.7850      0.5283   -1.486     0.6345


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name                    N    Mean  Grouping
Anas discors (alcohol)  1  11.520  A
Anas discors (skin)     2  10.735  A
Anas discors            4  10.625  A

Means that do not share a letter are significantly different.

Name = Anas discors  subtracted from:

                        Difference       SE of            Adjusted
Name                      of Means  Difference  T-Value    P-Value
Anas discors (alcohol)      0.8950      0.4823   1.8557     0.2646
Anas discors (skin)         0.1100      0.3736   0.2944     0.9539


Name = Anas discors (alcohol)  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.7850	0.5283	-1.486	0.3877

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Anas discors	4	15.070	A
Anas discors (skin)	2	9.865	B
Anas discors (alcohol)	1	7.860	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-7.210	0.9805	-7.353	0.0055
Anas discors (skin)	-5.205	0.7595	-6.853	0.0071

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	2.005	1.074	1.867	0.4061

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Anas discors	4	15.070	A
Anas discors (skin)	2	9.865	B
Anas discors (alcohol)	1	7.860	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-7.210	0.9805	-7.353	0.0040
Anas discors (skin)	-5.205	0.7595	-6.853	0.0052

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	2.005	1.074	1.867	0.2616

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Anas discors	4	10.435	A
Anas discors (skin)	2	6.745	A
Anas discors (alcohol)	1	5.380	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-5.055	1.562	-3.236	0.0954
Anas discors (skin)	-3.690	1.210	-3.049	0.1142

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	1.365	1.711	0.7976	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Anas discors	4	10.435	A
Anas discors (skin)	2	6.745	A
Anas discors (alcohol)	1	5.380	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-5.055	1.562	-3.236	0.0670
Anas discors (skin)	-3.690	1.210	-3.049	0.0797

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	1.365	1.711	0.7976	0.7242

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Anas discors (skin)	2	12.210	A
Anas discors (alcohol)	1	11.950	A
Anas discors	4	8.545	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	3.405	1.548	2.200	0.2780
Anas discors (skin)	3.665	1.199	3.057	0.1133

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.2600	1.696	0.1533	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Anas discors (skin)	2	12.210	A
Anas discors (alcohol)	1	11.950	A
Anas discors	4	8.545	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	3.405	1.548	2.200	0.1849
Anas discors (skin)	3.665	1.199	3.057	0.0791

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.2600	1.696	0.1533	0.9872

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Anas discors	4	11.950	A
Anas discors (skin)	2	7.530	B
Anas discors (alcohol)	1	7.350	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-4.600	1.0435	-4.408	0.0348
Anas discors (skin)	-4.420	0.8083	-5.468	0.0163

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.1800	1.143	0.1575	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Anas discors	4	11.950	A
Anas discors (skin)	2	7.530	B
Anas discors (alcohol)	1	7.350	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-4.600	1.0435	-4.408	0.0251
Anas discors (skin)	-4.420	0.8083	-5.468	0.0119

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.1800	1.143	0.1575	0.9865

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Anas discors	4	8.232	A
Anas discors (skin)	2	7.355	A
Anas discors (alcohol)	1	5.370	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-2.862	1.2172	-2.352	0.2351
Anas discors (skin)	-0.878	0.9428	-0.931	1.0000

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	1.985	1.333	1.489	0.6324

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Anas discors	4	8.232	A
Anas discors (skin)	2	7.355	A
Anas discors (alcohol)	1	5.370	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-2.862	1.2172	-2.352	0.1582
Anas discors (skin)	-0.878	0.9428	-0.931	0.6522

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	1.985	1.333	1.489	0.3866

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping

Anas discors	4	6.245	A
Anas discors (skin)	2	5.570	A
Anas discors (alcohol)	1	5.300	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-0.9450	0.8113	-1.165	0.9264
Anas discors (skin)	-0.6750	0.6284	-1.074	1.0000

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.2700	0.8887	0.3038	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Anas discors	4	6.245	A
Anas discors (skin)	2	5.570	A
Anas discors (alcohol)	1	5.300	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	-0.9450	0.8113	-1.165	0.5306
Anas discors (skin)	-0.6750	0.6284	-1.074	0.5764

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	0.2700	0.8887	0.3038	0.9510

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	8.450	A
Anas discors (skin)	2	7.400	A
Anas discors	4	6.778	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.6725	0.4814	3.475	0.0764
Anas discors (skin)	0.6225	0.3729	1.670	0.5110

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-1.050	0.5273	-1.991	0.3518

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Anas discors (alcohol)	1	8.450	A
Anas discors (skin)	2	7.400	A
Anas discors	4	6.778	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.6725	0.4814	3.475	0.0541
Anas discors (skin)	0.6225	0.3729	1.670	0.3211

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-1.050	0.5273	-1.991	0.2297

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Anas discors (alcohol)	1	41.730	A
Anas discors (skin)	2	41.650	A
Anas discors	4	39.985	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.745	2.597	0.6720	1.000
Anas discors (skin)	1.665	2.011	0.8278	1.000

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.08000	2.845	-0.02812	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Anas discors (alcohol)	1	41.730	A
Anas discors (skin)	2	41.650	A
Anas discors	4	39.985	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.745	2.597	0.6720	0.7911
Anas discors (skin)	1.665	2.011	0.8278	0.7079

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.08000	2.845	-0.02812	0.9996

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Anas discors (alcohol)	1	34.260	A
Anas discors (skin)	2	33.725	A
Anas discors	4	30.385	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	3.875	1.720	2.253	0.2621
Anas discors (skin)	3.340	1.332	2.507	0.1988

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.5350	1.884	-0.2840	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Anas discors (alcohol)	1	34.260	A
Anas discors (skin)	2	33.725	A
Anas discors	4	30.385	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	3.875	1.720	2.253	0.1750
Anas discors (skin)	3.340	1.332	2.507	0.1351

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.5350	1.884	-0.2840	0.9570

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Anas discors (alcohol)	1	7.600	A
Anas discors (skin)	2	7.280	A
Anas discors	4	6.005	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.595	0.3077	5.184	0.0198
Anas discors (skin)	1.275	0.2383	5.350	0.0177

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.3200	0.3370	-0.9495	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Anas discors (alcohol)	1	7.600	A
Anas discors (skin)	2	7.280	A
Anas discors	4	6.005	B

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	1.595	0.3077	5.184	0.0144
Anas discors (skin)	1.275	0.2383	5.350	0.0129

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.3200	0.3370	-0.9495	0.6421

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Anas discors (alcohol)	1	6.900	A
Anas discors (skin)	2	6.560	A
Anas discors	4	6.005	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Difference	SE of	Adjusted

Name	of Means	Difference	T-Value	P-Value
Anas discors (alcohol)	0.8950	0.5069	1.766	0.4566
Anas discors (skin)	0.5550	0.3926	1.414	0.6911

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.3400	0.5552	-0.6124	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Anas discors (alcohol)	1	6.900	A
Anas discors (skin)	2	6.560	A
Anas discors	4	6.005	A

Means that do not share a letter are significantly different.

Name = Anas discors subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (alcohol)	0.8950	0.5069	1.766	0.2906
Anas discors (skin)	0.5550	0.3926	1.414	0.4170

Name = Anas discors (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Anas discors (skin)	-0.3400	0.5552	-0.6124	0.8216

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	2	Ardea alba, Ardea alba (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	1.152	1.152	1.152	0.51	0.528
Error	3	6.832	6.832	2.277		
Total	4	7.984				

S = 1.50906   R-Sq = 14.43%   R-Sq(adj) = 0.00%

Unusual Observations for LoDI

Obs	LoDI	Fit	SE Fit	Residual	St Resid	
5	40.0400	40.0400	1.5091	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDII, using Adjusted SS for Tests

```
Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  42.632  42.632  42.632  6.47  0.084
Error    3  19.773  19.773   6.591
Total    4  62.405


S = 2.56727   R-Sq = 68.32%   R-Sq(adj) = 57.75%


Unusual Observations for LoDII

                                            St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  60.5800  60.5800  2.5673   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF   Seq SS  Adj SS  Adj MS      F      P
Name     1   86.486  86.486  86.486  10.45  0.048
Error    3   24.828  24.828   8.276
Total    4  111.315


S = 2.87682   R-Sq = 77.70%   R-Sq(adj) = 70.26%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  85.8800  85.8800  2.8768    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   62.30   62.30   62.30  5.42  0.102
Error    3   34.52   34.52   11.51
Total    4   96.82


S = 3.39197   R-Sq = 64.35%   R-Sq(adj) = 52.47%


Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  74.6100  74.6100  3.3920    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.1953  4.1953  4.1953  52.27  0.005
```

```
Error    3  0.2408  0.2408  0.0803
Total    4  4.4361


S = 0.283314   R-Sq = 94.57%   R-Sq(adj) = 92.76%


Unusual Observations for W@Pjoint II

                                                St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      6.05000  6.05000  0.28331  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.3524  4.3524  4.3524  74.16  0.003
Error    3  0.1761  0.1761  0.0587
Total    4  4.5285


S = 0.242264   R-Sq = 96.11%   R-Sq(adj) = 94.82%


Unusual Observations for W@Pjoint III

     W@Pjoint                              St
Obs       III      Fit   SE Fit  Residual  Resid
  5   6.75000  6.75000  0.24226   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  3.1442  3.1442  3.1442  160.76  0.001
Error    3  0.0587  0.0587  0.0196
Total    4  3.2029


S = 0.139851   R-Sq = 98.17%   R-Sq(adj) = 97.56%


Unusual Observations for W@Pjoint IV

                                                St
Obs  W@Pjoint IV      Fit   SE Fit  Residual  Resid
  5      6.35000  6.35000  0.13985   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.3618  4.3618  4.3618  80.33  0.003
Error    3  0.1629  0.1629  0.0543
Total    4  4.5247
```

S = 0.233024   R-Sq = 96.40%   R-Sq(adj) = 95.20%

Unusual Observations for W@2joint III

Obs	W@2joint III	Fit	SE Fit	Residual	St Resid
5	5.71000	5.71000	0.23302	-0.00000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	3.1601	3.1601	3.1601	71.35	0.003
Error	3	0.1329	0.1329	0.0443		
Total	4	3.2930				

S = 0.210456   R-Sq = 95.96%   R-Sq(adj) = 94.62%

Unusual Observations for W@2joint IV

Obs	W@2joint IV	Fit	SE Fit	Residual	St Resid
5	5.48000	5.48000	0.21046	0.00000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	1.6646	1.6646	1.6646	61.44	0.004
Error	3	0.0813	0.0813	0.0271		
Total	4	1.7459				

S = 0.164595   R-Sq = 95.34%   R-Sq(adj) = 93.79%

Unusual Observations for W@3joint IV

Obs	W@3joint IV	Fit	SE Fit	Residual	St Resid
5	4.33000	4.33000	0.16460	0.00000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	222.71	222.71	222.71	241.82	0.001
Error	3	2.76	2.76	0.92		
Total	4	225.47				

S = 0.959670   R-Sq = 98.77%   R-Sq(adj) = 98.37%

```
Unusual Observations for LoPhI,II

                                                 St
Obs  LoPhI,II      Fit  SE Fit  Residual  Resid
  5   22.6100  22.6100  0.9597    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF   Seq SS  Adj SS  Adj MS      F      P
Name     1   91.293  91.293  91.293  27.60  0.013
Error    3    9.922   9.922   3.307
Total    4  101.215


S = 1.81865   R-Sq = 90.20%   R-Sq(adj) = 86.93%


Unusual Observations for LoPhII,II

                                                  St
Obs  LoPhII,II      Fit  SE Fit  Residual  Resid
  5    18.6100  18.6100  1.8187    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  179.46  179.46  179.46  348.63  0.000
Error    3    1.54    1.54    0.51
Total    4  181.00


S = 0.717467   R-Sq = 99.15%   R-Sq(adj) = 98.86%


Unusual Observations for LoPhI,III

                                                  St
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  5    20.1300  20.1300  0.7175    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  135.46  135.46  135.46  137.73  0.001
Error    3    2.95    2.95    0.98
Total    4  138.41


S = 0.991711   R-Sq = 97.87%   R-Sq(adj) = 97.16%


Unusual Observations for LoPhII,III
```

```
                                                    St
Obs  LoPhII,III      Fit  SE Fit  Residual  Resid
  5     24.4000  24.4000  0.9917    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  107.37  107.37  107.37  44.34  0.007
Error    3    7.26    7.26    2.42
Total    4  114.63


S = 1.55607   R-Sq = 93.66%   R-Sq(adj) = 91.55%


Unusual Observations for LoPhIII,III

                                                     St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  5      14.4300  14.4300  1.5561   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  135.51  135.51  135.51  85.05  0.003
Error    3    4.78    4.78    1.59
Total    4  140.29


S = 1.26229   R-Sq = 96.59%   R-Sq(adj) = 95.46%


Unusual Observations for LoPhI,IV

                                                  St
Obs  LoPhI,IV      Fit  SE Fit  Residual  Resid
  5   14.9900  14.9900  1.2623   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  79.561  79.561  79.561  93.01  0.002
Error    3   2.566   2.566   0.855
Total    4  82.127


S = 0.924856   R-Sq = 96.88%   R-Sq(adj) = 95.83%


Unusual Observations for LoPhII,IV

                                                   St
Obs  LoPhII,IV      Fit  SE Fit  Residual  Resid
  5    12.9000  12.9000  0.9249    0.0000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  48.578  48.578  48.578  103.48  0.002
Error    3   1.408   1.408   0.469
Total    4  49.987


S = 0.685146   R-Sq = 97.18%   R-Sq(adj) = 96.24%


Unusual Observations for LoPhIII,IV

                                                St
Obs  LoPhIII,IV      Fit  SE Fit  Residual  Resid
  5     11.3000  11.3000  0.6851    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  79.720  79.720  79.720  113.33  0.002
Error    3   2.110   2.110   0.703
Total    4  81.831


S = 0.838704   R-Sq = 97.42%   R-Sq(adj) = 96.56%


Unusual Observations for LoPhIV,IV

                                              St
Obs  LoPhIV,IV     Fit  SE Fit  Residual  Resid
  5     6.4000  6.4000  0.8387    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  208.66  208.66  208.66  26.21  0.014
Error    3   23.88   23.88    7.96
Total    4  232.54


S = 2.82148   R-Sq = 89.73%   R-Sq(adj) = 86.31%


Unusual Observations for Foot Length

       Foot                                  St
Obs  Length     Fit  SE Fit  Residual  Resid
  5  92.220  92.220   2.821     0.000      * X

X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	101.2	101.2	101.2	1.01	0.389
Error	3	300.7	300.7	100.2		
Total	4	401.9				

S = 10.0109   R-Sq = 25.18%   R-Sq(adj) = 0.25%

Unusual Observations for Lotmt

Obs	Lotmt	Fit	SE Fit	Residual	St Resid
5	147.110	147.110	10.011	0.000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	2.5920	2.5920	2.5920	5.61	0.099
Error	3	1.3860	1.3860	0.4620		
Total	4	3.9780				

S = 0.679706   R-Sq = 65.16%   R-Sq(adj) = 53.54%

Unusual Observations for Wotmt@prox

Obs	Wotmt@prox	Fit	SE Fit	Residual	St Resid
5	14.1400	14.1400	0.6797	0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	8.8978	8.8978	8.8978	41.65	0.008
Error	3	0.6409	0.6409	0.2136		
Total	4	9.5387				

S = 0.462205   R-Sq = 93.28%   R-Sq(adj) = 91.04%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid
5	17.0000	17.0000	0.4622	0.0000	* X

X denotes an observation whose X value gives it large leverage.

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

```
Name                N    Mean  Grouping
Ardea alba (skin)  1  40.040  A
Ardea alba          4  38.840  A

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of           Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)       1.200       1.687   0.7112    0.5282


Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name                N    Mean  Grouping
Ardea alba (skin)  1  40.040  A
Ardea alba          4  38.840  A

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of           Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)       1.200       1.687   0.7112    0.5283


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name                N    Mean  Grouping
Ardea alba          4  67.880  A
Ardea alba (skin)  1  60.580  A

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of           Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -7.300       2.870   -2.543    0.0844


Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                N    Mean  Grouping
Ardea alba          4  67.880  A
Ardea alba (skin)  1  60.580  A

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of           Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -7.300       2.870   -2.543    0.0844


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name                N    Mean  Grouping
Ardea alba          4  96.278  A
Ardea alba (skin)  1  85.880    B
```

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-10.40	3.216	-3.233	0.0481

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Ardea alba	4	96.278	A
Ardea alba (skin)	1	85.880	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-10.40	3.216	-3.233	0.0481

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Ardea alba	4	83.435	A
Ardea alba (skin)	1	74.610	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-8.825	3.792	-2.327	0.1024

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Ardea alba	4	83.435	A
Ardea alba (skin)	1	74.610	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-8.825	3.792	-2.327	0.1024

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.050	A
Ardea alba	4	3.760	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.290	0.3168	7.230	0.0055

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.050	A
Ardea alba	4	3.760	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.290	0.3168	7.230	0.0055

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.750	A
Ardea alba	4	4.418	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.332	0.2709	8.611	0.0033

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.750	A
Ardea alba	4	4.418	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.332	0.2709	8.611	0.0033

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.350	A
Ardea alba	4	4.367	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.982	0.1564	12.68	0.0011

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	6.350	A
Ardea alba	4	4.367	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.982	0.1564	12.68	0.0011

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Ardea alba (skin)	1	5.710	A
Ardea alba	4	3.375	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.335	0.2605	8.963	0.0029

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Ardea alba (skin)	1	5.710	A
Ardea alba	4	3.375	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	2.335	0.2605	8.963	0.0029

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	5.480	A
Ardea alba	4	3.492	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.988	0.2353	8.447	0.0035

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	5.480	A
Ardea alba	4	3.492	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.988	0.2353	8.447	0.0035

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	4.330	A
Ardea alba	4	2.888	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.442	0.1840	7.839	0.0043

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Ardea alba (skin)	1	4.330	A
Ardea alba	4	2.888	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.442	0.1840	7.839	0.0043

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Ardea alba	4	39.295	A
Ardea alba (skin)	1	22.610	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Difference	SE of		Adjusted

Name	of Means	Difference	T-Value	P-Value
Ardea alba (skin)	-16.68	1.073	-15.55	0.0006

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Ardea alba	4	39.295	A
Ardea alba (skin)	1	22.610	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-16.68	1.073	-15.55	0.0006

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Ardea alba	4	29.292	A
Ardea alba (skin)	1	18.610	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-10.68	2.033	-5.254	0.0134

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Ardea alba	4	29.292	A
Ardea alba (skin)	1	18.610	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-10.68	2.033	-5.254	0.0134

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Ardea alba	4	35.108	A
Ardea alba (skin)	1	20.130	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-14.98	0.8022	-18.67	0.0003

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Ardea alba	4	35.108	A
Ardea alba (skin)	1	20.130	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-14.98	0.8022	-18.67	0.0003

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Ardea alba	4	37.413	A
Ardea alba (skin)	1	24.400	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-13.01	1.109	-11.74	0.0013

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Ardea alba	4	37.413	A
Ardea alba (skin)	1	24.400	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-13.01	1.109	-11.74	0.0013

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Ardea alba	4	26.015	A
Ardea alba (skin)	1	14.430	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-11.58	1.740	-6.659	0.0069

```
Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name               N    Mean  Grouping
Ardea alba         4  26.015  A
Ardea alba (skin)  1  14.430    B

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of            Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -11.58       1.740   -6.659    0.0069


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name               N    Mean  Grouping
Ardea alba         4  28.005  A
Ardea alba (skin)  1  14.990    B

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of            Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -13.01       1.411   -9.222    0.0027


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name               N    Mean  Grouping
Ardea alba         4  28.005  A
Ardea alba (skin)  1  14.990    B

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of            Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -13.01       1.411   -9.222    0.0027


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name               N    Mean  Grouping
Ardea alba         4  22.873  A
Ardea alba (skin)  1  12.900    B

Means that do not share a letter are significantly different.

Name = Ardea alba  subtracted from:

                   Difference       SE of            Adjusted
Name                 of Means  Difference  T-Value   P-Value
Ardea alba (skin)      -9.973       1.034   -9.644    0.0024


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name               N    Mean  Grouping
```

Name	N	Mean	Grouping
Ardea alba	4	22.873	A
Ardea alba (skin)	1	12.900	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-9.973	1.034	-9.644	0.0024

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Ardea alba	4	19.093	A
Ardea alba (skin)	1	11.300	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-7.792	0.7660	-10.17	0.0020

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Ardea alba	4	19.093	A
Ardea alba (skin)	1	11.300	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-7.792	0.7660	-10.17	0.0020

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Ardea alba	4	16.383	A
Ardea alba (skin)	1	6.400	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-9.982	0.9377	-10.65	0.0018

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Ardea alba	4	16.383	A
Ardea alba (skin)	1	6.400	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-9.982	0.9377	-10.65	0.0018

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Ardea alba	4	108.370	A
Ardea alba (skin)	1	92.220	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-16.15	3.155	-5.120	0.0144

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Ardea alba	4	108.370	A
Ardea alba (skin)	1	92.220	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-16.15	3.155	-5.120	0.0144

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Ardea alba	4	158.358	A
Ardea alba (skin)	1	147.110	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-11.25	11.19	-1.005	0.3890

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Ardea alba	4	158.358	A
Ardea alba (skin)	1	147.110	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	-11.25	11.19	-1.005	0.3890

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Ardea alba (skin)	1	14.140	A
Ardea alba	4	12.340	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.800	0.7599	2.369	0.0986

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Ardea alba (skin)	1	14.140	A
Ardea alba	4	12.340	A

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	1.800	0.7599	2.369	0.0986

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Ardea alba (skin)	1	17.000	A
Ardea alba	4	13.665	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	3.335	0.5168	6.454	0.0075

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Ardea alba (skin)	1	17.000	A
Ardea alba	4	13.665	B

Means that do not share a letter are significantly different.

Name = Ardea alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Ardea alba (skin)	3.335	0.5168	6.454	0.0076

General Linear Model: LoDII, LoDIII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	3	Calidris alba, Calidris alba (alcohol), Calidris alba (skin)

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	2.8771	2.8771	1.4386	7.33	0.033
Error	5	0.9807	0.9807	0.1961		
Total	7	3.8578				

S = 0.442871   R-Sq = 74.58%   R-Sq(adj) = 64.41%

Unusual Observations for LoDII

Obs	LoDII	Fit	SE Fit	Residual	St Resid	
5	10.5200	10.5200	0.4429	-0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	4.6273	4.6273	2.3137	4.44	0.078
Error	5	2.6083	2.6083	0.5217		
Total	7	7.2356				

S = 0.722257   R-Sq = 63.95%   R-Sq(adj) = 49.53%

Unusual Observations for LoDIII

Obs	LoDIII	Fit	SE Fit	Residual	St Resid	
5	13.5900	13.5900	0.7223	-0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	2.593	2.593	1.296	1.16	0.385
Error	5	5.571	5.571	1.114		
Total	7	8.164				

S = 1.05557   R-Sq = 31.76%   R-Sq(adj) = 4.46%

```
Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  11.7800  11.7800  1.0556    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.84031  0.84031  0.42016  21.55  0.003
Error    5  0.09747  0.09747  0.01949
Total    7  0.93779


S = 0.139624   R-Sq = 89.61%   R-Sq(adj) = 85.45%


Unusual Observations for W@Pjoint II

Obs  W@Pjoint II      Fit   SE Fit  Residual  St Resid
  5      1.68000  1.68000  0.13962  -0.00000         * X
  6      2.07000  1.82000  0.08061   0.25000      2.19 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.73975  0.73975  0.36987  9.57  0.020
Error    5  0.19334  0.19334  0.03867
Total    7  0.93309


S = 0.196643   R-Sq = 79.28%   R-Sq(adj) = 70.99%


Unusual Observations for W@Pjoint III

     W@Pjoint
Obs       III      Fit   SE Fit  Residual  St Resid
  5   2.04000  2.04000  0.19664  -0.00000         * X
  7   2.34000  1.99333  0.11353   0.34667      2.16 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.30521  0.30521  0.15260  85.33  0.000
Error    5  0.00894  0.00894  0.00179
Total    7  0.31415


S = 0.0422887   R-Sq = 97.15%   R-Sq(adj) = 96.02%
```

Unusual Observations for W@Pjoint IV

Obs	W@Pjoint IV	Fit	SE Fit	Residual	St Resid	
5	1.60000	1.60000	0.04229	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.70381	0.70381	0.35190	13.52	0.010
Error	5	0.13014	0.13014	0.02603		
Total	7	0.83395				

S = 0.161333   R-Sq = 84.39%   R-Sq(adj) = 78.15%

Unusual Observations for W@2joint III

Obs	W@2joint III	Fit	SE Fit	Residual	St Resid	
5	1.92000	1.92000	0.16133	-0.00000	*	X
7	2.00000	1.71667	0.09315	0.28333	2.15	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.39988	0.39988	0.19994	30.59	0.002
Error	5	0.03268	0.03268	0.00654		
Total	7	0.43255				

S = 0.0808393   R-Sq = 92.45%   R-Sq(adj) = 89.42%

Unusual Observations for W@2joint IV

Obs	W@2joint IV	Fit	SE Fit	Residual	St Resid	
5	1.35000	1.35000	0.08084	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.54469	0.54469	0.27234	97.27	0.000
Error	5	0.01400	0.01400	0.00280		
Total	7	0.55869				

S = 0.0529150   R-Sq = 97.49%   R-Sq(adj) = 96.49%

Unusual Observations for W@3joint IV

Obs	W@3joint IV	Fit	SE Fit	Residual	St Resid	
5	1.20000	1.20000	0.05292	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	18.8954	18.8954	9.4477	29.35	0.002
Error	5	1.6094	1.6094	0.3219		
Total	7	20.5048				

S = 0.567339   R-Sq = 92.15%   R-Sq(adj) = 89.01%

Unusual Observations for LoPhI,II

Obs	LoPhI,II	Fit	SE Fit	Residual	St Resid	
5	3.37000	3.37000	0.56734	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	5.0642	5.0642	2.5321	9.19	0.021
Error	5	1.3779	1.3779	0.2756		
Total	7	6.4422				

S = 0.524965   R-Sq = 78.61%   R-Sq(adj) = 70.05%

Unusual Observations for LoPhII,II

Obs	LoPhII,II	Fit	SE Fit	Residual	St Resid	
5	3.02000	3.02000	0.52497	0.00000	*	X
8	4.37000	3.44333	0.30309	0.92667	2.16	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	36.129	36.129	18.064	42.75	0.001
Error	5	2.113	2.113	0.423		
Total	7	38.242				

S = 0.650058   R-Sq = 94.47%   R-Sq(adj) = 92.26%

Unusual Observations for LoPhI,III

```
                                                St
Obs  LoPhI,III      Fit   SE Fit  Residual  Resid
  5    1.99000  1.99000  0.65006   0.00000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS  Adj MS       F      P
Name     2  13.5510  13.5510  6.7755  140.37  0.000
Error    5   0.2413   0.2413  0.0483
Total    7  13.7924
```

S = 0.219701   R-Sq = 98.25%   R-Sq(adj) = 97.55%

Unusual Observations for LoPhII,III

```
                                                 St
Obs  LoPhII,III      Fit   SE Fit  Residual  Resid
  5     1.83000  1.83000  0.21970   0.00000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

```
Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  3.3829  3.3829  1.6915  49.48  0.001
Error    5  0.1709  0.1709  0.0342
Total    7  3.5539
```

S = 0.184901   R-Sq = 95.19%   R-Sq(adj) = 93.27%

Unusual Observations for LoPhIII,III

```
                                                  St
Obs  LoPhIII,III      Fit   SE Fit  Residual  Resid
  5      1.85000  1.85000  0.18490   0.00000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  14.0380  14.0380  7.0190  23.72  0.003
Error    5   1.4795   1.4795  0.2959
Total    7  15.5176
```

S = 0.543975   R-Sq = 90.47%   R-Sq(adj) = 86.65%

Unusual Observations for LoPhI,IV

```
                                               St
Obs  LoPhI,IV      Fit   SE Fit  Residual  Resid
```

```
  5   2.96000  2.96000  0.54397   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  7.5723  7.5723  3.7861  77.41  0.000
Error    5  0.2445  0.2445  0.0489
Total    7  7.8168


S = 0.221152   R-Sq = 96.87%   R-Sq(adj) = 95.62%


Unusual Observations for LoPhII,IV

                                                   St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  5    1.14000  1.14000  0.22115   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  4.4121  4.4121  2.2060  118.01  0.000
Error    5  0.0935  0.0935  0.0187
Total    7  4.5056


S = 0.136724   R-Sq = 97.93%   R-Sq(adj) = 97.10%


Unusual Observations for LoPhIII,IV

                                                    St
Obs  LoPhIII,IV      Fit   SE Fit  Residual  Resid
  5     1.26000  1.26000  0.13672   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  1.69006  1.69006  0.84503  59.56  0.000
Error    5  0.07094  0.07094  0.01419
Total    7  1.76100


S = 0.119115   R-Sq = 95.97%   R-Sq(adj) = 94.36%


Unusual Observations for LoPhIV,IV

                                                   St
Obs  LoPhIV,IV      Fit   SE Fit  Residual  Resid
  5    1.37000  1.37000  0.11911   0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

```
Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2   1.583   1.583   0.792  0.52  0.623
Error    5   7.603   7.603   1.521
Total    7   9.186


S = 1.23312   R-Sq = 17.24%   R-Sq(adj) = 0.00%


Unusual Observations for Lotmt

Obs    Lotmt      Fit  SE Fit  Residual  St Resid
  1  28.3500  26.0250  0.6166    2.3250      2.18 R
  5  26.0600  26.0600  1.2331    0.0000         * X

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.03741  0.03741  0.01870  0.29  0.762
Error    5  0.32574  0.32574  0.06515
Total    7  0.36315


S = 0.255242   R-Sq = 10.30%   R-Sq(adj) = 0.00%


Unusual Observations for Wotmt@prox

Obs  Wotmt@prox      Fit   SE Fit  Residual  St Resid
  5     3.60000  3.60000  0.25524   0.00000         * X
  8     4.27000  3.82333  0.14736   0.44667      2.14 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.41492  0.41492  0.20746  3.37  0.118
Error    5  0.30767  0.30767  0.06153
Total    7  0.72259


S = 0.248059   R-Sq = 57.42%   R-Sq(adj) = 40.39%


Unusual Observations for Wotmt@cond

                                                St
Obs  Wotmt@cond      Fit   SE Fit  Residual  Resid
  5     4.23000  4.23000  0.24806   0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	12.1500	A
Calidris alba	4	11.0775	A
Calidris alba (skin)	1	10.5200	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	1.0725	0.3382	3.171	0.0744
Calidris alba (skin)	-0.5575	0.4951	-1.126	0.9339

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-1.630	0.5114	-3.187	0.0730

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	12.1500	A
Calidris alba	4	11.0775	A
Calidris alba (skin)	1	10.5200	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	1.0725	0.3382	3.171	0.0547
Calidris alba (skin)	-0.5575	0.4951	-1.126	0.5408

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-1.630	0.5114	-3.187	0.0537

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	15.4400	A
Calidris alba	4	13.9625	A
Calidris alba (skin)	1	13.5900	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	1.4775	0.5516	2.6784	0.1317

Calidris alba (skin)	-0.3725	0.8075	-0.4613	1.0000

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-1.850	0.8340	-2.218	0.2319

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	15.4400	A
Calidris alba	4	13.9625	A
Calidris alba (skin)	1	13.5900	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	1.4775	0.5516	2.6784	0.0945
Calidris alba (skin)	-0.3725	0.8075	-0.4613	0.8917

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-1.850	0.8340	-2.218	0.1607

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	13.6067	A
Calidris alba	4	12.9375	A
Calidris alba (skin)	1	11.7800	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.669	0.8062	0.8300	1.000
Calidris alba (skin)	-1.158	1.1802	-0.9808	1.000

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-1.827	1.219	-1.499	0.5827

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	13.6067	A
Calidris alba	4	12.9375	A

```
Calidris alba (skin)     1  11.7800  A

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)       0.669      0.8062   0.8300    0.7026
Calidris alba (skin)         -1.158      1.1802  -0.9808    0.6188


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of            Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)      -1.827       1.219   -1.499    0.3671


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                     N    Mean  Grouping
Calidris alba (alcohol)  3  1.8200  A
Calidris alba (skin)     1  1.6800  A B
Calidris alba            4  1.1425    B

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.6775      0.1066    6.353    0.0043
Calidris alba (skin)         0.5375      0.1561    3.443    0.0551


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of            Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)     -0.1400      0.1612  -0.8684     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                     N    Mean  Grouping
Calidris alba (alcohol)  3  1.8200  A
Calidris alba (skin)     1  1.6800  A
Calidris alba            4  1.1425    B

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.6775      0.1066    6.353    0.0033
Calidris alba (skin)         0.5375      0.1561    3.443    0.0409


Name = Calidris alba (alcohol)  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.1400	0.1612	-0.8684	0.6812

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Calidris alba (skin)	1	2.0400	A B
Calidris alba (alcohol)	3	1.9933	A
Calidris alba	4	1.3975	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.5958	0.1502	3.967	0.0320
Calidris alba (skin)	0.6425	0.2199	2.922	0.0988

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.04667	0.2271	0.2055	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Calidris alba (skin)	1	2.0400	A B
Calidris alba (alcohol)	3	1.9933	A
Calidris alba	4	1.3975	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.5958	0.1502	3.967	0.0241
Calidris alba (skin)	0.6425	0.2199	2.922	0.0718

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.04667	0.2271	0.2055	0.9771

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	1.6367	A
Calidris alba (skin)	1	1.6000	A
Calidris alba	4	1.2375	B

Means that do not share a letter are significantly different.

```
Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Calidris alba (alcohol)      0.3992     0.03230   12.359     0.0002
Calidris alba (skin)         0.3625     0.04728    7.667     0.0018


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of            Adjusted
Name                    of Means  Difference  T-Value    P-Value
Calidris alba (skin)    -0.03667     0.04883  -0.7509      1.000


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name                     N    Mean  Grouping
Calidris alba (alcohol)  3  1.6367  A
Calidris alba (skin)     1  1.6000  A
Calidris alba            4  1.2375    B

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Calidris alba (alcohol)      0.3992     0.03230   12.359     0.0002
Calidris alba (skin)         0.3625     0.04728    7.667     0.0014


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of            Adjusted
Name                    of Means  Difference  T-Value    P-Value
Calidris alba (skin)    -0.03667     0.04883  -0.7509     0.7463


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     III

Name                     N    Mean  Grouping
Calidris alba (skin)     1  1.9200  A
Calidris alba (alcohol)  3  1.7167  A
Calidris alba            4  1.1875    B

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Calidris alba (alcohol)      0.5292      0.1232    4.294     0.0233
Calidris alba (skin)         0.7325      0.1804    4.061     0.0292


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of            Adjusted
Name                    of Means  Difference  T-Value    P-Value
Calidris alba (skin)      0.2033      0.1863    1.091     0.9745
```

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Calidris alba (skin)	1	1.9200	A
Calidris alba (alcohol)	3	1.7167	A
Calidris alba	4	1.1875	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.5292	0.1232	4.294	0.0177
Calidris alba (skin)	0.7325	0.1804	4.061	0.0220

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.2033	0.1863	1.091	0.5589

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	1.4800	A
Calidris alba (skin)	1	1.3500	A
Calidris alba	4	1.0075	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.4725	0.06174	7.653	0.0018
Calidris alba (skin)	0.3425	0.09038	3.790	0.0383

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.1300	0.09335	-1.393	0.6674

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	1.4800	A
Calidris alba (skin)	1	1.3500	A
Calidris alba	4	1.0075	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Difference	SE of	Adjusted

```
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.4725     0.06174    7.653    0.0014
Calidris alba (skin)         0.3425     0.09038    3.790    0.0287


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of           Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)     -0.1300     0.09335   -1.393    0.4118


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint
     IV

Name                     N    Mean  Grouping
Calidris alba (alcohol)  3  1.4300  A
Calidris alba (skin)     1  1.2000    B
Calidris alba            4  0.8700      C

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.5600     0.04041   13.856    0.0001
Calidris alba (skin)         0.3300     0.05916    5.578    0.0077


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of           Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)     -0.2300     0.06110   -3.764    0.0393


Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name                     N    Mean  Grouping
Calidris alba (alcohol)  3  1.4300  A
Calidris alba (skin)     1  1.2000    B
Calidris alba            4  0.8700      C

Means that do not share a letter are significantly different.

Name = Calidris alba  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.5600     0.04041   13.856    0.0001
Calidris alba (skin)         0.3300     0.05916    5.578    0.0059


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of           Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)     -0.2300     0.06110   -3.764    0.0295


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II
```

Name	N	Mean	Grouping
Calidris alba	4	6.2550	A
Calidris alba (skin)	1	3.3700	B
Calidris alba (alcohol)	3	3.1233	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-3.132	0.4333	-7.227	0.0024
Calidris alba (skin)	-2.885	0.6343	-4.548	0.0184

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.2467	0.6551	0.3765	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Calidris alba	4	6.2550	A
Calidris alba (skin)	1	3.3700	B
Calidris alba (alcohol)	3	3.1233	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-3.132	0.4333	-7.227	0.0019
Calidris alba (skin)	-2.885	0.6343	-4.548	0.0140

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.2467	0.6551	0.3765	0.9260

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Calidris alba	4	4.9075	A
Calidris alba (alcohol)	3	3.4433	B
Calidris alba (skin)	1	3.0200	A B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.464	0.4009	-3.652	0.0442
Calidris alba (skin)	-1.888	0.5869	-3.216	0.0707

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.4233	0.6062	-0.6984	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Calidris alba	4	4.9075	A
Calidris alba (alcohol)	3	3.4433	B
Calidris alba (skin)	1	3.0200	A B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.464	0.4009	-3.652	0.0330
Calidris alba (skin)	-1.888	0.5869	-3.216	0.0521

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.4233	0.6062	-0.6984	0.7749

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Calidris alba	4	6.1875	A
Calidris alba (skin)	1	1.9900	B
Calidris alba (alcohol)	3	1.9200	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-4.268	0.4965	-8.595	0.0011
Calidris alba (skin)	-4.198	0.7268	-5.775	0.0066

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.07000	0.7506	0.09326	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Calidris alba	4	6.1875	A
Calidris alba (skin)	1	1.9900	B
Calidris alba (alcohol)	3	1.9200	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-4.268	0.4965	-8.595	0.0008
Calidris alba (skin)	-4.198	0.7268	-5.775	0.0051

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.07000	0.7506	0.09326	0.9952

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Calidris alba	4	4.5825	A
Calidris alba (alcohol)	3	2.0333	B
Calidris alba (skin)	1	1.8300	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-2.549	0.1678	-15.19	0.0001
Calidris alba (skin)	-2.753	0.2456	-11.21	0.0003

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2033	0.2537	-0.8015	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Calidris alba	4	4.5825	A
Calidris alba (alcohol)	3	2.0333	B
Calidris alba (skin)	1	1.8300	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-2.549	0.1678	-15.19	0.0001
Calidris alba (skin)	-2.753	0.2456	-11.21	0.0002

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2033	0.2537	-0.8015	0.7184

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Calidris alba	4	3.5775	A
Calidris alba (alcohol)	3	2.5033	B
Calidris alba (skin)	1	1.8500	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.074	0.1412	-7.606	0.0019
Calidris alba (skin)	-1.728	0.2067	-8.356	0.0012

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.6533	0.2135	-3.060	0.0843

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Calidris alba	4	3.5775	A
Calidris alba (alcohol)	3	2.5033	B
Calidris alba (skin)	1	1.8500	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.074	0.1412	-7.606	0.0015
Calidris alba (skin)	-1.728	0.2067	-8.356	0.0009

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.6533	0.2135	-3.060	0.0617

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Calidris alba	4	4.8025	A
Calidris alba (skin)	1	2.9600	A B
Calidris alba (alcohol)	3	1.9767	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Difference	SE of	Adjusted

Name	of Means	Difference	T-Value	P-Value
Calidris alba (alcohol)	-2.826	0.4155	-6.802	0.0031
Calidris alba (skin)	-1.843	0.6082	-3.030	0.0873

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.9833	0.6281	1.565	0.5347

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Calidris alba	4	4.8025	A
Calidris alba (skin)	1	2.9600	A B
Calidris alba (alcohol)	3	1.9767	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-2.826	0.4155	-6.802	0.0024
Calidris alba (skin)	-1.843	0.6082	-3.030	0.0638

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.9833	0.6281	1.565	0.3409

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Calidris alba	4	3.4125	A
Calidris alba (alcohol)	3	1.6033	B
Calidris alba (skin)	1	1.1400	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.809	0.1689	-10.71	0.0004
Calidris alba (skin)	-2.273	0.2473	-9.19	0.0008

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.4633	0.2554	-1.814	0.3880

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping

Calidris alba	4	3.4125	A
Calidris alba (alcohol)	3	1.6033	B
Calidris alba (skin)	1	1.1400	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.809	0.1689	-10.71	0.0003
Calidris alba (skin)	-2.273	0.2473	-9.19	0.0006

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.4633	0.2554	-1.814	0.2570

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Calidris alba	4	2.7100	A
Calidris alba (skin)	1	1.2600	B
Calidris alba (alcohol)	3	1.2133	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.497	0.1044	-14.33	0.0001
Calidris alba (skin)	-1.450	0.1529	-9.49	0.0007

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.04667	0.1579	0.2956	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Calidris alba	4	2.7100	A
Calidris alba (skin)	1	1.2600	B
Calidris alba (alcohol)	3	1.2133	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-1.497	0.1044	-14.33	0.0001
Calidris alba (skin)	-1.450	0.1529	-9.49	0.0005

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.04667	0.1579	0.2956	0.9534

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Calidris alba	4	2.4725	A
Calidris alba (alcohol)	3	1.6333	B
Calidris alba (skin)	1	1.3700	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-0.839	0.09098	-9.224	0.0008
Calidris alba (skin)	-1.103	0.13317	-8.279	0.0013

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2633	0.1375	-1.915	0.3412

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Calidris alba	4	2.4725	A
Calidris alba (alcohol)	3	1.6333	B
Calidris alba (skin)	1	1.3700	B

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-0.839	0.09098	-9.224	0.0006
Calidris alba (skin)	-1.103	0.13317	-8.279	0.0010

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2633	0.1375	-1.915	0.2289

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Calidris alba (skin)	1	26.0600	A
Calidris alba	4	26.0250	A
Calidris alba (alcohol)	3	25.1133	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-0.9117	0.9418	-0.9680	1.000
Calidris alba (skin)	0.0350	1.3787	0.0254	1.000

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.9467	1.424	0.6648	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Calidris alba (skin)	1	26.0600	A
Calidris alba	4	26.0250	A
Calidris alba (alcohol)	3	25.1133	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	-0.9117	0.9418	-0.9680	0.6259
Calidris alba (skin)	0.0350	1.3787	0.0254	0.9996

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.9467	1.424	0.6648	0.7927

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	3.8233	A
Calidris alba	4	3.7675	A
Calidris alba (skin)	1	3.6000	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.0558	0.1949	0.2864	1.000
Calidris alba (skin)	-0.1675	0.2854	-0.5870	1.000

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2233	0.2947	-0.7578	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Calidris alba (alcohol)	3	3.8233	A
Calidris alba	4	3.7675	A
Calidris alba (skin)	1	3.6000	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.0558	0.1949	0.2864	0.9562
Calidris alba (skin)	-0.1675	0.2854	-0.5870	0.8328

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	-0.2233	0.2947	-0.7578	0.7426

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Calidris alba (skin)	1	4.2300	A
Calidris alba (alcohol)	3	3.9733	A
Calidris alba	4	3.6100	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (alcohol)	0.3633	0.1895	1.918	0.3398
Calidris alba (skin)	0.6200	0.2773	2.236	0.2269

Name = Calidris alba (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Calidris alba (skin)	0.2567	0.2864	0.8961	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Calidris alba (skin)	1	4.2300	A
Calidris alba (alcohol)	3	3.9733	A
Calidris alba	4	3.6100	A

Means that do not share a letter are significantly different.

Name = Calidris alba subtracted from:

	Difference	SE of		Adjusted

```
Name                       of Means  Difference  T-Value   P-Value
Calidris alba (alcohol)      0.3633      0.1895    1.918    0.2280
Calidris alba (skin)         0.6200      0.2773    2.236    0.1575


Name = Calidris alba (alcohol)  subtracted from:

                      Difference       SE of           Adjusted
Name                    of Means  Difference  T-Value   P-Value
Calidris alba (skin)      0.2567      0.2864   0.8961    0.6658
```

General Linear Model: LoDII, LoDIII, ... versus Name

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Factor  Type   Levels  Values
Name    fixed       2  Cepphus columba, Chepphus columba (skin)


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  53.694  53.694  53.694  38.02  0.009
Error    3   4.236   4.236   1.412
Total    4  57.930


S = 1.18831   R-Sq = 92.69%   R-Sq(adj) = 90.25%


Unusual Observations for LoDII

                                            St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  35.7700  35.7700  1.1883    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  63.475  63.475  63.475  100.21  0.002
Error    3   1.900   1.900   0.633
Total    4  65.375


S = 0.795880   R-Sq = 97.09%   R-Sq(adj) = 96.12%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  46.6200  46.6200  0.7959    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  14.999  14.999  14.999  14.68  0.031
Error    3   3.064   3.064   1.021
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Total    4  18.064


S = 1.01068   R-Sq = 83.04%   R-Sq(adj) = 77.38%


Unusual Observations for LoDIV

                                               St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  42.7400  42.7400  1.0107    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.47125  0.47125  0.47125  15.87  0.028
Error    3  0.08908  0.08908  0.02969
Total    4  0.56032


S = 0.172313   R-Sq = 84.10%   R-Sq(adj) = 78.80%


Unusual Observations for W@Pjoint II

                                                    St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      3.10000  3.10000  0.17231   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     1  0.84050  0.84050  0.84050  201.72  0.001
Error    3  0.01250  0.01250  0.00417
Total    4  0.85300


S = 0.0645497   R-Sq = 98.53%   R-Sq(adj) = 98.05%


Unusual Observations for W@Pjoint III

     W@Pjoint                                  St
Obs       III      Fit   SE Fit  Residual  Resid
  5   3.65000  3.65000  0.06455  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.10658  0.10658  0.10658  2.91  0.187
Error    3  0.10990  0.10990  0.03663
Total    4  0.21648
```

```
S = 0.191398   R-Sq = 49.23%   R-Sq(adj) = 32.31%


Unusual Observations for W@Pjoint IV

                                                  St
Obs  W@Pjoint IV      Fit   SE Fit  Residual  Resid
  5      2.70000  2.70000  0.19140   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.91592  0.91592  0.91592  56.54  0.005
Error    3  0.04860  0.04860  0.01620
Total    4  0.96452


S = 0.127279   R-Sq = 94.96%   R-Sq(adj) = 93.28%


Unusual Observations for W@2joint III

     W@2joint                               St
Obs       III      Fit   SE Fit  Residual  Resid
  5   3.42000  3.42000  0.12728   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.35113  0.35113  0.35113  9.01  0.058
Error    3  0.11688  0.11688  0.03896
Total    4  0.46800


S = 0.197379   R-Sq = 75.03%   R-Sq(adj) = 66.70%


Unusual Observations for W@2joint IV

                                                  St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  5      2.64000  2.64000  0.19738   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     1  0.60552  0.60552  0.60552  119.51  0.002
Error    3  0.01520  0.01520  0.00507
Total    4  0.62072


S = 0.0711805   R-Sq = 97.55%   R-Sq(adj) = 96.73%
```

```
Unusual Observations for W@3joint IV

                                                      St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  5      2.53000  2.53000  0.07118   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  6.0170  6.0170  6.0170  19.04  0.022
Error    3  0.9481  0.9481  0.3160
Total    4  6.9651


S = 0.562161   R-Sq = 86.39%   R-Sq(adj) = 81.85%


Unusual Observations for LoPhI,II

                                                  St
Obs  LoPhI,II      Fit  SE Fit  Residual  Resid
  5   17.7800  17.7800  0.5622    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.2509  0.2509  0.2509  0.82  0.432
Error    3  0.9162  0.9162  0.3054
Total    4  1.1671


S = 0.552630   R-Sq = 21.50%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhII,II

                                                   St
Obs  LoPhII,II      Fit  SE Fit  Residual  Resid
  5    12.6100  12.6100  0.5526   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  1.8727  1.8727  1.8727  7.81  0.068
Error    3  0.7192  0.7192  0.2397
Total    4  2.5919


S = 0.489626   R-Sq = 72.25%   R-Sq(adj) = 63.00%


Unusual Observations for LoPhI,III

                                                   St
```

```
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  5    14.8000  14.8000  0.4896   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  2.6938  2.6938  2.6938  55.62  0.005
Error    3  0.1453  0.1453  0.0484
Total    4  2.8391


S = 0.220076   R-Sq = 94.88%   R-Sq(adj) = 93.18%


Unusual Observations for LoPhII,III

                                               St
Obs  LoPhII,III      Fit  SE Fit  Residual  Resid
  5     10.2500  10.2500  0.2201    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  11.582  11.582  11.582  45.36  0.007
Error    3   0.766   0.766   0.255
Total    4  12.349


S = 0.505338   R-Sq = 93.80%   R-Sq(adj) = 91.73%


Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  5      14.6900  14.6900  0.5053    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  11.086  11.086  11.086  112.55  0.002
Error    3   0.295   0.295   0.098
Total    4  11.381


S = 0.313834   R-Sq = 97.40%   R-Sq(adj) = 96.54%


Unusual Observations for LoPhI,IV

                                            St
Obs  LoPhI,IV     Fit  SE Fit  Residual  Resid
  5    9.2000  9.2000  0.3138    0.0000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.17112  0.17112  0.17112  7.01  0.077
Error    3  0.07327  0.07327  0.02442
Total    4  0.24440


S = 0.156285   R-Sq = 70.02%   R-Sq(adj) = 60.02%


Unusual Observations for LoPhII,IV

                                               St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  5    9.62000  9.62000  0.15628   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.0151  0.0151  0.0151  0.10  0.771
Error    3  0.4485  0.4485  0.1495
Total    4  0.4636


S = 0.386642   R-Sq = 3.26%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhIII,IV

                                                St
Obs  LoPhIII,IV      Fit   SE Fit  Residual  Resid
  5     8.75000  8.75000  0.38664   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.7106  0.7106  0.7106  0.97  0.397
Error    3  2.1895  2.1895  0.7298
Total    4  2.9001


S = 0.854298   R-Sq = 24.50%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhIV,IV

                                              St
Obs  LoPhIV,IV      Fit  SE Fit  Residual  Resid
  5    10.3200  10.3200  0.8543    0.0000      * X

X denotes an observation whose X value gives it large leverage.
```

```
Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.3200  0.3200  0.3200  0.40  0.571
Error    3  2.3875  2.3875  0.7958
Total    4  2.7075


S = 0.892090   R-Sq = 11.82%   R-Sq(adj) = 0.00%


Unusual Observations for Foot Length

                                                St
Obs  Foot Length      Fit  SE Fit  Residual  Resid
  5      46.2500  46.2500  0.8921    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  84.543  84.543  84.543  299.58  0.000
Error    3   0.847   0.847   0.282
Total    4  85.389


S = 0.531225   R-Sq = 99.01%   R-Sq(adj) = 98.68%


Unusual Observations for Lotmt

                                            St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  5  45.1000  45.1000  0.5312    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.45602  0.45602  0.45602  21.82  0.019
Error    3  0.06270  0.06270  0.02090
Total    4  0.51872


S = 0.144568   R-Sq = 87.91%   R-Sq(adj) = 83.88%


Unusual Observations for Wotmt@prox

                                                St
Obs  Wotmt@prox      Fit   SE Fit  Residual  Resid
  5     7.96000  7.96000  0.14457  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
```

```
Name      1  0.4176  0.4176  0.4176  3.29  0.168
Error     3  0.3813  0.3813  0.1271
Total     4  0.7989


S = 0.356499   R-Sq = 52.27%   R-Sq(adj) = 36.37%


Unusual Observations for Wotmt@cond

                                                St
Obs  Wotmt@cond      Fit   SE Fit  Residual  Resid
  5     7.44000  7.44000  0.35650   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  35.770  A
Cepphus columba          4  27.578    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       8.193       1.329    6.166    0.0086


Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  35.770  A
Cepphus columba          4  27.578    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       8.193       1.329    6.166    0.0086


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  46.620  A
Cepphus columba          4  37.712    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       8.907      0.8898    10.01    0.0021


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII
```

```
Name                     N    Mean  Grouping
Chepphus columba (skin)  1  46.620  A
Cepphus columba          4  37.712    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       8.907      0.8898    10.01    0.0021


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  42.740  A
Cepphus columba          4  38.410    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       4.330       1.130    3.832    0.0313


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  42.740  A
Cepphus columba          4  38.410    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       4.330       1.130    3.832    0.0313


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                     N   Mean  Grouping
Chepphus columba (skin)  1  3.100  A
Cepphus columba          4  2.333    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)      0.7675      0.1927    3.984    0.0283


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                     N   Mean  Grouping
```

Name	N	Mean	Grouping
Chepphus columba (skin)	1	3.100	A
Cepphus columba	4	2.333	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.7675	0.1927	3.984	0.0283

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	3.650	A
Cepphus columba	4	2.625	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	1.025	0.07217	14.20	0.0008

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	3.650	A
Cepphus columba	4	2.625	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	1.025	0.07217	14.20	0.0008

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	2.700	A
Cepphus columba	4	2.335	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.3650	0.2140	1.706	0.1866

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	2.700	A

Cepphus columba	4	2.335	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.3650	0.2140	1.706	0.1866

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	3.420	A
Cepphus columba	4	2.350	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	1.070	0.1423	7.519	0.0049

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	3.420	A
Cepphus columba	4	2.350	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	1.070	0.1423	7.519	0.0049

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	2.640	A
Cepphus columba	4	1.977	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.6625	0.2207	3.002	0.0576

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	2.640	A
Cepphus columba	4	1.977	A

```
Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)      0.6625      0.2207    3.002    0.0576


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint
     IV

Name                     N   Mean  Grouping
Chepphus columba (skin)  1  2.530  A
Cepphus columba          4  1.660    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)      0.8700     0.07958    10.93    0.0016


Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name                     N   Mean  Grouping
Chepphus columba (skin)  1  2.530  A
Cepphus columba          4  1.660    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)      0.8700     0.07958    10.93    0.0016


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  17.780  A
Cepphus columba          4  15.038    B

Means that do not share a letter are significantly different.

Name = Cepphus columba  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value   P-Value
Chepphus columba (skin)       2.743      0.6285    4.363    0.0223


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name                     N    Mean  Grouping
Chepphus columba (skin)  1  17.780  A
Cepphus columba          4  15.038    B

Means that do not share a letter are significantly different.
```

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	2.743	0.6285	4.363	0.0223

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Cepphus columba	4	13.170	A
Chepphus columba (skin)	1	12.610	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-0.5600	0.6179	-0.9064	0.4316

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Cepphus columba	4	13.170	A
Chepphus columba (skin)	1	12.610	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-0.5600	0.6179	-0.9064	0.4316

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Cepphus columba	4	16.330	A
Chepphus columba (skin)	1	14.800	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-1.530	0.5474	-2.795	0.0681

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Cepphus columba	4	16.330	A
Chepphus columba (skin)	1	14.800	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-1.530	0.5474	-2.795	0.0681

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Cepphus columba	4	12.085	A
Chepphus columba (skin)	1	10.250	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-1.835	0.2461	-7.458	0.0050

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Cepphus columba	4	12.085	A
Chepphus columba (skin)	1	10.250	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-1.835	0.2461	-7.458	0.0050

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	14.690	A
Cepphus columba	4	10.885	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	3.805	0.5650	6.735	0.0067

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Chepphus columba (skin)	1	14.690	A
Cepphus columba	4	10.885	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Difference	SE of	Adjusted

Name	of Means	Difference	T-Value	P-Value
Chepphus columba (skin)	3.805	0.5650	6.735	0.0067

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Cepphus columba	4	12.922	A
Chepphus columba (skin)	1	9.200	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-3.723	0.3509	-10.61	0.0018

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Cepphus columba	4	12.922	A
Chepphus columba (skin)	1	9.200	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-3.723	0.3509	-10.61	0.0018

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	9.620	A
Cepphus columba	4	9.158	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.4625	0.1747	2.647	0.0772

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	9.620	A
Cepphus columba	4	9.158	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.4625	0.1747	2.647	0.0772

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Cepphus columba	4	8.887	A
Chepphus columba (skin)	1	8.750	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-0.1375	0.4323	-0.3181	0.7713

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Cepphus columba	4	8.887	A
Chepphus columba (skin)	1	8.750	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	-0.1375	0.4323	-0.3181	0.7713

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	10.320	A
Cepphus columba	4	9.378	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.9425	0.9551	0.9868	0.3965

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Chepphus columba (skin)	1	10.320	A
Cepphus columba	4	9.378	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.9425	0.9551	0.9868	0.3965

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot

Length

Name	N	Mean	Grouping
Chepphus columba (skin)	1	46.250	A
Cepphus columba	4	45.618	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.6325	0.9974	0.6342	0.5710

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Chepphus columba (skin)	1	46.250	A
Cepphus columba	4	45.618	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.6325	0.9974	0.6342	0.5710

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Chepphus columba (skin)	1	45.100	A
Cepphus columba	4	34.820	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	10.28	0.5939	17.31	0.0004

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Chepphus columba (skin)	1	45.100	A
Cepphus columba	4	34.820	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	10.28	0.5939	17.31	0.0004

Grouping Information Using Bonferroni Method and 95.0% Confidence for
Wotmt@prox

Name	N	Mean	Grouping
Chepphus columba (skin)	1	7.960	A
Cepphus columba	4	7.205	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.7550	0.1616	4.671	0.0185

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Chepphus columba (skin)	1	7.960	A
Cepphus columba	4	7.205	B

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.7550	0.1616	4.671	0.0185

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Chepphus columba (skin)	1	7.440	A
Cepphus columba	4	6.718	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.7225	0.3986	1.813	0.1675

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Chepphus columba (skin)	1	7.440	A
Cepphus columba	4	6.718	A

Means that do not share a letter are significantly different.

Name = Cepphus columba subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Chepphus columba (skin)	0.7225	0.3986	1.813	0.1675

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	2	Corvus corax, Corvus corax (skin)

```
Analysis of Variance for LoDI, using Adjusted SS for Tests

Source  DF   Seq SS  Adj SS  Adj MS      F      P
Name     1   8.9378  8.9378  8.9378  21.76  0.019
Error    3   1.2321  1.2321  0.4107
Total    4  10.1699


S = 0.640852   R-Sq = 87.89%   R-Sq(adj) = 83.85%


Unusual Observations for LoDI

                                            St
Obs     LoDI      Fit  SE Fit  Residual  Resid
  5  28.3300  28.3300  0.6409    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   0.890   0.890   0.890  0.67  0.473
Error    3   3.983   3.983   1.328
Total    4   4.873


S = 1.15220   R-Sq = 18.27%   R-Sq(adj) = 0.00%


Unusual Observations for LoDII

                                            St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  28.5500  28.5500  1.1522    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   0.652   0.652   0.652  0.31  0.615
Error    3   6.245   6.245   2.082
Total    4   6.896


S = 1.44276   R-Sq = 9.45%   R-Sq(adj) = 0.00%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  42.5600  42.5600  1.4428    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests
```

```
Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  1.4418  1.4418  1.4418  2.72  0.197
Error    3  1.5887  1.5887  0.5296
Total    4  3.0305


S = 0.727708   R-Sq = 47.58%   R-Sq(adj) = 30.10%


Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  33.1800  33.1800  0.7277    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  5.4392  5.4392  5.4392  205.84  0.001
Error    3  0.0793  0.0793  0.0264
Total    4  5.5185


S = 0.162558   R-Sq = 98.56%   R-Sq(adj) = 98.08%


Unusual Observations for W@Pjoint II

                                                 St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      6.53000  6.53000  0.16256   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  5.6498  5.6498  5.6498  335.80  0.000
Error    3  0.0505  0.0505  0.0168
Total    4  5.7003


S = 0.129711   R-Sq = 99.11%   R-Sq(adj) = 98.82%


Unusual Observations for W@Pjoint III

     W@Pjoint                                  St
Obs       III      Fit   SE Fit  Residual  Resid
  5   6.98000  6.98000  0.12971   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  5.1005  5.1005  5.1005  905.41  0.000
```

```
Error    3  0.0169  0.0169  0.0056
Total    4  5.1174


S = 0.0750555   R-Sq = 99.67%   R-Sq(adj) = 99.56%


Unusual Observations for W@2joint III

     W@2joint                                 St
Obs       III      Fit   SE Fit  Residual  Resid
  5   6.42000  6.42000  0.07506   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  6.9149  6.9149  6.9149  340.08  0.000
Error    3  0.0610  0.0610  0.0203
Total    4  6.9759


S = 0.142595   R-Sq = 99.13%   R-Sq(adj) = 98.83%


Unusual Observations for W@2joint IV

                                                 St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  5      6.20000  6.20000  0.14259   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  7.5031  7.5031  7.5031  510.71  0.000
Error    3  0.0441  0.0441  0.0147
Total    4  7.5472


S = 0.121209   R-Sq = 99.42%   R-Sq(adj) = 99.22%


Unusual Observations for W@3joint IV

                                                 St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  5      6.02000  6.02000  0.12121   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  76.167  76.167  76.167  327.14  0.000
Error    3   0.698   0.698   0.233
Total    4  76.866
```

```
S = 0.482519   R-Sq = 99.09%   R-Sq(adj) = 98.79%


Unusual Observations for LoPhI,II

                                            St
Obs  LoPhI,II     Fit  SE Fit  Residual  Resid
  5    5.0600  5.0600  0.4825    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.0045  0.0045  0.0045  0.01  0.918
Error    3  1.0731  1.0731  0.3577
Total    4  1.0776


S = 0.598080   R-Sq = 0.42%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhII,II

                                              St
Obs  LoPhII,II      Fit  SE Fit  Residual  Resid
  5    16.1300  16.1300  0.5981    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  39.060  39.060  39.060  554.11  0.000
Error    3   0.211   0.211   0.070
Total    4  39.272


S = 0.265503   R-Sq = 99.46%   R-Sq(adj) = 99.28%


Unusual Observations for LoPhI,III

                                             St
Obs  LoPhI,III     Fit  SE Fit  Residual  Resid
  5     6.9200  6.9200  0.2655   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  49.424  49.424  49.424  170.15  0.001
Error    3   0.871   0.871   0.290
Total    4  50.295


S = 0.538950   R-Sq = 98.27%   R-Sq(adj) = 97.69%
```

```
Unusual Observations for LoPhII,III

                                              St
Obs  LoPhII,III     Fit  SE Fit  Residual  Resid
  5      5.7900  5.7900  0.5389   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  12.309  12.309  12.309  91.20  0.002
Error    3   0.405   0.405   0.135
Total    4  12.714


S = 0.367367   R-Sq = 96.82%   R-Sq(adj) = 95.75%


Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  5      20.0300  20.0300  0.3674    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.12012  0.12012  0.12012  1.22  0.351
Error    3  0.29648  0.29648  0.09883
Total    4  0.41660


S = 0.314364   R-Sq = 28.83%   R-Sq(adj) = 5.11%


Unusual Observations for LoPhII,IV

                                               St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  5    8.25000  8.25000  0.31436   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.2228  4.2228  4.2228  23.01  0.017
Error    3  0.5505  0.5505  0.1835
Total    4  4.7733


S = 0.428359   R-Sq = 88.47%   R-Sq(adj) = 84.62%


Unusual Observations for LoPhIII,IV
```

```
                                                St
Obs  LoPhIII,IV      Fit   SE Fit  Residual  Resid
  5     5.97000  5.97000  0.42836  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.6658  4.6658  4.6658  26.43  0.014
Error    3  0.5297  0.5297  0.1766
Total    4  5.1955


S = 0.420198   R-Sq = 89.80%   R-Sq(adj) = 86.41%


Unusual Observations for LoPhIV,IV

                                              St
Obs  LoPhIV,IV      Fit  SE Fit  Residual  Resid
  5    12.1200  12.1200  0.4202    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   0.000   0.000   0.000  0.00  0.986
Error    3   4.391   4.391   1.464
Total    4   4.391


S = 1.20981   R-Sq = 0.01%   R-Sq(adj) = 0.00%


Unusual Observations for Foot Length

                                                St
Obs  Foot Length      Fit  SE Fit  Residual  Resid
  5      48.9000  48.9000  1.2098   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  142.95  142.95  142.95  24.41  0.016
Error    3   17.57   17.57    5.86
Total    4  160.52


S = 2.41984   R-Sq = 89.06%   R-Sq(adj) = 85.41%


Unusual Observations for Lotmt

                                          St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  5  81.0000  81.0000  2.4198    0.0000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  13.514  13.514  13.514  116.90  0.002
Error    3   0.347   0.347   0.116
Total    4  13.860


S = 0.34   R-Sq = 97.50%   R-Sq(adj) = 96.66%


Unusual Observations for Wotmt@prox

                                                 St
Obs  Wotmt@prox      Fit  SE Fit  Residual  Resid
  5     16.2100  16.2100  0.3400    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  15.913  15.913  15.913  524.61  0.000
Error    3   0.091   0.091   0.030
Total    4  16.004


S = 0.174165   R-Sq = 99.43%   R-Sq(adj) = 99.24%


Unusual Observations for Wotmt@cond

                                                 St
Obs  Wotmt@cond      Fit  SE Fit  Residual  Resid
  5     13.2300  13.2300  0.1742    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name                 N    Mean  Grouping
Corvus corax (skin)  1  28.330  A
Corvus corax         4  24.988    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of           Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       3.342      0.7165    4.665    0.0186


Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name                 N    Mean  Grouping
Corvus corax (skin)  1  28.330  A
```

```
Corvus corax         4  24.988    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       3.342      0.7165    4.665    0.0186


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name                 N    Mean  Grouping
Corvus corax         4  29.605  A
Corvus corax (skin)  1  28.550  A

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)      -1.055       1.288  -0.8190    0.4728


Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                 N    Mean  Grouping
Corvus corax         4  29.605  A
Corvus corax (skin)  1  28.550  A

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)      -1.055       1.288  -0.8190    0.4728


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name                 N    Mean  Grouping
Corvus corax (skin)  1  42.560  A
Corvus corax         4  41.657  A

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)      0.9025       1.613   0.5595    0.6149


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name                 N    Mean  Grouping
Corvus corax (skin)  1  42.560  A
Corvus corax         4  41.657  A

Means that do not share a letter are significantly different.
```

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.9025	1.613	0.5595	0.6149

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Corvus corax (skin)	1	33.180	A
Corvus corax	4	31.837	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	1.343	0.8136	1.650	0.1975

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Corvus corax (skin)	1	33.180	A
Corvus corax	4	31.837	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	1.343	0.8136	1.650	0.1975

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.530	A
Corvus corax	4	3.923	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.607	0.1817	14.35	0.0007

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.530	A
Corvus corax	4	3.923	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.607	0.1817	14.35	0.0007

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.980	A
Corvus corax	4	4.322	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.658	0.1450	18.32	0.0004

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.980	A
Corvus corax	4	4.322	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.658	0.1450	18.32	0.0004

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.420	A
Corvus corax	4	3.895	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.525	0.08391	30.09	0.0001

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Corvus corax (skin)	1	6.420	A
Corvus corax	4	3.895	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

```
                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       2.525     0.08391    30.09    0.0001


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     IV

Name                 N   Mean  Grouping
Corvus corax (skin)  1  6.200  A
Corvus corax         4  3.260    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       2.940      0.1594    18.44    0.0003


Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name                 N   Mean  Grouping
Corvus corax (skin)  1  6.200  A
Corvus corax         4  3.260    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       2.940      0.1594    18.44    0.0004


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint
     IV

Name                 N   Mean  Grouping
Corvus corax (skin)  1  6.020  A
Corvus corax         4  2.958    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       3.062      0.1355    22.60    0.0002


Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name                 N   Mean  Grouping
Corvus corax (skin)  1  6.020  A
Corvus corax         4  2.958    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
```

Name	of Means	Difference	T-Value	P-Value
Corvus corax (skin)	3.062	0.1355	22.60	0.0002

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Corvus corax	4	14.817	A
Corvus corax (skin)	1	5.060	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-9.758	0.5395	-18.09	0.0004

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Corvus corax	4	14.817	A
Corvus corax (skin)	1	5.060	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-9.758	0.5395	-18.09	0.0004

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Corvus corax (skin)	1	16.130	A
Corvus corax	4	16.055	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.07500	0.6687	0.1122	0.9178

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Corvus corax (skin)	1	16.130	A
Corvus corax	4	16.055	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.07500	0.6687	0.1122	0.9178

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Corvus corax	4	13.907	A
Corvus corax (skin)	1	6.920	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-6.987	0.2968	-23.54	0.0002

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Corvus corax	4	13.907	A
Corvus corax (skin)	1	6.920	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-6.987	0.2968	-23.54	0.0002

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Corvus corax	4	13.650	A
Corvus corax (skin)	1	5.790	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-7.860	0.6026	-13.04	0.0010

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Corvus corax	4	13.650	A
Corvus corax (skin)	1	5.790	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-7.860	0.6026	-13.04	0.0010

Grouping Information Using Bonferroni Method and 95.0% Confidence for

LoPhIII,III

Name	N	Mean	Grouping
Corvus corax (skin)	1	20.030	A
Corvus corax	4	16.108	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	3.923	0.4107	9.550	0.0024

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Corvus corax (skin)	1	20.030	A
Corvus corax	4	16.108	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	3.923	0.4107	9.550	0.0024

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Corvus corax (skin)	1	8.250	A
Corvus corax	4	7.863	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.3875	0.3515	1.103	0.3507

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Corvus corax (skin)	1	8.250	A
Corvus corax	4	7.863	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.3875	0.3515	1.103	0.3508

Grouping Information Using Bonferroni Method and 95.0% Confidence for
LoPhIII,IV

Name	N	Mean	Grouping
Corvus corax	4	8.268	A
Corvus corax (skin)	1	5.970	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-2.298	0.4789	-4.797	0.0172

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Corvus corax	4	8.268	A
Corvus corax (skin)	1	5.970	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	-2.298	0.4789	-4.797	0.0172

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Corvus corax (skin)	1	12.120	A
Corvus corax	4	9.705	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.415	0.4698	5.141	0.0143

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Corvus corax (skin)	1	12.120	A
Corvus corax	4	9.705	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	2.415	0.4698	5.141	0.0143

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Corvus corax (skin)	1	48.900	A

Corvus corax	4	48.875	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.02500	1.353	0.01848	0.9864

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Corvus corax (skin)	1	48.900	A
Corvus corax	4	48.875	A

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	0.02500	1.353	0.01848	0.9864

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Corvus corax (skin)	1	81.000	A
Corvus corax	4	67.632	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	13.37	2.705	4.941	0.0159

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Corvus corax (skin)	1	81.000	A
Corvus corax	4	67.632	B

Means that do not share a letter are significantly different.

Name = Corvus corax subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Corvus corax (skin)	13.37	2.705	4.941	0.0159

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Corvus corax (skin)	1	16.210	A
Corvus corax	4	12.100	B

```
Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       4.110      0.3801    10.81    0.0017


Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name                 N    Mean  Grouping
Corvus corax (skin)  1  16.210  A
Corvus corax         4  12.100    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       4.110      0.3801    10.81    0.0017


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     Wotmt@cond

Name                 N    Mean  Grouping
Corvus corax (skin)  1  13.230  A
Corvus corax         4   8.770    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       4.460      0.1947    22.90    0.0002


Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name                 N    Mean  Grouping
Corvus corax (skin)  1  13.230  A
Corvus corax         4   8.770    B

Means that do not share a letter are significantly different.

Name = Corvus corax  subtracted from:

                     Difference       SE of            Adjusted
Name                   of Means  Difference  T-Value   P-Value
Corvus corax (skin)       4.460      0.1947    22.90    0.0002
```

General Linear Model: LoDIII, LoDIV, ... versus Name

```
Factor  Type   Levels  Values
Name    fixed       2  Gavia pacifica, Gavia pacifica (skin)


Analysis of Variance for LoDIII, using Adjusted SS for Tests
```

```
Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  57.029  57.029  57.029  66.14  0.015
Error    2   1.725   1.725   0.862
Total    3  58.753


S = 0.928601   R-Sq = 97.06%   R-Sq(adj) = 95.60%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  4  85.9900  85.9900  0.9286    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  49.491  49.491  49.491  43.96  0.022
Error    2   2.252   2.252   1.126
Total    3  51.743


S = 1.06105   R-Sq = 95.65%   R-Sq(adj) = 93.47%


Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  4  91.3900  91.3900  1.0611    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  3.1110  3.1110  3.1110  51.65  0.019
Error    2  0.1205  0.1205  0.0602
Total    3  3.2315


S = 0.245425   R-Sq = 96.27%   R-Sq(adj) = 94.41%


Unusual Observations for W@Pjoint III

     W@Pjoint                                 St
Obs       III      Fit   SE Fit  Residual  Resid
  4   6.20000  6.20000  0.24542   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  5.8660  5.8660  5.8660  114.94  0.009
Error    2  0.1021  0.1021  0.0510
```

```
Total    3  5.9681


S = 0.225906   R-Sq = 98.29%   R-Sq(adj) = 97.43%


Unusual Observations for W@2joint III

     W@2joint                                St
Obs       III      Fit   SE Fit  Residual  Resid
  4   6.18000  6.18000  0.22591   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  1.2936  1.2936  1.2936  6.12  0.132
Error    2  0.4229  0.4229  0.2114
Total    3  1.7165


S = 0.459819   R-Sq = 75.36%   R-Sq(adj) = 63.05%


Unusual Observations for W@2joint IV

                                                St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  4      5.09000  5.09000  0.45982   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.61201  0.61201  0.61201  7.57  0.111
Error    2  0.16167  0.16167  0.08083
Total    3  0.77367


S = 0.284312   R-Sq = 79.10%   R-Sq(adj) = 68.66%


Unusual Observations for W@3joint IV

                                                St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  4      4.42000  4.42000  0.28431   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS        F      P
Name     1  179.49  179.49  179.49  1968.10  0.001
Error    2    0.18    0.18    0.09
Total    3  179.67
```

```
S = 0.301993   R-Sq = 99.90%   R-Sq(adj) = 99.85%


Unusual Observations for LoPhI,II

                                                St
Obs  LoPhI,II      Fit  SE Fit  Residual  Resid
  4   27.2300  27.2300  0.3020   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  51.336  51.336  51.336  141.72  0.007
Error    2   0.724   0.724   0.362
Total    3  52.061


S = 0.601858   R-Sq = 98.61%   R-Sq(adj) = 97.91%


Unusual Observations for LoPhI,III

                                                 St
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  4    27.8800  27.8800  0.6019    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  1.6651  1.6651  1.6651  7.99  0.106
Error    2  0.4166  0.4166  0.2083
Total    3  2.0817


S = 0.456399   R-Sq = 79.99%   R-Sq(adj) = 69.98%


Unusual Observations for LoPhII,III

                                                  St
Obs  LoPhII,III      Fit  SE Fit  Residual  Resid
  4     24.3700  24.3700  0.4564    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF   Seq SS  Adj SS  Adj MS       F      P
Name     1   99.821  99.821  99.821  391.40  0.003
Error    2    0.510   0.510   0.255
Total    3  100.331


S = 0.505008   R-Sq = 99.49%   R-Sq(adj) = 99.24%
```

```
Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  4      31.7000  31.7000  0.5050    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  26.314  26.314  26.314  140.69  0.007
Error    2   0.374   0.374   0.187
Total    3  26.688


S = 0.432474   R-Sq = 98.60%   R-Sq(adj) = 97.90%


Unusual Observations for LoPhI,IV

                                             St
Obs  LoPhI,IV      Fit  SE Fit  Residual  Resid
  4   24.7800  24.7800  0.4325    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  6.7650  6.7650  6.7650  228.29  0.004
Error    2  0.0593  0.0593  0.0296
Total    3  6.8243


S = 0.172143   R-Sq = 99.13%   R-Sq(adj) = 98.70%


Unusual Observations for LoPhII,IV

                                              St
Obs  LoPhII,IV      Fit  SE Fit  Residual  Resid
  4    15.2300  15.2300  0.1721    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.0252  0.0252  0.0252  0.09  0.791
Error    2  0.5523  0.5523  0.2761
Total    3  0.5775


S = 0.525484   R-Sq = 4.37%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhIII,IV

                                               St
```

```
Obs  LoPhIII,IV      Fit  SE Fit  Residual  Resid
  4     16.8800  16.8800  0.5255    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  16.521  16.521  16.521  82.92  0.012
Error    2   0.398   0.398   0.199
Total    3  16.919


S = 0.446356   R-Sq = 97.64%   R-Sq(adj) = 96.47%


Unusual Observations for LoPhIV,IV

                                             St
Obs  LoPhIV,IV      Fit  SE Fit  Residual  Resid
  4    24.0400  24.0400  0.4464    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  47.521  47.521  47.521  8.67  0.099
Error    2  10.966  10.966   5.483
Total    3  58.487


S = 2.34156   R-Sq = 81.25%   R-Sq(adj) = 71.88%


Unusual Observations for Foot Length

                                               St
Obs  Foot Length      Fit  SE Fit  Residual  Resid
  4      102.800  102.800   2.342     0.000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  100.80  100.80  100.80  113.65  0.009
Error    2    1.77    1.77    0.89
Total    3  102.58


S = 0.941771   R-Sq = 98.27%   R-Sq(adj) = 97.41%


Unusual Observations for Lotmt

                                           St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  4  84.4400  84.4400  0.9418    0.0000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	4.7880	4.7880	4.7880	294.95	0.003
Error	2	0.0325	0.0325	0.0162		
Total	3	4.8205				

S = 0.127410   R-Sq = 99.33%   R-Sq(adj) = 98.99%

Unusual Observations for Wotmt@prox

Obs	Wotmt@prox	Fit	SE Fit	Residual	St Resid	
4	14.7800	14.7800	0.1274	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.8112	0.8112	0.8112	2.97	0.227
Error	2	0.5462	0.5462	0.2731		
Total	3	1.3574				

S = 0.522590   R-Sq = 59.76%   R-Sq(adj) = 39.64%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid	
4	10.2500	10.2500	0.5226	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	85.990	A
Gavia pacifica	3	77.270	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	8.720	1.072	8.132	0.0148

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	85.990	A
Gavia pacifica	3	77.270	B

```
Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value    P-Value
Gavia pacifica (skin)       8.720       1.072    8.132     0.0148


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name                   N    Mean  Grouping
Gavia pacifica (skin)  1  91.390  A
Gavia pacifica         3  83.267    B

Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value    P-Value
Gavia pacifica (skin)       8.123       1.225    6.630     0.0220


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                   N    Mean  Grouping
Gavia pacifica (skin)  1  91.390  A
Gavia pacifica         3  83.267    B

Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value    P-Value
Gavia pacifica (skin)       8.123       1.225    6.630     0.0220


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     III

Name                   N   Mean  Grouping
Gavia pacifica (skin)  1  6.200  A
Gavia pacifica         3  4.163    B

Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value    P-Value
Gavia pacifica (skin)       2.037      0.2834    7.187     0.0188


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name                   N   Mean  Grouping
Gavia pacifica (skin)  1  6.200  A
Gavia pacifica         3  4.163    B

Means that do not share a letter are significantly different.
```

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	2.037	0.2834	7.187	0.0188

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	6.180	A
Gavia pacifica	3	3.383	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	2.797	0.2609	10.72	0.0086

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	6.180	A
Gavia pacifica	3	3.383	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	2.797	0.2609	10.72	0.0086

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	5.090	A
Gavia pacifica	3	3.777	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	1.313	0.5310	2.474	0.1319

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	5.090	A
Gavia pacifica	3	3.777	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	1.313	0.5310	2.474	0.1319

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	4.420	A
Gavia pacifica	3	3.517	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	0.9033	0.3283	2.752	0.1106

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	4.420	A
Gavia pacifica	3	3.517	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	0.9033	0.3283	2.752	0.1106

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Gavia pacifica	3	42.700	A
Gavia pacifica (skin)	1	27.230	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-15.47	0.3487	-44.36	0.0005

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Gavia pacifica	3	42.700	A
Gavia pacifica (skin)	1	27.230	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-15.47	0.3487	-44.36	0.0005

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Gavia pacifica	3	36.153	A
Gavia pacifica (skin)	1	27.880	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-8.273	0.6950	-11.90	0.0070

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Gavia pacifica	3	36.153	A
Gavia pacifica (skin)	1	27.880	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-8.273	0.6950	-11.90	0.0070

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	24.370	A
Gavia pacifica	3	22.880	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	1.490	0.5270	2.827	0.1056

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	24.370	A
Gavia pacifica	3	22.880	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Gavia pacifica (skin)	1.490	0.5270	2.827	0.1057

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	31.700	A
Gavia pacifica	3	20.163	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	11.54	0.5831	19.78	0.0025

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	31.700	A
Gavia pacifica	3	20.163	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	11.54	0.5831	19.78	0.0026

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Gavia pacifica	3	30.703	A
Gavia pacifica (skin)	1	24.780	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-5.923	0.4994	-11.86	0.0070

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Gavia pacifica	3	30.703	A
Gavia pacifica (skin)	1	24.780	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-5.923	0.4994	-11.86	0.0070

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Gavia pacifica	3	18.233	A
Gavia pacifica (skin)	1	15.230	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-3.003	0.1988	-15.11	0.0044

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Gavia pacifica	3	18.233	A
Gavia pacifica (skin)	1	15.230	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	-3.003	0.1988	-15.11	0.0044

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	16.880	A
Gavia pacifica	3	16.697	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	0.1833	0.6068	0.3021	0.7911

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	16.880	A
Gavia pacifica	3	16.697	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	0.1833	0.6068	0.3021	0.7911

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	24.040	A
Gavia pacifica	3	19.347	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	4.693	0.5154	9.106	0.0118

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	24.040	A
Gavia pacifica	3	19.347	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	4.693	0.5154	9.106	0.0119

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	102.800	A
Gavia pacifica	3	94.840	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	7.960	2.704	2.944	0.0986

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	102.800	A
Gavia pacifica	3	94.840	A

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	7.960	2.704	2.944	0.0986

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	84.440	A
Gavia pacifica	3	72.847	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	11.59	1.087	10.66	0.0087

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	84.440	A
Gavia pacifica	3	72.847	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	11.59	1.087	10.66	0.0087

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	14.780	A
Gavia pacifica	3	12.253	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	2.527	0.1471	17.17	0.0034

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	14.780	A
Gavia pacifica	3	12.253	B

Means that do not share a letter are significantly different.

Name = Gavia pacifica subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Gavia pacifica (skin)	2.527	0.1471	17.17	0.0034

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Gavia pacifica (skin)	1	10.250	A

```
Gavia pacifica         3   9.210  A

Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of           Adjusted
Name                     of Means  Difference  T-Value   P-Value
Gavia pacifica (skin)       1.040      0.6034    1.723    0.2269


Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name                   N    Mean  Grouping
Gavia pacifica (skin)  1  10.250  A
Gavia pacifica         3   9.210  A

Means that do not share a letter are significantly different.

Name = Gavia pacifica  subtracted from:

                       Difference       SE of           Adjusted
Name                     of Means  Difference  T-Value   P-Value
Gavia pacifica (skin)       1.040      0.6034    1.723    0.2270
```

General Linear Model: LoDI, LoDII, ... versus Name

```
* WARNING * Not all response variables have the same missing value pattern. You
            would get different univariate results if you ran this command
            separately for each of these response variables. See the Help topic
            'missing values' for details.


Factor  Type   Levels  Values
Name    fixed       2  Lecucophaeus pipixcan, Lecucophaeus pipixcan (skin)


Analysis of Variance for LoDI, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  5.5488  5.5488  5.5488  24.72  0.126
Error    1  0.2244  0.2244  0.2244
Total    2  5.7733


S = 0.473762   R-Sq = 96.11%   R-Sq(adj) = 92.22%


Unusual Observations for LoDI

                                                  St
Obs     LoDI      Fit   SE Fit  Residual  Resid
  5  6.19000  6.19000  0.47376   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   4.133   4.133   4.133  2.73  0.346
```

```
Error    1   1.514   1.514   1.514
Total    2   5.647


S = 1.23037   R-Sq = 73.19%   R-Sq(adj) = 46.39%


Unusual Observations for LoDII

                                            St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  22.0100  22.0100  1.2304   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   1.344   1.344   1.344  0.34  0.665
Error    1   3.976   3.976   3.976
Total    2   5.320


S = 1.99404   R-Sq = 25.27%   R-Sq(adj) = 0.00%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  30.2000  30.2000  1.9940    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.0400  0.0400  0.0400  0.07  0.838
Error    1  0.5940  0.5940  0.5940
Total    2  0.6341


S = 0.770746   R-Sq = 6.31%   R-Sq(adj) = 0.00%


Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  30.2000  30.2000  0.7707    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.00735  0.00735  0.00735  0.65  0.567
Error    1  0.01125  0.01125  0.01125
Total    2  0.01860
```

```
S = 0.106066   R-Sq = 39.52%   R-Sq(adj) = 0.00%


Unusual Observations for W@Pjoint II

                                                     St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      1.82000  1.82000  0.10607   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.28167  0.28167  0.28167  88.02  0.068
Error    1  0.00320  0.00320  0.00320
Total    2  0.28487


S = 0.0565685   R-Sq = 98.88%   R-Sq(adj) = 97.75%


Unusual Observations for W@Pjoint III

     W@Pjoint                               St
Obs       III      Fit   SE Fit  Residual  Resid
  5   2.81000  2.81000  0.05657   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     1  0.12615  0.12615  0.12615  100.92  0.063
Error    1  0.00125  0.00125  0.00125
Total    2  0.12740


S = 0.0353553   R-Sq = 99.02%   R-Sq(adj) = 98.04%


Unusual Observations for W@Pjoint IV

                                                     St
Obs  W@Pjoint IV      Fit   SE Fit  Residual  Resid
  5      2.21000  2.21000  0.03536   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.57660  0.57660  0.57660  80.08  0.071
Error    1  0.00720  0.00720  0.00720
Total    2  0.58380


S = 0.0848528   R-Sq = 98.77%   R-Sq(adj) = 97.53%
```

```
Unusual Observations for W@2joint III

     W@2joint                                 St
Obs       III      Fit   SE Fit  Residual  Resid
  5   2.82000  2.82000  0.08485   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.35527  0.35527  0.35527  27.76  0.119
Error    1  0.01280  0.01280  0.01280
Total    2  0.36807


S = 0.113137   R-Sq = 96.52%   R-Sq(adj) = 93.04%


Unusual Observations for W@2joint IV

                                                 St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  5      2.20000  2.20000  0.11314   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     1  0.27735  0.27735  0.27735  32.82  0.110
Error    1  0.00845  0.00845  0.00845
Total    2  0.28580


S = 0.0919239   R-Sq = 97.04%   R-Sq(adj) = 94.09%


Unusual Observations for W@3joint IV

                                                 St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  5      1.84000  1.84000  0.09192   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  31.099  31.099  31.099  92.50  0.066
Error    1   0.336   0.336   0.336
Total    2  31.435


S = 0.579828   R-Sq = 98.93%   R-Sq(adj) = 97.86%


Unusual Observations for LoPhI,II
```

```
                                                 St
Obs  LoPhI,II     Fit  SE Fit  Residual  Resid
  5    6.2800  6.2800  0.5798   -0.0000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS   Adj MS        F      P
Name     1  0.54602  0.54602  0.54602  1213.37  0.018
Error    1  0.00045  0.00045  0.00045
Total    2  0.54647
```

S = 0.0212132   R-Sq = 99.92%   R-Sq(adj) = 99.84%

Unusual Observations for LoPhII,II

```
                                                   St
Obs  LoPhII,II      Fit  SE Fit  Residual  Resid
  5    12.3200  12.3200  0.0212    0.0000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

```
Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  2.7338  2.7338  2.7338  2.75  0.345
Error    1  0.9940  0.9940  0.9940
Total    2  3.7278
```

S = 0.997021   R-Sq = 73.33%   R-Sq(adj) = 46.67%

Unusual Observations for LoPhI,III

```
                                                   St
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  5    13.0300  13.0300  0.9970   -0.0000      * X
```

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

```
Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  4.8062  4.8062  4.8062  24.22  0.128
Error    1  0.1984  0.1984  0.1984
Total    2  5.0046
```

S = 0.445477   R-Sq = 96.03%   R-Sq(adj) = 92.07%

Unusual Observations for LoPhII,III

```
                                                   St
Obs  LoPhII,III     Fit  SE Fit  Residual  Resid
  5      7.0100  7.0100  0.4455    0.0000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.6734  0.6734  0.6734  0.74  0.548
Error    1  0.9113  0.9113  0.9113
Total    2  1.5846


S = 0.954594   R-Sq = 42.49%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit   SE Fit  Residual  Resid
  5      8.88000  8.88000  0.95459   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.0067  0.0067  0.0067  0.01  0.931
Error    1  0.5618  0.5618  0.5618
Total    2  0.5685


S = 0.749533   R-Sq = 1.17%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhI,IV

                                            St
Obs  LoPhI,IV      Fit  SE Fit  Residual  Resid
  5   10.7700  10.7700  0.7495    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.05227  0.05227  0.05227  0.59  0.582
Error    1  0.08820  0.08820  0.08820
Total    2  0.14047


S = 0.296985   R-Sq = 37.21%   R-Sq(adj) = 0.00%


Unusual Observations for LoPhII,IV

                                              St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  5    7.24000  7.24000  0.29698   0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.021600	0.021600	0.021600	12.00	0.179
Error	1	0.001800	0.001800	0.001800		
Total	2	0.023400				

S = 0.0424264   R-Sq = 92.31%   R-Sq(adj) = 84.62%

Unusual Observations for LoPhIII,IV

Obs	LoPhIII,IV	Fit	SE Fit	Residual	St Resid	
5	7.09000	7.09000	0.04243	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.29040	0.29040	0.29040	58.08	0.083
Error	1	0.00500	0.00500	0.00500		
Total	2	0.29540				

S = 0.0707107   R-Sq = 98.31%   R-Sq(adj) = 96.61%

Unusual Observations for LoPhIV,IV

Obs	LoPhIV,IV	Fit	SE Fit	Residual	St Resid	
5	5.58000	5.58000	0.07071	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	1.643	1.643	1.643	0.26	0.702
Error	1	6.408	6.408	6.408		
Total	2	8.051				

S = 2.53144   R-Sq = 20.41%   R-Sq(adj) = 0.00%

Unusual Observations for Foot Length

Obs	Foot Length	Fit	SE Fit	Residual	St Resid	
5	38.3600	38.3600	2.5314	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	9.985	9.985	9.985	4.13	0.291
Error	1	2.420	2.420	2.420		
Total	2	12.405				

S = 1.55563   R-Sq = 80.49%   R-Sq(adj) = 60.98%

Unusual Observations for Lotmt

Obs	Lotmt	Fit	SE Fit	Residual	St Resid	
5	48.2000	48.2000	1.5556	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	1.1704	1.1704	1.1704	81.00	0.070
Error	1	0.0145	0.0145	0.0145		
Total	2	1.1849				

S = 0.120208   R-Sq = 98.78%   R-Sq(adj) = 97.56%

Unusual Observations for Wotmt@prox

Obs	Wotmt@prox	Fit	SE Fit	Residual	St Resid	
5	5.43000	5.43000	0.12021	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	1	0.0181	0.0181	0.0181	0.16	0.755
Error	1	0.1105	0.1105	0.1105		
Total	2	0.1286				

S = 0.332340   R-Sq = 14.11%   R-Sq(adj) = 0.00%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid	
5	6.13000	6.13000	0.33234	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	6.190	A
Lecucophaeus pipixcan	2	3.305	A

```
Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value    P-Value
Lecucophaeus pipixcan (skin)       2.885      0.5802    4.972     0.1264


Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  6.190  A
Lecucophaeus pipixcan         2  3.305  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value    P-Value
Lecucophaeus pipixcan (skin)       2.885      0.5802    4.972     0.1264


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  24.500  A
Lecucophaeus pipixcan (skin)  1  22.010  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value    P-Value
Lecucophaeus pipixcan (skin)      -2.490       1.507   -1.652     0.3465


Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  24.500  A
Lecucophaeus pipixcan (skin)  1  22.010  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value    P-Value
Lecucophaeus pipixcan (skin)      -2.490       1.507   -1.652     0.3465


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  31.620  A
Lecucophaeus pipixcan (skin)  1  30.200  A

Means that do not share a letter are significantly different.
```

```
Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -1.420       2.442  -0.5814    0.6647


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  31.620  A
Lecucophaeus pipixcan (skin)  1  30.200  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -1.420       2.442  -0.5814    0.6647


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  30.445  A
Lecucophaeus pipixcan (skin)  1  30.200  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)     -0.2450      0.9440  -0.2595    0.8383


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                          N    Mean  Grouping
Lecucophaeus pipixcan         2  30.445  A
Lecucophaeus pipixcan (skin)  1  30.200  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)     -0.2450      0.9440  -0.2595    0.8383


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  1.820  A
Lecucophaeus pipixcan         2  1.715  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.1050	0.1299	0.8083	0.5672

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	1.820	A
Lecucophaeus pipixcan	2	1.715	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.1050	0.1299	0.8083	0.5672

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	2.810	A
Lecucophaeus pipixcan	2	2.160	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.6500	0.06928	9.382	0.0676

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	2.810	A
Lecucophaeus pipixcan	2	2.160	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.6500	0.06928	9.382	0.0676

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	2.210	A
Lecucophaeus pipixcan	2	1.775	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Difference	SE of	Adjusted

```
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      0.4350     0.04330    10.05    0.0632


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  2.210  A
Lecucophaeus pipixcan         2  1.775  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      0.4350     0.04330    10.05    0.0632


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     III

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  2.820  A
Lecucophaeus pipixcan         2  1.890  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      0.9300      0.1039    8.949    0.0708


Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  2.820  A
Lecucophaeus pipixcan         2  1.890  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      0.9300      0.1039    8.949    0.0709


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     IV

Name                          N   Mean  Grouping
Lecucophaeus pipixcan (skin)  1  2.200  A
Lecucophaeus pipixcan         2  1.470  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.7300	0.1386	5.268	0.1194

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	2.200	A
Lecucophaeus pipixcan	2	1.470	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.7300	0.1386	5.268	0.1194

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	1.840	A
Lecucophaeus pipixcan	2	1.195	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.6450	0.1126	5.729	0.1100

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	1.840	A
Lecucophaeus pipixcan	2	1.195	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.6450	0.1126	5.729	0.1100

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	13.110	A
Lecucophaeus pipixcan (skin)	1	6.280	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-6.830	0.7101	-9.618	0.0660

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	13.110	A
Lecucophaeus pipixcan (skin)	1	6.280	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-6.830	0.7101	-9.618	0.0660

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	12.320	A
Lecucophaeus pipixcan	2	11.415	B

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.9050	0.02598	34.83	0.0183

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	12.320	A
Lecucophaeus pipixcan	2	11.415	B

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.9050	0.02598	34.83	0.0183

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	15.055	A
Lecucophaeus pipixcan (skin)	1	13.030	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-2.025	1.221	-1.658	0.3454

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

```
Name                         N    Mean  Grouping
Lecucophaeus pipixcan        2  15.055  A
Lecucophaeus pipixcan (skin) 1  13.030  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -2.025       1.221   -1.658    0.3455


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     LoPhII,III

Name                         N   Mean  Grouping
Lecucophaeus pipixcan        2  9.695  A
Lecucophaeus pipixcan (skin) 1  7.010  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -2.685      0.5456   -4.921    0.1276


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name                         N   Mean  Grouping
Lecucophaeus pipixcan        2  9.695  A
Lecucophaeus pipixcan (skin) 1  7.010  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -2.685      0.5456   -4.921    0.1276


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     LoPhIII,III

Name                         N   Mean  Grouping
Lecucophaeus pipixcan (skin) 1  8.880  A
Lecucophaeus pipixcan        2  7.875  A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)       1.005       1.169   0.8596    0.5480


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name                         N   Mean  Grouping
```

Lecucophaeus pipixcan (skin)	1	8.880	A
Lecucophaeus pipixcan	2	7.875	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	1.005	1.169	0.8596	0.5480

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	10.870	A
Lecucophaeus pipixcan (skin)	1	10.770	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.1000	0.9180	-0.1089	0.9309

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	10.870	A
Lecucophaeus pipixcan (skin)	1	10.770	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.1000	0.9180	-0.1089	0.9309

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	7.520	A
Lecucophaeus pipixcan (skin)	1	7.240	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.2800	0.3637	-0.7698	0.5823

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	7.520	A
Lecucophaeus pipixcan (skin)	1	7.240	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.2800	0.3637	-0.7698	0.5823

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	7.090	A
Lecucophaeus pipixcan	2	6.910	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.1800	0.05196	3.464	0.1789

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	7.090	A
Lecucophaeus pipixcan	2	6.910	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	0.1800	0.05196	3.464	0.1789

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	6.240	A
Lecucophaeus pipixcan (skin)	1	5.580	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.6600	0.08660	-7.621	0.0831

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	6.240	A
Lecucophaeus pipixcan (skin)	1	5.580	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-0.6600	0.08660	-7.621	0.0831

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	39.930	A
Lecucophaeus pipixcan (skin)	1	38.360	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-1.570	3.100	-0.5064	0.7016

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Lecucophaeus pipixcan	2	39.930	A
Lecucophaeus pipixcan (skin)	1	38.360	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	-1.570	3.100	-0.5064	0.7016

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	48.200	A
Lecucophaeus pipixcan	2	44.330	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Lecucophaeus pipixcan (skin)	3.870	1.905	2.031	0.2912

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Lecucophaeus pipixcan (skin)	1	48.200	A
Lecucophaeus pipixcan	2	44.330	A

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

```
                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)       3.870       1.905    2.031    0.2912
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for
Wotmt@prox

```
Name                          N   Mean  Grouping
Lecucophaeus pipixcan         2  6.755  A
Lecucophaeus pipixcan (skin)  1  5.430  A
```

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

```
                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -1.325      0.1472   -9.000    0.0704
```

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

```
Name                          N   Mean  Grouping
Lecucophaeus pipixcan         2  6.755  A
Lecucophaeus pipixcan (skin)  1  5.430  A
```

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

```
                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)      -1.325      0.1472   -9.000    0.0705
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for
Wotmt@cond

```
Name                          N   Mean  Grouping
Lecucophaeus pipixcan         2  6.295  A
Lecucophaeus pipixcan (skin)  1  6.130  A
```

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

```
                              Difference       SE of            Adjusted
Name                            of Means  Difference  T-Value   P-Value
Lecucophaeus pipixcan (skin)     -0.1650      0.4070  -0.4054    0.7548
```

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

```
Name                          N   Mean  Grouping
Lecucophaeus pipixcan         2  6.295  A
Lecucophaeus pipixcan (skin)  1  6.130  A
```

Means that do not share a letter are significantly different.

Name = Lecucophaeus pipixcan subtracted from:

```
                              Difference       SE of            Adjusted
```

Name	of Means	Difference	T-Value	P-Value
Lecucophaeus pipixcan (skin)	-0.1650	0.4070	-0.4054	0.7548

General Linear Model: LoDI, LoDII, ... versus Name

```
* WARNING * Not all response variables have the same missing value pattern. You
            would get different univariate results if you ran this command
            separately for each of these response variables. See the Help topic
            'missing values' for details.


Factor  Type   Levels  Values
Name    fixed       2  Meleagris gallopavo, Meleagris gallopovo (skin)


Analysis of Variance for LoDI, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  0.4004  0.4004  0.4004  0.70  0.465
Error    3  1.7271  1.7271  0.5757
Total    4  2.1275


S = 0.758743   R-Sq = 18.82%   R-Sq(adj) = 0.00%


Unusual Observations for LoDI

                                            St
Obs     LoDI      Fit  SE Fit  Residual  Resid
  6  19.4900  19.4900  0.7587    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   0.808   0.808   0.808  0.31  0.618
Error    3   7.907   7.907   2.636
Total    4   8.715


S = 1.62342   R-Sq = 9.27%   R-Sq(adj) = 0.00%


Unusual Observations for LoDII

                                            St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  6  49.5500  49.5500  1.6234    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   1.104   1.104   1.104  0.15  0.728
Error    3  22.737  22.737   7.579
Total    4  23.842
```

```
S = 2.75302   R-Sq = 4.63%   R-Sq(adj) = 0.00%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  6  75.0700  75.0700  2.7530    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   16.82   16.82   16.82  1.39  0.323
Error    3   36.18   36.18   12.06
Total    4   53.00


S = 3.47289   R-Sq = 31.73%   R-Sq(adj) = 8.98%


Unusual Observations for LoDIV

                                            St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  6  53.4400  53.4400  3.4729    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  7.1760  7.1760  7.1760  14.53  0.032
Error    3  1.4819  1.4819  0.4940
Total    4  8.6579


S = 0.702828   R-Sq = 82.88%   R-Sq(adj) = 77.18%


Unusual Observations for W@Pjoint II

     W@Pjoint                               St
Obs        II     Fit  SE Fit  Residual  Resid
  6    9.6200  9.6200  0.7028   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   6.317   6.317   6.317  1.11  0.369
Error    3  17.074  17.074   5.691
Total    4  23.391


S = 2.38567   R-Sq = 27.01%   R-Sq(adj) = 2.67%
```

```
Unusual Observations for W@Pjoint III

     W@Pjoint                                St
Obs       III      Fit  SE Fit  Residual  Resid
  6   10.8800  10.8800  2.3857    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     1  0.22898  0.22898  0.22898  4.49  0.124
Error    3  0.15290  0.15290  0.05097
Total    4  0.38188


S = 0.225758   R-Sq = 59.96%   R-Sq(adj) = 46.61%


Unusual Observations for W@Pjoint IV

     W@Pjoint                               St
Obs        IV     Fit  SE Fit  Residual  Resid
  6    7.6600  7.6600  0.2258    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  3.8194  3.8194  3.8194  44.43  0.007
Error    3  0.2579  0.2579  0.0860
Total    4  4.0773


S = 0.293201   R-Sq = 93.67%   R-Sq(adj) = 91.57%


Unusual Observations for W@2joint III

     W@2joint                               St
Obs       III     Fit  SE Fit  Residual  Resid
  6    9.5600  9.5600  0.2932    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  2.4290  2.4290  2.4290  119.71  0.002
Error    3  0.0609  0.0609  0.0203
Total    4  2.4899


S = 0.142449   R-Sq = 97.56%   R-Sq(adj) = 96.74%


Unusual Observations for W@2joint IV
```

```
                                                        St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  6      7.91000  7.91000  0.14245   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  2.8577  2.8577  2.8577  104.04  0.002
Error    3  0.0824  0.0824  0.0275
Total    4  2.9401


S = 0.165731   R-Sq = 97.20%   R-Sq(adj) = 96.26%


Unusual Observations for W@3joint IV

                                                        St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  6      7.46000  7.46000  0.16573  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  177.61  177.61  177.61  119.88  0.002
Error    3    4.44    4.44    1.48
Total    4  182.05


S = 1.21718   R-Sq = 97.56%   R-Sq(adj) = 96.74%


Unusual Observations for LoPhI,II

                                                    St
Obs  LoPhI,II      Fit  SE Fit  Residual  Resid
  6   15.8400  15.8400  1.2172    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  12.672  12.672  12.672  11.57  0.042
Error    3   3.285   3.285   1.095
Total    4  15.957


S = 1.04636   R-Sq = 79.42%   R-Sq(adj) = 72.55%


Unusual Observations for LoPhII,II

                                                     St
Obs  LoPhII,II      Fit  SE Fit  Residual  Resid
```

```
  6    17.7400  17.7400  1.0464   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  124.65  124.65  124.65  55.69  0.005
Error    3    6.71    6.71    2.24
Total    4  131.36


S = 1.49607   R-Sq = 94.89%   R-Sq(adj) = 93.18%


Unusual Observations for LoPhI,III

                                              St
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  6    21.0700  21.0700  1.4961    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  34.034  34.034  34.034  65.38  0.004
Error    3   1.562   1.562   0.521
Total    4  35.596


S = 0.721497   R-Sq = 95.61%   R-Sq(adj) = 94.15%


Unusual Observations for LoPhII,III

                                               St
Obs  LoPhII,III      Fit  SE Fit  Residual  Resid
  6     17.9300  17.9300  0.7215    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  3.5112  3.5112  3.5112  3.92  0.142
Error    3  2.6885  2.6885  0.8962
Total    4  6.1997


S = 0.946661   R-Sq = 56.64%   R-Sq(adj) = 42.18%


Unusual Observations for LoPhIII,III

                                                St
Obs  LoPhIII,III      Fit  SE Fit  Residual  Resid
  6      17.2600  17.2600  0.9467    0.0000      * X

X denotes an observation whose X value gives it large leverage.
```

```
Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     1  310.24  310.24  310.24  386.37  0.000
Error    3    2.41    2.41    0.80
Total    4  312.64


S = 0.896079   R-Sq = 99.23%   R-Sq(adj) = 98.97%


Unusual Observations for LoPhI,IV

                                             St
Obs  LoPhI,IV     Fit  SE Fit  Residual  Resid
  6    3.9300  3.9300  0.8961   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  7.4298  7.4298  7.4298  13.36  0.035
Error    3  1.6687  1.6687  0.5562
Total    4  9.0985


S = 0.745805   R-Sq = 81.66%   R-Sq(adj) = 75.55%


Unusual Observations for LoPhII,IV

                                               St
Obs  LoPhII,IV      Fit  SE Fit  Residual  Resid
  6    11.2200  11.2200  0.7458    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1   9.426   9.426   9.426  8.93  0.058
Error    3   3.168   3.168   1.056
Total    4  12.594


S = 1.02763   R-Sq = 74.84%   R-Sq(adj) = 66.46%


Unusual Observations for LoPhIII,IV

                                               St
Obs  LoPhIII,IV     Fit  SE Fit  Residual  Resid
  6      8.5200  8.5200  1.0276    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests
```

```
Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  31.777  31.777  31.777  32.93  0.011
Error    3   2.895   2.895   0.965
Total    4  34.672


S = 0.982289   R-Sq = 91.65%   R-Sq(adj) = 88.87%


Unusual Observations for LoPhIV,IV

                                              St
Obs  LoPhIV,IV       Fit  SE Fit  Residual  Resid
  6    19.8900  19.8900  0.9823    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  301.24  301.24  301.24  30.57  0.012
Error    3   29.56   29.56    9.85
Total    4  330.81


S = 3.13910   R-Sq = 91.06%   R-Sq(adj) = 88.08%


Unusual Observations for Foot Length

       Foot                             St
Obs  Length     Fit  SE Fit  Residual  Resid
  6  81.170  81.170   3.139     0.000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     1  1179.5  1179.5  1179.5  22.75  0.018
Error    3   155.5   155.5    51.8
Total    4  1335.0


S = 7.20046   R-Sq = 88.35%   R-Sq(adj) = 84.47%


Unusual Observations for Lotmt

                                            St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  6  128.000  128.000   7.200     0.000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  3.4861  3.4861  3.4861  5.71  0.097
```

```
Error    3  1.8321  1.8321  0.6107
Total    4  5.3182


S = 0.781468   R-Sq = 65.55%   R-Sq(adj) = 54.07%


Unusual Observations for Wotmt@prox

                                                  St
Obs  Wotmt@prox      Fit  SE Fit  Residual  Resid
  6     22.3800  22.3800  0.7815    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     1  1.3676  1.3676  1.3676  2.00  0.252
Error    3  2.0517  2.0517  0.6839
Total    4  3.4193


S = 0.826977   R-Sq = 40.00%   R-Sq(adj) = 20.00%


Unusual Observations for Wotmt@cond

                                                  St
Obs  Wotmt@cond      Fit  SE Fit  Residual  Resid
  6     24.6800  24.6800  0.8270    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name                        N    Mean  Grouping
Meleagris gallopavo         4  20.198  A
Meleagris gallopovo (skin)  1  19.490  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Meleagris gallopovo (skin)     -0.7075      0.8483  -0.8340     0.4655


Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name                        N    Mean  Grouping
Meleagris gallopavo         4  20.198  A
Meleagris gallopovo (skin)  1  19.490  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
```

Meleagris gallopovo (skin)	-0.7075	0.8483	-0.8340	0.4655

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Meleagris gallopavo	4	50.555	A
Meleagris gallopovo (skin)	1	49.550	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-1.005	1.815	-0.5537	0.6184

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Meleagris gallopavo	4	50.555	A
Meleagris gallopovo (skin)	1	49.550	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-1.005	1.815	-0.5537	0.6184

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	75.070	A
Meleagris gallopavo	4	73.895	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.175	3.078	0.3817	0.7281

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	75.070	A
Meleagris gallopavo	4	73.895	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.175	3.078	0.3817	0.7281

```
Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name                         N    Mean  Grouping
Meleagris gallopavo          4  58.025  A
Meleagris gallopovo (skin)  1  53.440  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Meleagris gallopovo (skin)      -4.585       3.883   -1.181     0.3228


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                         N    Mean  Grouping
Meleagris gallopavo          4  58.025  A
Meleagris gallopovo (skin)  1  53.440  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Meleagris gallopovo (skin)      -4.585       3.883   -1.181     0.3228


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                         N   Mean  Grouping
Meleagris gallopovo (skin)  1  9.620  A
Meleagris gallopavo          4  6.625    B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Meleagris gallopovo (skin)       2.995      0.7858    3.811     0.0318


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                         N   Mean  Grouping
Meleagris gallopovo (skin)  1  9.620  A
Meleagris gallopavo          4  6.625    B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Meleagris gallopovo (skin)       2.995      0.7858    3.811     0.0318


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     III
```

```
Name                         N    Mean  Grouping
Meleagris gallopovo (skin)  1  10.880  A
Meleagris gallopavo         4   8.070  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)       2.810       2.667    1.054    0.3695


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name                         N    Mean  Grouping
Meleagris gallopovo (skin)  1  10.880  A
Meleagris gallopavo         4   8.070  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)       2.810       2.667    1.054    0.3695


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     IV

Name                         N   Mean  Grouping
Meleagris gallopovo (skin)  1  7.660  A
Meleagris gallopavo         4  7.125  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      0.5350      0.2524    2.120    0.1242


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name                         N   Mean  Grouping
Meleagris gallopovo (skin)  1  7.660  A
Meleagris gallopavo         4  7.125  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      0.5350      0.2524    2.120    0.1242


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     III
```

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	9.560	A
Meleagris gallopavo	4	7.375	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	2.185	0.3278	6.665	0.0069

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	9.560	A
Meleagris gallopavo	4	7.375	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	2.185	0.3278	6.665	0.0069

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	7.910	A
Meleagris gallopavo	4	6.168	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.743	0.1593	10.94	0.0016

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	7.910	A
Meleagris gallopavo	4	6.168	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.743	0.1593	10.94	0.0016

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping

Meleagris gallopovo (skin)	1	7.460	A
Meleagris gallopavo	4	5.570	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.890	0.1853	10.20	0.0020

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	7.460	A
Meleagris gallopavo	4	5.570	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.890	0.1853	10.20	0.0020

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Meleagris gallopavo	4	30.740	A
Meleagris gallopovo (skin)	1	15.840	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-14.90	1.361	-10.95	0.0016

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Meleagris gallopavo	4	30.740	A
Meleagris gallopovo (skin)	1	15.840	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-14.90	1.361	-10.95	0.0016

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Meleagris gallopavo	4	21.720	A
Meleagris gallopovo (skin)	1	17.740	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-3.980	1.170	-3.402	0.0424

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Meleagris gallopavo	4	21.720	A
Meleagris gallopovo (skin)	1	17.740	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-3.980	1.170	-3.402	0.0424

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	33.553	A
Meleagris gallopovo (skin)	1	21.070	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-12.48	1.673	-7.463	0.0050

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	33.553	A
Meleagris gallopovo (skin)	1	21.070	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-12.48	1.673	-7.463	0.0050

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	24.453	A
Meleagris gallopovo (skin)	1	17.930	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-6.523	0.8067	-8.086	0.0040

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	24.453	A
Meleagris gallopovo (skin)	1	17.930	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-6.523	0.8067	-8.086	0.0040

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	19.355	A
Meleagris gallopovo (skin)	1	17.260	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-2.095	1.058	-1.979	0.1421

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Meleagris gallopavo	4	19.355	A
Meleagris gallopovo (skin)	1	17.260	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-2.095	1.058	-1.979	0.1421

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	23.623	A
Meleagris gallopovo (skin)	1	3.930	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-19.69	1.002	-19.66	0.0003

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	23.623	A
Meleagris gallopovo (skin)	1	3.930	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-19.69	1.002	-19.66	0.0003

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	14.268	A
Meleagris gallopovo (skin)	1	11.220	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-3.047	0.8338	-3.655	0.0354

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	14.268	A
Meleagris gallopovo (skin)	1	11.220	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-3.047	0.8338	-3.655	0.0354

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	11.953	A
Meleagris gallopovo (skin)	1	8.520	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Meleagris gallopovo (skin)	-3.433	1.149	-2.988	0.0582

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Meleagris gallopavo	4	11.953	A
Meleagris gallopovo (skin)	1	8.520	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-3.433	1.149	-2.988	0.0583

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	19.890	A
Meleagris gallopavo	4	13.587	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	6.303	1.098	5.739	0.0105

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	19.890	A
Meleagris gallopavo	4	13.587	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	6.303	1.098	5.739	0.0105

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Meleagris gallopavo	4	100.575	A
Meleagris gallopovo (skin)	1	81.170	B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-19.40	3.510	-5.529	0.0117

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Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name                         N     Mean  Grouping
Meleagris gallopavo          4  100.575  A
Meleagris gallopovo (skin)   1   81.170    B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      -19.40       3.510   -5.529    0.0117


Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name                         N     Mean  Grouping
Meleagris gallopavo          4  166.397  A
Meleagris gallopovo (skin)   1  128.000    B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      -38.40       8.050   -4.770    0.0175


Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name                         N     Mean  Grouping
Meleagris gallopavo          4  166.397  A
Meleagris gallopovo (skin)   1  128.000    B

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      -38.40       8.050   -4.770    0.0175


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     Wotmt@prox

Name                         N    Mean  Grouping
Meleagris gallopavo          4  24.467  A
Meleagris gallopovo (skin)   1  22.380  A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Meleagris gallopovo (skin)      -2.088      0.8737   -2.389    0.0968


Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox
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Name	N	Mean	Grouping
Meleagris gallopavo	4	24.467	A
Meleagris gallopovo (skin)	1	22.380	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	-2.088	0.8737	-2.389	0.0968

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	24.680	A
Meleagris gallopavo	4	23.373	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.307	0.9246	1.414	0.2522

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Meleagris gallopovo (skin)	1	24.680	A
Meleagris gallopavo	4	23.373	A

Means that do not share a letter are significantly different.

Name = Meleagris gallopavo subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Meleagris gallopovo (skin)	1.307	0.9246	1.414	0.2522

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	3	Molothrus ater, Molothrus ater (alcohol), Molothrus ater (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.5441	0.5441	0.2721	0.75	0.529
Error	4	1.4494	1.4494	0.3624		
Total	6	1.9935				

S = 0.601955   R-Sq = 27.30%   R-Sq(adj) = 0.00%

```
Unusual Observations for LoDI

                                             St
Obs     LoDI      Fit  SE Fit  Residual  Resid
  5  10.3300  10.3300  0.6020    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.4835  0.4835  0.2418  0.57  0.605
Error    4  1.6907  1.6907  0.4227
Total    6  2.1742


S = 0.650130   R-Sq = 22.24%   R-Sq(adj) = 0.00%


Unusual Observations for LoDII

                                             St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  11.3800  11.3800  0.6501    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  3.5249  3.5249  1.7624  1.97  0.254
Error    4  3.5763  3.5763  0.8941
Total    6  7.1012


S = 0.945552   R-Sq = 49.64%   R-Sq(adj) = 24.46%


Unusual Observations for LoDIII

                                             St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  16.2300  16.2300  0.9456    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  1.3045  1.3045  0.6523  0.67  0.562
Error    4  3.9065  3.9065  0.9766
Total    6  5.2111


S = 0.988250   R-Sq = 25.03%   R-Sq(adj) = 0.00%


Unusual Observations for LoDIV

                                             St
```

```
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  14.4400  14.4400  0.9882    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.39147  0.39147  0.19573  5.78  0.066
Error    4  0.13547  0.13547  0.03387
Total    6  0.52694


S = 0.184035   R-Sq = 74.29%   R-Sq(adj) = 61.44%


Unusual Observations for W@Pjoint II

                                                 St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      1.50000  1.50000  0.18403   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.73959  0.73959  0.36979  10.35  0.026
Error    4  0.14290  0.14290  0.03572
Total    6  0.88249


S = 0.189011   R-Sq = 83.81%   R-Sq(adj) = 75.71%


Unusual Observations for W@Pjoint III

     W@Pjoint                              St
Obs       III      Fit   SE Fit  Residual  Resid
  5   1.69000  1.69000  0.18901   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.47427  0.47427  0.23713  5.27  0.076
Error    4  0.17988  0.17988  0.04497
Total    6  0.65414


S = 0.212058   R-Sq = 72.50%   R-Sq(adj) = 58.75%


Unusual Observations for W@2joint III

     W@2joint                              St
Obs       III      Fit   SE Fit  Residual  Resid
  5   1.62000  1.62000  0.21206   0.00000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  0.50690  0.50690  0.25345  248.78  0.000
Error    4  0.00407  0.00407  0.00102
Total    6  0.51097


S = 0.0319179   R-Sq = 99.20%   R-Sq(adj) = 98.80%


Unusual Observations for W@2joint IV

                                                 St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  5      1.45000  1.45000  0.03192   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.43976  0.43976  0.21988  24.76  0.006
Error    4  0.03552  0.03552  0.00888
Total    6  0.47529


S = 0.0942404   R-Sq = 92.53%   R-Sq(adj) = 88.79%


Unusual Observations for W@3joint IV

                                                 St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  5      1.29000  1.29000  0.09424   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  22.422  22.422  11.211  109.99  0.000
Error    4   0.408   0.408   0.102
Total    6  22.830


S = 0.319267   R-Sq = 98.21%   R-Sq(adj) = 97.32%


Unusual Observations for LoPhI,II

                                              St
Obs  LoPhI,II      Fit   SE Fit  Residual  Resid
  5   1.97000  1.97000  0.31927   0.00000      * X

X denotes an observation whose X value gives it large leverage.
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Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  8.6332  8.6332  4.3166  17.91  0.010
Error    4  0.9641  0.9641  0.2410
Total    6  9.5973


S = 0.490949   R-Sq = 89.95%   R-Sq(adj) = 84.93%


Unusual Observations for LoPhII,II

                                                St
Obs  LoPhII,II      Fit   SE Fit  Residual  Resid
  5    4.42000  4.42000  0.49095   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  7.3391  7.3391  3.6696  25.60  0.005
Error    4  0.5735  0.5735  0.1434
Total    6  7.9126


S = 0.378641   R-Sq = 92.75%   R-Sq(adj) = 89.13%


Unusual Observations for LoPhII,III

                                                 St
Obs  LoPhII,III      Fit   SE Fit  Residual  Resid
  5     5.01000  5.01000  0.37864  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  12.0131  12.0131  6.0065  18.19  0.010
Error    4   1.3209   1.3209  0.3302
Total    6  13.3340


S = 0.574652   R-Sq = 90.09%   R-Sq(adj) = 85.14%


Unusual Observations for LoPhIII,III

                                                  St
Obs  LoPhIII,III      Fit   SE Fit  Residual  Resid
  5      8.24000  8.24000  0.57465  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
```

```
Name      2  0.93947  0.93947  0.46974  7.29  0.046
Error     4  0.25790  0.25790  0.06448
Total     6  1.19737


S = 0.253919   R-Sq = 78.46%   R-Sq(adj) = 67.69%


Unusual Observations for LoPhII,IV

                                                   St
Obs  LoPhII,IV       Fit   SE Fit  Residual  Resid
  5    2.31000  2.31000  0.25392  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.6946  0.6946  0.3473  2.59  0.190
Error    4  0.5357  0.5357  0.1339
Total    6  1.2303


S = 0.365966   R-Sq = 56.46%   R-Sq(adj) = 34.69%


Unusual Observations for LoPhIII,IV

                                                    St
Obs  LoPhIII,IV       Fit   SE Fit  Residual  Resid
  5     2.30000  2.30000  0.36597  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  2.9510  2.9510  1.4755  7.98  0.040
Error    4  0.7398  0.7398  0.1850
Total    6  3.6908


S = 0.430058   R-Sq = 79.96%   R-Sq(adj) = 69.93%


Unusual Observations for LoPhIV,IV

                                                   St
Obs  LoPhIV,IV       Fit   SE Fit  Residual  Resid
  5    5.25000  5.25000  0.43006   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  53.579  53.579  26.789  14.06  0.016
Error    4   7.624   7.624   1.906
Total    6  61.203
```

```
S = 1.38058   R-Sq = 87.54%   R-Sq(adj) = 81.31%


Unusual Observations for Lotmt

                                            St
Obs    Lotmt      Fit  SE Fit  Residual  Resid
  5  32.6300  32.6300  1.3806    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.31339  0.31339  0.15670  1.61  0.307
Error    4  0.38975  0.38975  0.09744
Total    6  0.70314


S = 0.312150   R-Sq = 44.57%   R-Sq(adj) = 16.86%


Unusual Observations for Wotmt@prox

                                                St
Obs  Wotmt@prox      Fit   SE Fit  Residual  Resid
  5     3.61000  3.61000  0.31215  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  4.4737  4.4737  2.2369  4.33  0.100
Error    4  2.0682  2.0682  0.5170
Total    6  6.5419


S = 0.719053   R-Sq = 68.39%   R-Sq(adj) = 52.58%


Unusual Observations for Wotmt@cond

                                                St
Obs  Wotmt@cond      Fit   SE Fit  Residual  Resid
  5     3.90000  3.90000  0.71905  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name                      N    Mean  Grouping
Molothrus ater (alcohol)  2  10.500  A
Molothrus ater (skin)     1  10.330  A
Molothrus ater            4   9.890  A

Means that do not share a letter are significantly different.
```

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.6100	0.5213	1.1701	0.9207
Molothrus ater (skin)	0.4400	0.6730	0.6538	1.0000

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1700	0.7372	-0.2306	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	10.500	A
Molothrus ater (skin)	1	10.330	A
Molothrus ater	4	9.890	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.6100	0.5213	1.1701	0.5280
Molothrus ater (skin)	0.4400	0.6730	0.6538	0.8005

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1700	0.7372	-0.2306	0.9713

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	12.220	A
Molothrus ater	4	11.853	A
Molothrus ater (skin)	1	11.380	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.3675	0.5630	0.6527	1.000
Molothrus ater (skin)	-0.4725	0.7269	-0.6500	1.000

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.8400	0.7962	-1.055	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	12.220	A
Molothrus ater	4	11.853	A
Molothrus ater (skin)	1	11.380	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.3675	0.5630	0.6527	0.8010
Molothrus ater (skin)	-0.4725	0.7269	-0.6500	0.8024

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.8400	0.7962	-1.055	0.5863

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Molothrus ater	4	17.198	A
Molothrus ater (skin)	1	16.230	A
Molothrus ater (alcohol)	2	15.610	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-1.587	0.8189	-1.939	0.3737
Molothrus ater (skin)	-0.967	1.0572	-0.915	1.0000

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.6200	1.158	0.5354	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Molothrus ater	4	17.198	A
Molothrus ater (skin)	1	16.230	A
Molothrus ater (alcohol)	2	15.610	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-1.587	0.8189	-1.939	0.2426
Molothrus ater (skin)	-0.967	1.0572	-0.915	0.6606

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.6200	1.158	0.5354	0.8590

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Molothrus ater (skin)	1	14.440	A
Molothrus ater (alcohol)	2	13.695	A
Molothrus ater	4	13.205	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.4900	0.8558	0.5725	1.0000
Molothrus ater (skin)	1.2350	1.1049	1.1178	0.9788

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.7450	1.210	0.6155	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Molothrus ater (skin)	1	14.440	A
Molothrus ater (alcohol)	2	13.695	A
Molothrus ater	4	13.205	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.4900	0.8558	0.5725	0.8413
Molothrus ater (skin)	1.2350	1.1049	1.1178	0.5541

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.7450	1.210	0.6155	0.8200

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.730	A
Molothrus ater (skin)	1	1.500	A

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Molothrus ater            4  1.198  A

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      0.5325      0.1594    3.341    0.0864
Molothrus ater (skin)         0.3025      0.2058    1.470    0.6464


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)     -0.2300      0.2254   -1.020     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                      N   Mean  Grouping
Molothrus ater (alcohol)  2  1.730  A
Molothrus ater (skin)     1  1.500  A
Molothrus ater            4  1.198  A

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      0.5325      0.1594    3.341    0.0609
Molothrus ater (skin)         0.3025      0.2058    1.470    0.3939


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)     -0.2300      0.2254   -1.020    0.6044


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     III

Name                      N   Mean  Grouping
Molothrus ater (alcohol)  2  2.030  A
Molothrus ater (skin)     1  1.690  A B
Molothrus ater            4  1.295    B

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      0.7350      0.1637    4.490    0.0327
Molothrus ater (skin)         0.3950      0.2113    1.869    0.4049


Name = Molothrus ater (alcohol)  subtracted from:
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Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3400	0.2315	-1.469	0.6475

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	2.030	A
Molothrus ater (skin)	1	1.690	A B
Molothrus ater	4	1.295	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.7350	0.1637	4.490	0.0236
Molothrus ater (skin)	0.3950	0.2113	1.869	0.2609

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3400	0.2315	-1.469	0.3945

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.690	A
Molothrus ater (skin)	1	1.620	A
Molothrus ater	4	1.142	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.5475	0.1836	2.981	0.1221
Molothrus ater (skin)	0.4775	0.2371	2.014	0.3428

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.07000	0.2597	-0.2695	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.690	A
Molothrus ater (skin)	1	1.620	A
Molothrus ater	4	1.142	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.5475	0.1836	2.981	0.0849
Molothrus ater (skin)	0.4775	0.2371	2.014	0.2243

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.07000	0.2597	-0.2695	0.9611

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.770	A
Molothrus ater (skin)	1	1.450	B
Molothrus ater	4	1.158	C

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.6125	0.02764	22.159	0.0001
Molothrus ater (skin)	0.2925	0.03569	8.197	0.0036

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3200	0.03909	-8.186	0.0036

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.770	A
Molothrus ater (skin)	1	1.450	B
Molothrus ater	4	1.158	C

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.6125	0.02764	22.159	0.0001
Molothrus ater (skin)	0.2925	0.03569	8.197	0.0027

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3200	0.03909	-8.186	0.0027

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.615	A
Molothrus ater (skin)	1	1.290	A B
Molothrus ater	4	1.043	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.5725	0.08161	7.015	0.0065
Molothrus ater (skin)	0.2475	0.10536	2.349	0.2358

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3250	0.1154	-2.816	0.1441

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	1.615	A
Molothrus ater (skin)	1	1.290	A B
Molothrus ater	4	1.043	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	0.5725	0.08161	7.015	0.0048
Molothrus ater (skin)	0.2475	0.10536	2.349	0.1586

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.3250	0.1154	-2.816	0.0996

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Molothrus ater	4	5.662	A
Molothrus ater (alcohol)	2	2.085	B
Molothrus ater (skin)	1	1.970	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Molothrus ater (alcohol)	-3.578	0.2765	-12.94	0.0006
Molothrus ater (skin)	-3.692	0.3570	-10.34	0.0015

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1150	0.3910	-0.2941	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Molothrus ater	4	5.662	A
Molothrus ater (alcohol)	2	2.085	B
Molothrus ater (skin)	1	1.970	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-3.578	0.2765	-12.94	0.0005
Molothrus ater (skin)	-3.692	0.3570	-10.34	0.0011

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1150	0.3910	-0.2941	0.9540

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	7.935	A
Molothrus ater	4	6.282	A B
Molothrus ater (skin)	1	4.420	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	1.652	0.4252	3.887	0.0532
Molothrus ater (skin)	-1.863	0.5489	-3.393	0.0823

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-3.515	0.6013	-5.846	0.0128

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	7.935	A

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Molothrus ater            4  6.282    B
Molothrus ater (skin)     1  4.420    B

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)       1.652      0.4252    3.887    0.0380
Molothrus ater (skin)         -1.863      0.5489   -3.393    0.0581


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)      -3.515      0.6013   -5.846    0.0094


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     LoPhII,III

Name                      N   Mean  Grouping
Molothrus ater            4  5.473  A
Molothrus ater (skin)     1  5.010  A
Molothrus ater (alcohol)  2  3.140    B

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      -2.332      0.3279   -7.113    0.0062
Molothrus ater (skin)         -0.462      0.4233   -1.093    1.0000


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)       1.870      0.4637    4.032    0.0471


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name                      N   Mean  Grouping
Molothrus ater            4  5.473  A
Molothrus ater (skin)     1  5.010  A
Molothrus ater (alcohol)  2  3.140    B

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      -2.332      0.3279   -7.113    0.0046
Molothrus ater (skin)         -0.462      0.4233   -1.093    0.5669


Name = Molothrus ater (alcohol)  subtracted from:
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Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	1.870	0.4637	4.032	0.0338

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	8.900	A
Molothrus ater (skin)	1	8.240	A B
Molothrus ater	4	6.065	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	2.835	0.4977	5.697	0.0141
Molothrus ater (skin)	2.175	0.6425	3.385	0.0829

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.6600	0.7038	-0.9378	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	8.900	A
Molothrus ater (skin)	1	8.240	A B
Molothrus ater	4	6.065	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	2.835	0.4977	5.697	0.0103
Molothrus ater (skin)	2.175	0.6425	3.385	0.0585

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.6600	0.7038	-0.9378	0.6484

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Molothrus ater	4	2.875	A
Molothrus ater (skin)	1	2.310	A
Molothrus ater (alcohol)	2	2.070	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-0.8050	0.2199	-3.661	0.0647
Molothrus ater (skin)	-0.5650	0.2839	-1.990	0.3523

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.2400	0.3110	0.7717	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Molothrus ater	4	2.875	A
Molothrus ater (skin)	1	2.310	A B
Molothrus ater (alcohol)	2	2.070	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-0.8050	0.2199	-3.661	0.0460
Molothrus ater (skin)	-0.5650	0.2839	-1.990	0.2299

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	0.2400	0.3110	0.7717	0.7382

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Molothrus ater	4	3.032	A
Molothrus ater (alcohol)	2	2.455	A
Molothrus ater (skin)	1	2.300	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-0.5775	0.3169	-1.822	0.4276
Molothrus ater (skin)	-0.7325	0.4092	-1.790	0.4437

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1550	0.4482	-0.3458	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Molothrus ater	4	3.032	A
Molothrus ater (alcohol)	2	2.455	A
Molothrus ater (skin)	1	2.300	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	-0.5775	0.3169	-1.822	0.2740
Molothrus ater (skin)	-0.7325	0.4092	-1.790	0.2833

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1550	0.4482	-0.3458	0.9372

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	5.440	A
Molothrus ater (skin)	1	5.250	A
Molothrus ater	4	4.070	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	1.370	0.3724	3.678	0.0637
Molothrus ater (skin)	1.180	0.4808	2.454	0.2104

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1900	0.5267	-0.3607	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	5.440	A
Molothrus ater (skin)	1	5.250	A B
Molothrus ater	4	4.070	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Molothrus ater (alcohol)	1.370	0.3724	3.678	0.0453
Molothrus ater (skin)	1.180	0.4808	2.454	0.1425

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.1900	0.5267	-0.3607	0.9320

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Molothrus ater (skin)	1	32.630	A
Molothrus ater (alcohol)	2	29.180	A B
Molothrus ater	4	25.170	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	4.010	1.196	3.354	0.0854
Molothrus ater (skin)	7.460	1.544	4.833	0.0253

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	3.450	1.691	2.040	0.3327

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Molothrus ater (skin)	1	32.630	A
Molothrus ater (alcohol)	2	29.180	A B
Molothrus ater	4	25.170	B

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	4.010	1.196	3.354	0.0602
Molothrus ater (skin)	7.460	1.544	4.833	0.0184

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	3.450	1.691	2.040	0.2182

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping

```
Molothrus ater (alcohol)  2  3.775  A
Molothrus ater (skin)     1  3.610  A
Molothrus ater            4  3.305  A

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      0.4700      0.2703   1.7386    0.4713
Molothrus ater (skin)         0.3050      0.3490   0.8739    1.0000


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)     -0.1650      0.3823  -0.4316     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name                      N   Mean  Grouping
Molothrus ater (alcohol)  2  3.775  A
Molothrus ater (skin)     1  3.610  A
Molothrus ater            4  3.305  A

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      0.4700      0.2703   1.7386    0.2989
Molothrus ater (skin)         0.3050      0.3490   0.8739    0.6829


Name = Molothrus ater (alcohol)  subtracted from:

                       Difference       SE of            Adjusted
Name                     of Means  Difference  T-Value   P-Value
Molothrus ater (skin)     -0.1650      0.3823  -0.4316    0.9048


Grouping Information Using Bonferroni Method and 95.0% Confidence for
     Wotmt@cond

Name                      N   Mean  Grouping
Molothrus ater (alcohol)  2  4.855  A
Molothrus ater (skin)     1  3.900  A
Molothrus ater            4  3.035  A

Means that do not share a letter are significantly different.

Name = Molothrus ater  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Molothrus ater (alcohol)      1.8200      0.6227    2.923    0.1294
Molothrus ater (skin)         0.8650      0.8039    1.076    1.0000
```

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.9550	0.8807	-1.084	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Molothrus ater (alcohol)	2	4.855	A
Molothrus ater (skin)	1	3.900	A
Molothrus ater	4	3.035	A

Means that do not share a letter are significantly different.

Name = Molothrus ater subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (alcohol)	1.8200	0.6227	2.923	0.0898
Molothrus ater (skin)	0.8650	0.8039	1.076	0.5754

Name = Molothrus ater (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Molothrus ater (skin)	-0.9550	0.8807	-1.084	0.5711

General Linear Model: LoDI, LoDII, ... versus Name

* WARNING * Not all response variables have the same missing value pattern. You would get different univariate results if you ran this command separately for each of these response variables. See the Help topic 'missing values' for details.

Factor	Type	Levels	Values
Name	fixed	3	Passer domesticus, Passer domesticus (alcohol), Passer domesticus (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.4511	1.4511	0.7256	1.02	0.410
Error	7	5.0013	5.0013	0.7145		
Total	9	6.4524				

S = 0.845260   R-Sq = 22.49%   R-Sq(adj) = 0.34%

Unusual Observations for LoDI

Obs	LoDI	Fit	SE Fit	Residual	St Resid
5	6.42000	8.20000	0.37801	-1.78000	-2.35 R

R denotes an observation with a large standardized residual.

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.5215	0.5215	0.2607	0.43	0.667
Error	7	4.2580	4.2580	0.6083		
Total	9	4.7795				

S = 0.779926   R-Sq = 10.91%   R-Sq(adj) = 0.00%

Unusual Observations for LoDII

Obs	LoDII	Fit	SE Fit	Residual	St Resid
5	7.22000	8.77800	0.34879	-1.55800	-2.23 R

R denotes an observation with a large standardized residual.

Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.791	0.791	0.396	0.14	0.870
Error	7	19.441	19.441	2.777		
Total	9	20.232				

S = 1.66651   R-Sq = 3.91%   R-Sq(adj) = 0.00%

Unusual Observations for LoDIII

Obs	LoDIII	Fit	SE Fit	Residual	St Resid
5	10.3500	14.2020	0.7453	-3.8520	-2.58 R

R denotes an observation with a large standardized residual.

Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.3835	0.3835	0.1917	0.46	0.648
Error	7	2.9087	2.9087	0.4155		
Total	9	3.2922				

S = 0.644617   R-Sq = 11.65%   R-Sq(adj) = 0.00%

Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.21860	0.21860	0.10930	12.54	0.005
Error	7	0.06104	0.06104	0.00872		
Total	9	0.27964				

S = 0.0933784   R-Sq = 78.17%   R-Sq(adj) = 71.94%

Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.32284  0.32284  0.16142  24.69  0.001
Error    7  0.04577  0.04577  0.00654
Total    9  0.36861


S = 0.0808614   R-Sq = 87.58%   R-Sq(adj) = 84.04%


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.23548  0.23548  0.11774  12.31  0.005
Error    7  0.06693  0.06693  0.00956
Total    9  0.30241


S = 0.0977826   R-Sq = 77.87%   R-Sq(adj) = 71.54%


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.42725  0.42725  0.21363  24.44  0.001
Error    7  0.06119  0.06119  0.00874
Total    9  0.48844


S = 0.0934931   R-Sq = 87.47%   R-Sq(adj) = 83.89%


Unusual Observations for W@2joint IV

Obs  W@2joint IV      Fit   SE Fit  Residual  St Resid
  5      1.41000  1.21400  0.04181   0.19600      2.34 R

R denotes an observation with a large standardized residual.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.20449  0.20449  0.10225  12.43  0.005
Error    7  0.05760  0.05760  0.00823
Total    9  0.26209


S = 0.0907088   R-Sq = 78.02%   R-Sq(adj) = 71.75%


Unusual Observations for W@3joint IV

Obs  W@3joint IV      Fit   SE Fit  Residual  St Resid
  1      1.05000  0.90500  0.06414   0.14500      2.26 R
  2      0.76000  0.90500  0.06414  -0.14500     -2.26 R

R denotes an observation with a large standardized residual.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  5.7303  5.7303  2.8652  12.13  0.005
```

```
Error    7  1.6537  1.6537  0.2362
Total    9  7.3840


S = 0.486051   R-Sq = 77.60%   R-Sq(adj) = 71.21%


Unusual Observations for LoPhI,II

Obs  LoPhI,II      Fit   SE Fit  Residual  St Resid
  1   2.90000  3.68500  0.34369  -0.78500     -2.28 R
  2   4.47000  3.68500  0.34369   0.78500      2.28 R

R denotes an observation with a large standardized residual.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.5922  0.5922  0.2961  1.01  0.413
Error    7  2.0584  2.0584  0.2941
Total    9  2.6506


S = 0.542270   R-Sq = 22.34%   R-Sq(adj) = 0.16%


Unusual Observations for LoPhII,II

Obs  LoPhII,II      Fit   SE Fit  Residual  St Resid
  5    4.03000  5.12200  0.24251  -1.09200     -2.25 R

R denotes an observation with a large standardized residual.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  15.0265  15.0265  7.5133  25.38  0.001
Error    7   2.0720   2.0720  0.2960
Total    9  17.0985


S = 0.544055   R-Sq = 87.88%   R-Sq(adj) = 84.42%


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  5.1648  5.1648  2.5824  6.52  0.025
Error    7  2.7708  2.7708  0.3958
Total    9  7.9356


S = 0.629146   R-Sq = 65.08%   R-Sq(adj) = 55.11%


Unusual Observations for LoPhII,III

Obs  LoPhII,III      Fit   SE Fit  Residual  St Resid
  7     4.44000  3.23600  0.28136   1.20400      2.14 R

R denotes an observation with a large standardized residual.
```

Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	3.5611	3.5611	1.7805	5.10	0.043
Error	7	2.4452	2.4452	0.3493		
Total	9	6.0062				

S = 0.591028   R-Sq = 59.29%   R-Sq(adj) = 47.66%

Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.20196	0.20196	0.10098	1.38	0.312
Error	7	0.51184	0.51184	0.07312		
Total	9	0.71380				

S = 0.270406   R-Sq = 28.29%   R-Sq(adj) = 7.81%

Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.07109	1.07109	0.53555	24.85	0.001
Error	7	0.15087	0.15087	0.02155		
Total	9	1.22196				

S = 0.146807   R-Sq = 87.65%   R-Sq(adj) = 84.13%

Unusual Observations for LoPhIII,IV

Obs	LoPhIII,IV	Fit	SE Fit	Residual	St Resid
5	1.52000	1.79000	0.06565	-0.27000	-2.06 R

R denotes an observation with a large standardized residual.

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	2.0735	2.0735	1.0367	2.99	0.115
Error	7	2.4269	2.4269	0.3467		
Total	9	4.5004				

S = 0.588818   R-Sq = 46.07%   R-Sq(adj) = 30.66%

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	13.2387	13.2387	6.6193	11.95	0.006
Error	7	3.8770	3.8770	0.5539		
Total	9	17.1157				

S = 0.744219   R-Sq = 77.35%   R-Sq(adj) = 70.88%

```
Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  12.3515  12.3515  6.1758  15.34  0.003
Error    7   2.8185   2.8185  0.4026
Total    9  15.1701


S = 0.634547   R-Sq = 81.42%   R-Sq(adj) = 76.11%


Unusual Observations for Lotmt

Obs    Lotmt      Fit  SE Fit  Residual  St Resid
  5  20.2300  21.4720  0.2838   -1.2420     -2.19 R

R denotes an observation with a large standardized residual.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.0509  0.0509  0.0255  0.15  0.862
Error    7  1.1721  1.1721  0.1674
Total    9  1.2230


S = 0.409201   R-Sq = 4.16%   R-Sq(adj) = 0.00%


Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  1.5681  1.5681  0.7840  1.79  0.236
Error    7  3.0651  3.0651  0.4379
Total    9  4.6332


S = 0.661724   R-Sq = 33.84%   R-Sq(adj) = 14.94%


Unusual Observations for Wotmt@cond

Obs  Wotmt@cond      Fit   SE Fit  Residual  St Resid
 11     1.36000  2.71333  0.38205  -1.35333     -2.50 R

R denotes an observation with a large standardized residual.


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name                         N    Mean  Grouping
Passer domesticus (alcohol)  3  8.5100  A
Passer domesticus (skin)     5  8.2000  A
Passer domesticus            2  7.4250  A

Means that do not share a letter are significantly different.

Name = Passer domesticus  subtracted from:

                             Difference       SE of           Adjusted
```

Name	of Means	Difference	T-Value	P-Value
Passer domesticus (alcohol)	1.0850	0.7716	1.406	0.6075
Passer domesticus (skin)	0.7750	0.7072	1.096	0.9282

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.3100	0.6173	-0.5022	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	8.5100	A
Passer domesticus (skin)	5	8.2000	A
Passer domesticus	2	7.4250	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	1.0850	0.7716	1.406	0.3884
Passer domesticus (skin)	0.7750	0.7072	1.096	0.5461

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.3100	0.6173	-0.5022	0.8726

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Passer domesticus (skin)	5	8.7780	A
Passer domesticus (alcohol)	3	8.6367	A
Passer domesticus	2	8.1750	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4617	0.7120	0.6484	1.000
Passer domesticus (skin)	0.6030	0.6525	0.9241	1.000

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.1413	0.5696	0.2481	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping

Passer domesticus (skin)	5	8.7780	A
Passer domesticus (alcohol)	3	8.6367	A
Passer domesticus	2	8.1750	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4617	0.7120	0.6484	0.7991
Passer domesticus (skin)	0.6030	0.6525	0.9241	0.6435

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.1413	0.5696	0.2481	0.9668

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	14.2633	A
Passer domesticus (skin)	5	14.2020	A
Passer domesticus	2	13.5250	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.7383	1.521	0.4853	1.000
Passer domesticus (skin)	0.6770	1.394	0.4855	1.000

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.06133	1.217	-0.05040	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	14.2633	A
Passer domesticus (skin)	5	14.2020	A
Passer domesticus	2	13.5250	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.7383	1.521	0.4853	0.8804
Passer domesticus (skin)	0.6770	1.394	0.4855	0.8803

Name = Passer domesticus (alcohol) subtracted from:

```
                          Difference       SE of            Adjusted
Name                        of Means  Difference   T-Value   P-Value
Passer domesticus (skin)    -0.06133       1.217  -0.05040    0.9986
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

```
Name                         N    Mean  Grouping
Passer domesticus (skin)     5  9.4360  A
Passer domesticus (alcohol)  3  9.2500  A
Passer domesticus            2  8.9200  A
```

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

```
                             Difference       SE of           Adjusted
Name                           of Means  Difference  T-Value   P-Value
Passer domesticus (alcohol)      0.3300      0.5885   0.5608     1.000
Passer domesticus (skin)         0.5160      0.5393   0.9568     1.000
```

Name = Passer domesticus (alcohol) subtracted from:

```
                          Difference       SE of           Adjusted
Name                        of Means  Difference  T-Value   P-Value
Passer domesticus (skin)      0.1860      0.4708   0.3951     1.000
```

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

```
Name                         N    Mean  Grouping
Passer domesticus (skin)     5  9.4360  A
Passer domesticus (alcohol)  3  9.2500  A
Passer domesticus            2  8.9200  A
```

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

```
                             Difference       SE of           Adjusted
Name                           of Means  Difference  T-Value   P-Value
Passer domesticus (alcohol)      0.3300      0.5885   0.5608    0.8444
Passer domesticus (skin)         0.5160      0.5393   0.9568    0.6247
```

Name = Passer domesticus (alcohol) subtracted from:

```
                          Difference       SE of           Adjusted
Name                        of Means  Difference  T-Value   P-Value
Passer domesticus (skin)      0.1860      0.4708   0.3951    0.9185
```

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

```
Name                         N    Mean  Grouping
Passer domesticus (alcohol)  3  1.3467  A
Passer domesticus (skin)     5  1.2860  A
Passer domesticus            2  0.9450    B
```

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4017	0.08524	4.712	0.0065
Passer domesticus (skin)	0.3410	0.07813	4.365	0.0099

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.06067	0.06819	-0.8896	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.3467	A
Passer domesticus (skin)	5	1.2860	A
Passer domesticus	2	0.9450	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4017	0.08524	4.712	0.0054
Passer domesticus (skin)	0.3410	0.07813	4.365	0.0081

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.06067	0.06819	-0.8896	0.6633

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.7400	A
Passer domesticus (skin)	5	1.4560	B
Passer domesticus	2	1.2350	C

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.5050	0.07382	6.841	0.0007
Passer domesticus (skin)	0.2210	0.06765	3.267	0.0412

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.2840	0.05905	-4.809	0.0058

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Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name                         N    Mean  Grouping
Passer domesticus (alcohol)  3  1.7400  A
Passer domesticus (skin)     5  1.4560    B
Passer domesticus            2  1.2350      C

Means that do not share a letter are significantly different.

Name = Passer domesticus  subtracted from:

                             Difference       SE of            Adjusted
Name                           of Means  Difference  T-Value   P-Value
Passer domesticus (alcohol)      0.5050     0.07382    6.841    0.0006
Passer domesticus (skin)         0.2210     0.06765    3.267    0.0324


Name = Passer domesticus (alcohol)  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Passer domesticus (skin)     -0.2840     0.05905   -4.809    0.0048


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     III

Name                         N    Mean  Grouping
Passer domesticus (alcohol)  3  1.5400  A
Passer domesticus (skin)     5  1.3080    B
Passer domesticus            2  1.1050    B

Means that do not share a letter are significantly different.

Name = Passer domesticus  subtracted from:

                             Difference       SE of            Adjusted
Name                           of Means  Difference  T-Value   P-Value
Passer domesticus (alcohol)      0.4350     0.08926    4.873    0.0054
Passer domesticus (skin)         0.2030     0.08181    2.481    0.1264


Name = Passer domesticus (alcohol)  subtracted from:

                          Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Passer domesticus (skin)     -0.2320     0.07141   -3.249    0.0422


Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name                         N    Mean  Grouping
Passer domesticus (alcohol)  3  1.5400  A
Passer domesticus (skin)     5  1.3080    B
Passer domesticus            2  1.1050    B

Means that do not share a letter are significantly different.

Name = Passer domesticus  subtracted from:

                             Difference       SE of            Adjusted
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4350	0.08926	4.873	0.0045
Passer domesticus (skin)	0.2030	0.08181	2.481	0.0945

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.2320	0.07141	-3.249	0.0332

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.4567	A
Passer domesticus (skin)	5	1.2140	B
Passer domesticus	2	0.8600	C

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.5967	0.08535	6.991	0.0006
Passer domesticus (skin)	0.3540	0.07822	4.526	0.0081

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.2427	0.06828	-3.554	0.0279

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.4567	A
Passer domesticus (skin)	5	1.2140	B
Passer domesticus	2	0.8600	C

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.5967	0.08535	6.991	0.0005
Passer domesticus (skin)	0.3540	0.07822	4.526	0.0067

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.2427	0.06828	-3.554	0.0222

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.3067	A
Passer domesticus (skin)	5	1.2120	A
Passer domesticus	2	0.9050	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4017	0.08281	4.851	0.0056
Passer domesticus (skin)	0.3070	0.07589	4.045	0.0147

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.09467	0.06624	-1.429	0.5882

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	1.3067	A
Passer domesticus (skin)	5	1.2120	A
Passer domesticus	2	0.9050	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4017	0.08281	4.851	0.0046
Passer domesticus (skin)	0.3070	0.07589	4.045	0.0119

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.09467	0.06624	-1.429	0.3781

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Passer domesticus	2	3.6850	A
Passer domesticus (alcohol)	3	1.8767	B
Passer domesticus (skin)	5	1.7500	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-1.808	0.4437	-4.076	0.0141
Passer domesticus (skin)	-1.935	0.4067	-4.758	0.0062

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1267	0.3550	-0.3568	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Passer domesticus	2	3.6850	A
Passer domesticus (alcohol)	3	1.8767	B
Passer domesticus (skin)	5	1.7500	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-1.808	0.4437	-4.076	0.0115
Passer domesticus (skin)	-1.935	0.4067	-4.758	0.0051

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1267	0.3550	-0.3568	0.9329

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	5.4267	A
Passer domesticus (skin)	5	5.1220	A
Passer domesticus	2	4.7250	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.7017	0.4950	1.4174	0.5979
Passer domesticus (skin)	0.3970	0.4537	0.8750	1.0000

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.3047	0.3960	-0.7693	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	5.4267	A
Passer domesticus (skin)	5	5.1220	A
Passer domesticus	2	4.7250	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.7017	0.4950	1.4174	0.3833
Passer domesticus (skin)	0.3970	0.4537	0.8750	0.6718

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.3047	0.3960	-0.7693	0.7323

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Passer domesticus	2	4.5450	A
Passer domesticus (skin)	5	1.6740	B
Passer domesticus (alcohol)	3	1.2500	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-3.295	0.4967	-6.634	0.0009
Passer domesticus (skin)	-2.871	0.4552	-6.307	0.0012

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.4240	0.3973	1.067	0.9640

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Passer domesticus	2	4.5450	A
Passer domesticus (skin)	5	1.6740	B
Passer domesticus (alcohol)	3	1.2500	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-3.295	0.4967	-6.634	0.0007
Passer domesticus (skin)	-2.871	0.4552	-6.307	0.0010

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.4240	0.3973	1.067	0.5621

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Passer domesticus	2	4.7050	A
Passer domesticus (skin)	5	3.2360	A B
Passer domesticus (alcohol)	3	2.6600	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-2.045	0.5743	-3.561	0.0276
Passer domesticus (skin)	-1.469	0.5264	-2.791	0.0806

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.5760	0.4595	1.254	0.7507

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Passer domesticus	2	4.7050	A
Passer domesticus (skin)	5	3.2360	A B
Passer domesticus (alcohol)	3	2.6600	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-2.045	0.5743	-3.561	0.0220
Passer domesticus (skin)	-1.469	0.5264	-2.791	0.0617

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.5760	0.4595	1.254	0.4622

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Passer domesticus (skin)	5	6.7120	A
Passer domesticus (alcohol)	3	6.6067	A
Passer domesticus	2	5.1850	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	1.422	0.5395	2.635	0.1010
Passer domesticus (skin)	1.527	0.4945	3.088	0.0528

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.1053	0.4316	0.2440	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Passer domesticus (skin)	5	6.7120	A
Passer domesticus (alcohol)	3	6.6067	A B
Passer domesticus	2	5.1850	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	1.422	0.5395	2.635	0.0765
Passer domesticus (skin)	1.527	0.4945	3.088	0.0412

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.1053	0.4316	0.2440	0.9679

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Passer domesticus	2	2.5550	A
Passer domesticus (skin)	5	2.3840	A
Passer domesticus (alcohol)	3	2.1567	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-0.3983	0.2468	-1.614	0.4519
Passer domesticus (skin)	-0.1710	0.2262	-0.756	1.0000

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.2273	0.1975	1.151	0.8624

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Passer domesticus	2	2.5550	A
Passer domesticus (skin)	5	2.3840	A
Passer domesticus (alcohol)	3	2.1567	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-0.3983	0.2468	-1.614	0.3018
Passer domesticus (skin)	-0.1710	0.2262	-0.756	0.7399

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.2273	0.1975	1.151	0.5159

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Passer domesticus	2	2.6400	A
Passer domesticus (alcohol)	3	1.8967	B
Passer domesticus (skin)	5	1.7900	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-0.7433	0.1340	-5.547	0.0026
Passer domesticus (skin)	-0.8500	0.1228	-6.920	0.0007

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1067	0.1072	-0.9949	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Passer domesticus	2	2.6400	A
Passer domesticus (alcohol)	3	1.8967	B
Passer domesticus (skin)	5	1.7900	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	-0.7433	0.1340	-5.547	0.0022
Passer domesticus (skin)	-0.8500	0.1228	-6.920	0.0006

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1067	0.1072	-0.9949	0.6029

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	3.5833	A
Passer domesticus (skin)	5	3.5420	A
Passer domesticus	2	2.4200	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	1.163	0.5375	2.164	0.2015
Passer domesticus (skin)	1.122	0.4926	2.278	0.1705

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.04133	0.4300	-0.09612	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	3.5833	A
Passer domesticus (skin)	5	3.5420	A
Passer domesticus	2	2.4200	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	1.163	0.5375	2.164	0.1460
Passer domesticus (skin)	1.122	0.4926	2.278	0.1251

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.04133	0.4300	-0.09612	0.9949

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	16.7433	A
Passer domesticus (skin)	5	15.8460	A
Passer domesticus	2	13.4750	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	3.268	0.6794	4.811	0.0058
Passer domesticus (skin)	2.371	0.6227	3.808	0.0199

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.8973	0.5435	-1.651	0.4282

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	16.7433	A
Passer domesticus (skin)	5	15.8460	A
Passer domesticus	2	13.4750	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	3.268	0.6794	4.811	0.0048
Passer domesticus (skin)	2.371	0.6227	3.808	0.0160

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.8973	0.5435	-1.651	0.2879

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Passer domesticus (skin)	5	21.4720	A
Passer domesticus (alcohol)	3	19.2833	B
Passer domesticus	2	19.2000	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.08333	0.5793	0.1439	1.0000
Passer domesticus (skin)	2.27200	0.5309	4.2795	0.0110

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Passer domesticus (skin)	2.189	0.4634	4.723	0.0065

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Passer domesticus (skin)	5	21.4720	A
Passer domesticus (alcohol)	3	19.2833	B
Passer domesticus	2	19.2000	B

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.08333	0.5793	0.1439	0.9887
Passer domesticus (skin)	2.27200	0.5309	4.2795	0.0089

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	2.189	0.4634	4.723	0.0053

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	2.8900	A
Passer domesticus	2	2.8500	A
Passer domesticus (skin)	5	2.7340	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.0400	0.3735	0.1071	1.000
Passer domesticus (skin)	-0.1160	0.3424	-0.3388	1.000

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1560	0.2988	-0.5220	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Passer domesticus (alcohol)	3	2.8900	A
Passer domesticus	2	2.8500	A
Passer domesticus (skin)	5	2.7340	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.0400	0.3735	0.1071	0.9937
Passer domesticus (skin)	-0.1160	0.3424	-0.3388	0.9392

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	-0.1560	0.2988	-0.5220	0.8633

Grouping Information Using Bonferroni Method and 95.0% Confidence for
Wotmt@cond

Name	N	Mean	Grouping
Passer domesticus (skin)	5	3.2520	A
Passer domesticus (alcohol)	3	2.7133	A
Passer domesticus	2	2.2500	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4633	0.6041	0.7670	1.0000
Passer domesticus (skin)	1.0020	0.5536	1.8098	0.3397

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.5387	0.4833	1.115	0.9054

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Passer domesticus (skin)	5	3.2520	A
Passer domesticus (alcohol)	3	2.7133	A
Passer domesticus	2	2.2500	A

Means that do not share a letter are significantly different.

Name = Passer domesticus subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (alcohol)	0.4633	0.6041	0.7670	0.7336
Passer domesticus (skin)	1.0020	0.5536	1.8098	0.2347

Name = Passer domesticus (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Passer domesticus (skin)	0.5387	0.4833	1.115	0.5358

General Linear Model: LoDI, LoDII, ... versus Name

```
Factor  Type   Levels  Values
Name    fixed       3  Porzana carolina, Porzana carolina (alcohol), Porzana
                       carolina (skin)


Analysis of Variance for LoDI, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.1857  0.1857  0.0928  0.85  0.509
Error    3  0.3271  0.3271  0.1090
Total    5  0.5128


S = 0.330189   R-Sq = 36.21%   R-Sq(adj) = 0.00%


Unusual Observations for LoDI

                                              St
Obs     LoDI      Fit  SE Fit  Residual  Resid
  5  10.4700  10.4700  0.3302   -0.0000      * X
  6  10.2100  10.2100  0.3302    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  2.9309  2.9309  1.4654  2.00  0.280
Error    3  2.1971  2.1971  0.7324
Total    5  5.1280


S = 0.855784   R-Sq = 57.15%   R-Sq(adj) = 28.59%


Unusual Observations for LoDII

                                              St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  27.8600  27.8600  0.8558    0.0000      * X
  6  27.0400  27.0400  0.8558    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  19.496  19.496   9.748  8.80  0.056
Error    3   3.324   3.324   1.108
Total    5  22.820


S = 1.05269   R-Sq = 85.43%   R-Sq(adj) = 75.72%


Unusual Observations for LoDIII

                                              St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
```

```
  5  36.9800  36.9800  1.0527   -0.0000      * X
  6  37.3400  37.3400  1.0527    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  4.2659  4.2659  2.1329  2.29  0.249
Error    3  2.7973  2.7973  0.9324
Total    5  7.0631


S = 0.965622   R-Sq = 60.40%   R-Sq(adj) = 33.99%


Unusual Observations for LoDIV

                                              St
Obs    LoDIV      Fit  SE Fit  Residual  Resid
  5  30.9500  30.9500  0.9656    0.0000      * X
  6  30.0800  30.0800  0.9656    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.86607  0.86607  0.43304  49.44  0.005
Error    3  0.02627  0.02627  0.00876
Total    5  0.89235


S = 0.0935860   R-Sq = 97.06%   R-Sq(adj) = 95.09%


Unusual Observations for W@Pjoint II

                                                   St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      2.28000  2.28000  0.09359   0.00000      * X
  6      2.00000  2.00000  0.09359   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  1.00350  1.00350  0.50175  18.25  0.021
Error    3  0.08250  0.08250  0.02750
Total    5  1.08600


S = 0.165831   R-Sq = 92.40%   R-Sq(adj) = 87.34%


Unusual Observations for W@Pjoint III

     W@Pjoint                                St
Obs       III      Fit   SE Fit  Residual  Resid
```

```
  5   2.38000  2.38000  0.16583   0.00000      * X
  6   2.62000  2.62000  0.16583   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.47703  0.47703  0.23852  21.75  0.016
Error    3  0.03290  0.03290  0.01097
Total    5  0.50993


S = 0.104722   R-Sq = 93.55%   R-Sq(adj) = 89.25%


Unusual Observations for W@Pjoint IV

                                                 St
Obs  W@Pjoint IV      Fit   SE Fit  Residual  Resid
  5      2.16000  2.16000  0.10472   0.00000      * X
  6      2.06000  2.06000  0.10472   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.47781  0.47781  0.23890  40.55  0.007
Error    3  0.01768  0.01768  0.00589
Total    5  0.49548


S = 0.0767572   R-Sq = 96.43%   R-Sq(adj) = 94.05%


Unusual Observations for W@2joint III

     W@2joint                              St
Obs       III      Fit   SE Fit  Residual  Resid
  5   1.88000  1.88000  0.07676   0.00000      * X
  6   1.94000  1.94000  0.07676   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.48720  0.48720  0.24360  32.92  0.009
Error    3  0.02220  0.02220  0.00740
Total    5  0.50940


S = 0.0860233   R-Sq = 95.64%   R-Sq(adj) = 92.74%


Unusual Observations for W@2joint IV

                                                 St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
```

```
  5      1.93000  1.93000  0.08602   0.00000      * X
  6      1.81000  1.81000  0.08602   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.27106  0.27106  0.13553  64.79  0.003
Error    3  0.00627  0.00627  0.00209
Total    5  0.27733


S = 0.0457347   R-Sq = 97.74%   R-Sq(adj) = 96.23%


Unusual Observations for W@3joint IV

                                                  St
Obs  W@3joint IV      Fit   SE Fit  Residual  Resid
  5      1.65000  1.65000  0.04573   0.00000      * X
  6      1.56000  1.56000  0.04573   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  21.273  21.273  10.637  38.03  0.007
Error    3   0.839   0.839   0.280
Total    5  22.112


S = 0.528859   R-Sq = 96.21%   R-Sq(adj) = 93.68%


Unusual Observations for LoPhI,II

                                              St
Obs  LoPhI,II      Fit  SE Fit  Residual  Resid
  5   12.2400  12.2400  0.5289   -0.0000      * X
  6   10.0500  10.0500  0.5289    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  5.6646  5.6646  2.8323  8.42  0.059
Error    3  1.0091  1.0091  0.3364
Total    5  6.6737


S = 0.579971   R-Sq = 84.88%   R-Sq(adj) = 74.80%


Unusual Observations for LoPhII,II

                                              St
Obs  LoPhII,II     Fit  SE Fit  Residual  Resid
```

```
  5     9.3400  9.3400  0.5800    0.0000      * X
  6     9.6900  9.6900  0.5800   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  38.856  38.856  19.428  152.54  0.001
Error    3   0.382   0.382   0.127
Total    5  39.238


S = 0.356885   R-Sq = 99.03%   R-Sq(adj) = 98.38%


Unusual Observations for LoPhI,III

                                                St
Obs  LoPhI,III      Fit  SE Fit  Residual  Resid
  5    10.3800  10.3800  0.3569   -0.0000      * X
  6     7.4900   7.4900  0.3569    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  6.6926  6.6926  3.3463  11.40  0.040
Error    3  0.8805  0.8805  0.2935
Total    5  7.5731


S = 0.541756   R-Sq = 88.37%   R-Sq(adj) = 80.62%


Unusual Observations for LoPhII,III

                                                St
Obs  LoPhII,III     Fit  SE Fit  Residual  Resid
  5      8.6300  8.6300  0.5418    0.0000      * X
  6      7.7200  7.7200  0.5418    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  2.0055  2.0055  1.0027  3.24  0.178
Error    3  0.9295  0.9295  0.3098
Total    5  2.9349


S = 0.556619   R-Sq = 68.33%   R-Sq(adj) = 47.22%


Unusual Observations for LoPhIII,III

                                                 St
Obs  LoPhIII,III     Fit  SE Fit  Residual  Resid
```

```
  5       7.9500  7.9500  0.5566    0.0000      * X
  6       8.5100  8.5100  0.5566    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  22.060  22.060  11.030  110.20  0.002
Error    3   0.300   0.300   0.100
Total    5  22.360


S = 0.316373   R-Sq = 98.66%   R-Sq(adj) = 97.76%


Unusual Observations for LoPhI,IV

                                            St
Obs  LoPhI,IV     Fit  SE Fit  Residual  Resid
  5    6.5800  6.5800  0.3164    0.0000      * X
  6    6.6000  6.6000  0.3164    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  10.2562  10.2562  5.1281  62.98  0.004
Error    3   0.2443   0.2443  0.0814
Total    5  10.5005


S = 0.285351   R-Sq = 97.67%   R-Sq(adj) = 96.12%


Unusual Observations for LoPhII,IV

                                               St
Obs  LoPhII,IV      Fit   SE Fit  Residual  Resid
  5    4.85000  4.85000  0.28535   0.00000      * X
  6    3.61000  3.61000  0.28535  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  6.1596  6.1596  3.0798  11.80  0.038
Error    3  0.7833  0.7833  0.2611
Total    5  6.9429


S = 0.510979   R-Sq = 88.72%   R-Sq(adj) = 81.20%


Unusual Observations for LoPhIII,IV

                                                St
Obs  LoPhIII,IV      Fit   SE Fit  Residual  Resid
```

```
  5     3.66000  3.66000  0.51098   0.00000      * X
  6     3.19000  3.19000  0.51098   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  3.6222  3.6222  1.8111  11.08  0.041
Error    3  0.4905  0.4905  0.1635
Total    5  4.1127


S = 0.404341   R-Sq = 88.07%   R-Sq(adj) = 80.12%


Unusual Observations for LoPhIV,IV

                                               St
Obs  LoPhIV,IV       Fit   SE Fit  Residual  Resid
  5    4.87000  4.87000  0.40434   0.00000      * X
  6    4.79000  4.79000  0.40434   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2   5.717   5.717   2.858  1.54  0.347
Error    3   5.585   5.585   1.862
Total    5  11.302


S = 1.36449   R-Sq = 50.58%   R-Sq(adj) = 17.63%


Unusual Observations for Foot Length

                                                St
Obs  Foot Length       Fit  SE Fit  Residual  Resid
  5      41.3600  41.3600  1.3645    0.0000      * X
  6      38.8800  38.8800  1.3645    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.60501  0.60501  0.30250  10.30  0.045
Error    3  0.08808  0.08808  0.02936
Total    5  0.69308


S = 0.171343   R-Sq = 87.29%   R-Sq(adj) = 78.82%


Unusual Observations for Wotmt@prox

                                                St
Obs  Wotmt@prox      Fit   SE Fit  Residual  Resid
```

5	4.80000	4.80000	0.17134	0.00000	* X
6	5.20000	5.20000	0.17134	0.00000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	1.1658	1.1658	0.5829	5.57	0.098
Error	3	0.3137	0.3137	0.1046		
Total	5	1.4795				

S = 0.323368   R-Sq = 78.80%   R-Sq(adj) = 64.66%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid
5	5.53000	5.53000	0.32337	0.00000	* X
6	5.51000	5.51000	0.32337	0.00000	* X

X denotes an observation whose X value gives it large leverage.

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Porzana carolina (skin)	1	10.470	A
Porzana carolina (alcohol)	1	10.210	A
Porzana carolina	4	10.003	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.2075	0.3692	0.5621	1.0000
Porzana carolina (skin)	0.4675	0.3692	1.2664	0.8843

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.2600	0.4670	0.5568	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Porzana carolina (skin)	1	10.470	A
Porzana carolina (alcohol)	1	10.210	A
Porzana carolina	4	10.003	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Difference	SE of	Adjusted

Name	of Means	Difference	T-Value	P-Value
Porzana carolina (alcohol)	0.2075	0.3692	0.5621	0.8482
Porzana carolina (skin)	0.4675	0.3692	1.2664	0.5000

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.2600	0.4670	0.5568	0.8507

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Porzana carolina (skin)	1	27.860	A
Porzana carolina (alcohol)	1	27.040	A
Porzana carolina	4	26.055	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9850	0.9568	1.029	1.0000
Porzana carolina (skin)	1.8050	0.9568	1.887	0.4671

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.8200	1.210	0.6775	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Porzana carolina (skin)	1	27.860	A
Porzana carolina (alcohol)	1	27.040	A
Porzana carolina	4	26.055	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9850	0.9568	1.029	0.6112
Porzana carolina (skin)	1.8050	0.9568	1.887	0.2865

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.8200	1.210	0.6775	0.7917

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping

Porzana carolina (alcohol)	1	37.340	A
Porzana carolina (skin)	1	36.980	A
Porzana carolina	4	33.343	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	3.998	1.177	3.397	0.1277
Porzana carolina (skin)	3.637	1.177	3.091	0.1611

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.3600	1.489	-0.2418	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	37.340	A
Porzana carolina (skin)	1	36.980	A
Porzana carolina	4	33.343	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	3.998	1.177	3.397	0.0841
Porzana carolina (skin)	3.637	1.177	3.091	0.1053

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.3600	1.489	-0.2418	0.9686

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	30.950	A
Porzana carolina (alcohol)	1	30.080	A
Porzana carolina	4	28.808	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	1.272	1.080	1.179	0.9705
Porzana carolina (skin)	2.142	1.080	1.985	0.4243

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.8700	1.366	0.6371	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	30.950	A
Porzana carolina (alcohol)	1	30.080	A
Porzana carolina	4	28.808	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	1.272	1.080	1.179	0.5395
Porzana carolina (skin)	2.142	1.080	1.985	0.2624

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.8700	1.366	0.6371	0.8119

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Porzana carolina (skin)	1	2.280	A
Porzana carolina (alcohol)	1	2.000	A
Porzana carolina	4	1.353	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.6475	0.1046	6.188	0.0255
Porzana carolina (skin)	0.9275	0.1046	8.864	0.0091

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.2800	0.1324	2.116	0.3741

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Porzana carolina (skin)	1	2.280	A
Porzana carolina (alcohol)	1	2.000	A
Porzana carolina	4	1.353	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.6475	0.1046	6.188	0.0173
Porzana carolina (skin)	0.9275	0.1046	8.864	0.0062

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.2800	0.1324	2.116	0.2337

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	2.620	A
Porzana carolina (skin)	1	2.380	A B
Porzana carolina	4	1.645	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9750	0.1854	5.259	0.0402
Porzana carolina (skin)	0.7350	0.1854	3.964	0.0860

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.2400	0.2345	-1.023	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	2.620	A
Porzana carolina (skin)	1	2.380	A B
Porzana carolina	4	1.645	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9750	0.1854	5.259	0.0271
Porzana carolina (skin)	0.7350	0.1854	3.964	0.0573

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.2400	0.2345	-1.023	0.6142

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Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     IV

Name                         N   Mean  Grouping
Porzana carolina (skin)      1  2.160  A
Porzana carolina (alcohol)   1  2.060  A B
Porzana carolina             4  1.515    B

Means that do not share a letter are significantly different.

Name = Porzana carolina  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Porzana carolina (alcohol)      0.5450      0.1171    4.655     0.0561
Porzana carolina (skin)         0.6450      0.1171    5.509     0.0353


Name = Porzana carolina (alcohol)  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Porzana carolina (skin)      0.1000      0.1481   0.6752      1.000


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint IV

Name                         N   Mean  Grouping
Porzana carolina (skin)      1  2.160  A
Porzana carolina (alcohol)   1  2.060  A
Porzana carolina             4  1.515    B

Means that do not share a letter are significantly different.

Name = Porzana carolina  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Porzana carolina (alcohol)      0.5450      0.1171    4.655     0.0377
Porzana carolina (skin)         0.6450      0.1171    5.509     0.0239


Name = Porzana carolina (alcohol)  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Porzana carolina (skin)      0.1000      0.1481   0.6752     0.7929


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint
     III

Name                         N   Mean  Grouping
Porzana carolina (alcohol)   1  1.940  A
Porzana carolina (skin)      1  1.880  A
Porzana carolina             4  1.313    B

Means that do not share a letter are significantly different.

Name = Porzana carolina  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.6275	0.08582	7.312	0.0158
Porzana carolina (skin)	0.5675	0.08582	6.613	0.0211

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.06000	0.1086	-0.5527	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	1.940	A
Porzana carolina (skin)	1	1.880	A
Porzana carolina	4	1.313	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.6275	0.08582	7.312	0.0108
Porzana carolina (skin)	0.5675	0.08582	6.613	0.0144

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.06000	0.1086	-0.5527	0.8526

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	1.930	A
Porzana carolina (alcohol)	1	1.810	A
Porzana carolina	4	1.270	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.5400	0.09618	5.615	0.0335
Porzana carolina (skin)	0.6600	0.09618	6.862	0.0190

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.1200	0.1217	0.9864	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	1.930	A
Porzana carolina (alcohol)	1	1.810	A
Porzana carolina	4	1.270	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.5400	0.09618	5.615	0.0227
Porzana carolina (skin)	0.6600	0.09618	6.862	0.0129

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.1200	0.1217	0.9864	0.6328

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	1.650	A
Porzana carolina (alcohol)	1	1.560	A
Porzana carolina	4	1.158	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.4025	0.05113	7.872	0.0128
Porzana carolina (skin)	0.4925	0.05113	9.632	0.0071

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.09000	0.06468	1.391	0.7749

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Porzana carolina (skin)	1	1.650	A
Porzana carolina (alcohol)	1	1.560	A
Porzana carolina	4	1.158	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.4025	0.05113	7.872	0.0087
Porzana carolina (skin)	0.4925	0.05113	9.632	0.0049

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.09000	0.06468	1.391	0.4476

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Porzana carolina	4	14.908	A
Porzana carolina (skin)	1	12.240	A B
Porzana carolina (alcohol)	1	10.050	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-4.857	0.5913	-8.215	0.0113
Porzana carolina (skin)	-2.667	0.5913	-4.511	0.0611

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	2.190	0.7479	2.928	0.1833

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Porzana carolina	4	14.908	A
Porzana carolina (skin)	1	12.240	B
Porzana carolina (alcohol)	1	10.050	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-4.857	0.5913	-8.215	0.0077
Porzana carolina (skin)	-2.667	0.5913	-4.511	0.0409

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	2.190	0.7479	2.928	0.1192

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Porzana carolina	4	11.565	A
Porzana carolina (alcohol)	1	9.690	A
Porzana carolina (skin)	1	9.340	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-1.875	0.6484	-2.892	0.1888
Porzana carolina (skin)	-2.225	0.6484	-3.431	0.1245

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.3500	0.8202	-0.4267	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Porzana carolina	4	11.565	A
Porzana carolina (alcohol)	1	9.690	A
Porzana carolina (skin)	1	9.340	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-1.875	0.6484	-2.892	0.1226
Porzana carolina (skin)	-2.225	0.6484	-3.431	0.0821

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.3500	0.8202	-0.4267	0.9075

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Porzana carolina	4	14.035	A
Porzana carolina (skin)	1	10.380	B
Porzana carolina (alcohol)	1	7.490	C

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-6.545	0.3990	-16.40	0.0015
Porzana carolina (skin)	-3.655	0.3990	-9.16	0.0083

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Porzana carolina (skin)	2.890	0.5047	5.726	0.0317

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Porzana carolina	4	14.035	A
Porzana carolina (skin)	1	10.380	B
Porzana carolina (alcohol)	1	7.490	C

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-6.545	0.3990	-16.40	0.0010
Porzana carolina (skin)	-3.655	0.3990	-9.16	0.0056

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	2.890	0.5047	5.726	0.0215

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Porzana carolina	4	10.345	A
Porzana carolina (skin)	1	8.630	A
Porzana carolina (alcohol)	1	7.720	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-2.625	0.6057	-4.334	0.0680
Porzana carolina (skin)	-1.715	0.6057	-2.831	0.1983

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.9100	0.7662	1.188	0.9612

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Porzana carolina	4	10.345	A
Porzana carolina (skin)	1	8.630	A B
Porzana carolina (alcohol)	1	7.720	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-2.625	0.6057	-4.334	0.0455
Porzana carolina (skin)	-1.715	0.6057	-2.831	0.1285

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.9100	0.7662	1.188	0.5353

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Porzana carolina	4	9.408	A
Porzana carolina (alcohol)	1	8.510	A
Porzana carolina (skin)	1	7.950	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-0.897	0.6223	-1.442	0.7348
Porzana carolina (skin)	-1.457	0.6223	-2.342	0.3031

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.5600	0.7872	-0.7114	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Porzana carolina	4	9.408	A
Porzana carolina (alcohol)	1	8.510	A
Porzana carolina (skin)	1	7.950	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-0.897	0.6223	-1.442	0.4278
Porzana carolina (skin)	-1.457	0.6223	-2.342	0.1921

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.5600	0.7872	-0.7114	0.7745

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Porzana carolina	4	10.657	A
Porzana carolina (alcohol)	1	6.600	B
Porzana carolina (skin)	1	6.580	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-4.058	0.3537	-11.47	0.0043
Porzana carolina (skin)	-4.077	0.3537	-11.53	0.0042

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.02000	0.4474	-0.04470	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Porzana carolina	4	10.657	A
Porzana carolina (alcohol)	1	6.600	B
Porzana carolina (skin)	1	6.580	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-4.058	0.3537	-11.47	0.0029
Porzana carolina (skin)	-4.077	0.3537	-11.53	0.0029

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.02000	0.4474	-0.04470	0.9989

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Porzana carolina	4	6.898	A
Porzana carolina (skin)	1	4.850	B
Porzana carolina (alcohol)	1	3.610	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-3.287	0.3190	-10.30	0.0058
Porzana carolina (skin)	-2.047	0.3190	-6.42	0.0230

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	1.240	0.4035	3.073	0.1633

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Porzana carolina	4	6.898	A
Porzana carolina (skin)	1	4.850	B
Porzana carolina (alcohol)	1	3.610	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-3.287	0.3190	-10.30	0.0040
Porzana carolina (skin)	-2.047	0.3190	-6.42	0.0156

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	1.240	0.4035	3.073	0.1067

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Porzana carolina	4	5.555	A
Porzana carolina (skin)	1	3.660	A
Porzana carolina (alcohol)	1	3.190	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-2.365	0.5713	-4.140	0.0768
Porzana carolina (skin)	-1.895	0.5713	-3.317	0.1355

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.4700	0.7226	0.6504	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Porzana carolina	4	5.555	A
Porzana carolina (skin)	1	3.660	A
Porzana carolina (alcohol)	1	3.190	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-2.365	0.5713	-4.140	0.0512
Porzana carolina (skin)	-1.895	0.5713	-3.317	0.0891

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.4700	0.7226	0.6504	0.8053

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Porzana carolina	4	6.477	A
Porzana carolina (skin)	1	4.870	A
Porzana carolina (alcohol)	1	4.790	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-1.687	0.4521	-3.733	0.1005
Porzana carolina (skin)	-1.607	0.4521	-3.556	0.1138

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.08000	0.5718	0.1399	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Porzana carolina	4	6.477	A
Porzana carolina (skin)	1	4.870	A
Porzana carolina (alcohol)	1	4.790	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	-1.687	0.4521	-3.733	0.0667
Porzana carolina (skin)	-1.607	0.4521	-3.556	0.0752

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Porzana carolina (skin)	0.08000	0.5718	0.1399	0.9893

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Porzana carolina (skin)	1	41.360	A
Porzana carolina (alcohol)	1	38.880	A
Porzana carolina	4	38.712	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.1675	1.526	0.1098	1.0000
Porzana carolina (skin)	2.6475	1.526	1.7354	0.5432

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	2.480	1.930	1.285	0.8669

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Porzana carolina (skin)	1	41.360	A
Porzana carolina (alcohol)	1	38.880	A
Porzana carolina	4	38.712	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.1675	1.526	0.1098	0.9934
Porzana carolina (skin)	2.6475	1.526	1.7354	0.3282

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	2.480	1.930	1.285	0.4918

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	5.200	A
Porzana carolina (skin)	1	4.800	A
Porzana carolina	4	4.373	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.8275	0.1916	4.320	0.0686
Porzana carolina (skin)	0.4275	0.1916	2.232	0.3355

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.4000	0.2423	-1.651	0.5921

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Porzana carolina (alcohol)	1	5.200	A
Porzana carolina (skin)	1	4.800	A B
Porzana carolina	4	4.373	B

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.8275	0.1916	4.320	0.0459
Porzana carolina (skin)	0.4275	0.1916	2.232	0.2112

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	-0.4000	0.2423	-1.651	0.3544

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Porzana carolina (skin)	1	5.530	A
Porzana carolina (alcohol)	1	5.510	A
Porzana carolina	4	4.585	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9250	0.3615	2.559	0.2500
Porzana carolina (skin)	0.9450	0.3615	2.614	0.2383

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.02000	0.4573	0.04373	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Porzana carolina (skin)	1	5.530	A
Porzana carolina (alcohol)	1	5.510	A
Porzana carolina	4	4.585	A

Means that do not share a letter are significantly different.

Name = Porzana carolina subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (alcohol)	0.9250	0.3615	2.559	0.1602
Porzana carolina (skin)	0.9450	0.3615	2.614	0.1531

Name = Porzana carolina (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Porzana carolina (skin)	0.02000	0.4573	0.04373	0.9989

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	3	Sitta canadensis, Sitta canadensis (alcohol), Sitta canadensis (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	13.3485	13.3485	6.6742	32.50	0.001
Error	5	1.0269	1.0269	0.2054		
Total	7	14.3754				

S = 0.453198   R-Sq = 92.86%   R-Sq(adj) = 90.00%

Unusual Observations for LoDI

Obs	LoDI	Fit	SE Fit	Residual	St Resid	
5	10.4900	10.4900	0.4532	-0.0000	*	X
6	10.2500	10.9933	0.2617	-0.7433	-2.01	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	3.8526	3.8526	1.9263	5.36	0.057
Error	5	1.7977	1.7977	0.3595		
Total	7	5.6503				

S = 0.599612   R-Sq = 68.18%   R-Sq(adj) = 55.46%

```
Unusual Observations for LoDII

Obs    LoDII      Fit   SE Fit  Residual  St Resid
  5  6.17000  6.17000  0.59961   0.00000         * X
  7  7.05000  8.09000  0.34619  -1.04000     -2.12 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  10.0248  10.0248  5.0124  10.87  0.015
Error    5   2.3061   2.3061  0.4612
Total    7  12.3309


S = 0.679128   R-Sq = 81.30%   R-Sq(adj) = 73.82%


Unusual Observations for LoDIII

                                            St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  12.9800  12.9800  0.6791    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  6.2355  6.2355  3.1178  11.61  0.013
Error    5  1.3427  1.3427  0.2685
Total    7  7.5782


S = 0.518202   R-Sq = 82.28%   R-Sq(adj) = 75.20%


Unusual Observations for LoDIV

                                          St
Obs   LoDIV     Fit  SE Fit  Residual  Resid
  5  8.6100  8.6100  0.5182    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.58621  0.58621  0.29310  89.68  0.000
Error    5  0.01634  0.01634  0.00327
Total    7  0.60255


S = 0.0571693   R-Sq = 97.29%   R-Sq(adj) = 96.20%


Unusual Observations for W@Pjoint II
```

```
                                                      St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      1.17000  1.17000  0.05717  -0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.54871  0.54871  0.27436  23.87  0.003
Error    5  0.05748  0.05748  0.01150
Total    7  0.60619


S = 0.107215   R-Sq = 90.52%   R-Sq(adj) = 86.73%
```

Unusual Observations for W@Pjoint III

```
     W@Pjoint
Obs       III      Fit   SE Fit  Residual  St Resid
  5   1.31000  1.31000  0.10721  -0.00000         * X
  6   1.55000  1.37000  0.06190   0.18000      2.06 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for W@2joint III, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  1.02365  1.02365  0.51183  275.17  0.000
Error    5  0.00930  0.00930  0.00186
Total    7  1.03295


S = 0.0431277   R-Sq = 99.10%   R-Sq(adj) = 98.74%
```

Unusual Observations for W@2joint III

```
     W@2joint                                 St
Obs       III      Fit   SE Fit  Residual  Resid
  5   1.46000  1.46000  0.04313  -0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

```
Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  0.51568  0.51568  0.25784  187.75  0.000
Error    5  0.00687  0.00687  0.00137
Total    7  0.52255


S = 0.0370585   R-Sq = 98.69%   R-Sq(adj) = 98.16%
```

Unusual Observations for W@2joint IV

```
                                                St
Obs  W@2joint IV      Fit   SE Fit  Residual  Resid
  5      1.12000  1.12000  0.03706  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  0.56985  0.56985  0.28492  924.07  0.000
Error    5  0.00154  0.00154  0.00031
Total    7  0.57139


S = 0.0175594   R-Sq = 99.73%   R-Sq(adj) = 99.62%


Unusual Observations for W@3joint IV

Obs  W@3joint IV      Fit   SE Fit  Residual  St Resid
  2      0.59000  0.62250  0.00878  -0.03250     -2.14 R
  5      1.05000  1.05000  0.01756  -0.00000         * X

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  8.7395  8.7395  4.3698  452.67  0.000
Error    5  0.0483  0.0483  0.0097
Total    7  8.7878


S = 0.0982514   R-Sq = 99.45%   R-Sq(adj) = 99.23%


Unusual Observations for LoPhI,II

                                             St
Obs  LoPhI,II      Fit   SE Fit  Residual  Resid
  5   1.20000  1.20000  0.09825   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  4.2229  4.2229  2.1115  15.90  0.007
Error    5  0.6639  0.6639  0.1328
Total    7  4.8868


S = 0.364383   R-Sq = 86.41%   R-Sq(adj) = 80.98%


Unusual Observations for LoPhII,II

Obs  LoPhII,II      Fit   SE Fit  Residual  St Resid
  5    5.34000  5.34000  0.36438  -0.00000         * X
```

```
  8    5.71000  5.09000  0.21038   0.62000      2.08 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  13.9089  13.9089  6.9544  60.40  0.000
Error    5   0.5757   0.5757  0.1151
Total    7  14.4846


S = 0.339313   R-Sq = 96.03%   R-Sq(adj) = 94.44%


Unusual Observations for LoPhI,III

                                               St
Obs  LoPhI,III      Fit   SE Fit  Residual  Resid
  5    2.41000  2.41000  0.33931   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  3.5299  3.5299  1.7650  17.04  0.006
Error    5  0.5180  0.5180  0.1036
Total    7  4.0479


S = 0.321859   R-Sq = 87.20%   R-Sq(adj) = 82.09%


Unusual Observations for LoPhII,III

Obs  LoPhII,III      Fit   SE Fit  Residual  St Resid
  5     1.84000  1.84000  0.32186   0.00000         * X
  7     3.43000  3.96333  0.18583  -0.53333     -2.03 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS       F      P
Name     2  12.5814  12.5814  6.2907  179.18  0.000
Error    5   0.1755   0.1755  0.0351
Total    7  12.7569


S = 0.187372   R-Sq = 98.62%   R-Sq(adj) = 98.07%


Unusual Observations for LoPhIII,III

                                                 St
Obs  LoPhIII,III      Fit   SE Fit  Residual  Resid
  5      6.23000  6.23000  0.18737  -0.00000      * X
```

```
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  5.7331  5.7331  2.8666  37.51  0.001
Error    5  0.3821  0.3821  0.0764
Total    7  6.1152


S = 0.276433   R-Sq = 93.75%   R-Sq(adj) = 91.25%


Unusual Observations for LoPhI,IV

                                               St
Obs  LoPhI,IV      Fit   SE Fit  Residual  Resid
  5   0.87000  0.87000  0.27643   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS       F      P
Name     2  0.51288  0.51288  0.25644  243.46  0.000
Error    5  0.00527  0.00527  0.00105
Total    7  0.51815


S = 0.0324551   R-Sq = 98.98%   R-Sq(adj) = 98.58%


Unusual Observations for LoPhII,IV

Obs  LoPhII,IV      Fit   SE Fit  Residual  St Resid
  5    1.61000  1.61000  0.03246   0.00000         * X
  6    1.27000  1.32333  0.01874  -0.05333     -2.01 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  0.3282  0.3282  0.1641  1.49  0.312
Error    5  0.5524  0.5524  0.1105
Total    7  0.8806


S = 0.332375   R-Sq = 37.27%   R-Sq(adj) = 12.18%


Unusual Observations for LoPhIII,IV

                                                 St
Obs  LoPhIII,IV      Fit   SE Fit  Residual  Resid
  5     1.61000  1.61000  0.33238   0.00000      * X

X denotes an observation whose X value gives it large leverage.
```

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	6.2306	6.2306	3.1153	68.93	0.000
Error	5	0.2260	0.2260	0.0452		
Total	7	6.4566				

S = 0.212587   R-Sq = 96.50%   R-Sq(adj) = 95.10%

Unusual Observations for LoPhIV,IV

Obs	LoPhIV,IV	Fit	SE Fit	Residual	St Resid
5	4.86000	4.86000	0.21259	-0.00000	* X
7	4.48000	4.84667	0.12274	-0.36667	-2.11 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	12.5007	12.5007	6.2504	12.43	0.011
Error	5	2.5150	2.5150	0.5030		
Total	7	15.0158				

S = 0.709225   R-Sq = 83.25%   R-Sq(adj) = 76.55%

Unusual Observations for Foot Length

Obs	Foot Length	Fit	SE Fit	Residual	St Resid
5	15.6000	15.6000	0.7092	-0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	34.302	34.302	17.151	8.83	0.023
Error	5	9.711	9.711	1.942		
Total	7	44.013				

S = 1.39360   R-Sq = 77.94%   R-Sq(adj) = 69.11%

Unusual Observations for Lotmt

Obs	Lotmt	Fit	SE Fit	Residual	St Resid
5	22.3000	22.3000	1.3936	0.0000	* X
6	20.1000	17.6767	0.8046	2.4233	2.13 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.83285	0.83285	0.41643	24.70	0.003
Error	5	0.08430	0.08430	0.01686		
Total	7	0.91715				

S = 0.129846   R-Sq = 90.81%   R-Sq(adj) = 87.13%

Unusual Observations for Wotmt@prox

Obs	Wotmt@prox	Fit	SE Fit	Residual	St Resid	
5	1.81000	1.81000	0.12985	0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	8.0862	8.0862	4.0431	73.26	0.000
Error	5	0.2759	0.2759	0.0552		
Total	7	8.3622				

S = 0.234922   R-Sq = 96.70%   R-Sq(adj) = 95.38%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid	
5	3.75000	3.75000	0.23492	-0.00000	*	X
6	3.98000	3.56333	0.13563	0.41667	2.17	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.691	0.3461	7.774	0.0017
Sitta canadensis (skin)	2.188	0.5067	4.317	0.0228

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.5033	0.5233	-0.9618	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping	
Sitta canadensis (alcohol)	3	10.9933	A	
Sitta canadensis (skin)	1	10.4900	A	
Sitta canadensis	4	8.3025		B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.691	0.3461	7.774	0.0013
Sitta canadensis (skin)	2.188	0.5067	4.317	0.0173

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.5033	0.5233	-0.9618	0.6293

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	8.0900	A
Sitta canadensis	4	6.8725	A
Sitta canadensis (skin)	1	6.1700	A

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.2175	0.4580	2.659	0.1349
Sitta canadensis (skin)	-0.7025	0.6704	-1.048	1.0000

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-1.920	0.6924	-2.773	0.1177

Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	8.0900	A
Sitta canadensis	4	6.8725	A
Sitta canadensis (skin)	1	6.1700	A

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.2175	0.4580	2.659	0.0966
Sitta canadensis (skin)	-0.7025	0.6704	-1.048	0.5822

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-1.920	0.6924	-2.773	0.0849

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	13.7200	A
Sitta canadensis (skin)	1	12.9800	A B
Sitta canadensis	4	11.3425	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.377	0.5187	4.584	0.0178
Sitta canadensis (skin)	1.638	0.7593	2.157	0.2506

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.7400	0.7842	-0.9436	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	13.7200	A
Sitta canadensis (skin)	1	12.9800	A B
Sitta canadensis	4	11.3425	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.377	0.5187	4.584	0.0136
Sitta canadensis (skin)	1.638	0.7593	2.157	0.1726

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.7400	0.7842	-0.9436	0.6393

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	10.5433	A
Sitta canadensis	4	8.7500	B
Sitta canadensis (skin)	1	8.6100	A B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

```
Sitta canadensis (alcohol)      1.7933      0.3958   4.5311    0.0187
Sitta canadensis (skin)        -0.1400      0.5794  -0.2416    1.0000


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Sitta canadensis (skin)      -1.933      0.5984   -3.231    0.0695


Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name                        N     Mean  Grouping
Sitta canadensis (alcohol)  3  10.5433  A
Sitta canadensis            4   8.7500    B
Sitta canadensis (skin)     1   8.6100  A B

Means that do not share a letter are significantly different.

Name = Sitta canadensis  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Sitta canadensis (alcohol)      1.7933      0.3958   4.5311    0.0142
Sitta canadensis (skin)        -0.1400      0.5794  -0.2416    0.9685


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Sitta canadensis (skin)      -1.933      0.5984   -3.231    0.0512


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint
     II

Name                        N    Mean  Grouping
Sitta canadensis (alcohol)  3  1.2333  A
Sitta canadensis (skin)     1  1.1700  A
Sitta canadensis            4  0.6775    B

Means that do not share a letter are significantly different.

Name = Sitta canadensis  subtracted from:

                            Difference       SE of           Adjusted
Name                          of Means  Difference  T-Value   P-Value
Sitta canadensis (alcohol)      0.5558     0.04366   12.730    0.0002
Sitta canadensis (skin)         0.4925     0.06392    7.705    0.0018


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of           Adjusted
Name                       of Means  Difference  T-Value   P-Value
Sitta canadensis (skin)    -0.06333     0.06601  -0.9594     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name                        N    Mean  Grouping
```

Sitta canadensis (alcohol)	3	1.2333	A
Sitta canadensis (skin)	1	1.1700	A
Sitta canadensis	4	0.6775	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5558	0.04366	12.730	0.0001
Sitta canadensis (skin)	0.4925	0.06392	7.705	0.0014

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.06333	0.06601	-0.9594	0.6306

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.3700	A
Sitta canadensis (skin)	1	1.3100	A
Sitta canadensis	4	0.8325	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5375	0.08189	6.564	0.0037
Sitta canadensis (skin)	0.4775	0.11987	3.983	0.0315

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.06000	0.1238	-0.4846	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.3700	A
Sitta canadensis (skin)	1	1.3100	A
Sitta canadensis	4	0.8325	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5375	0.08189	6.564	0.0029
Sitta canadensis (skin)	0.4775	0.11987	3.983	0.0237

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.06000	0.1238	-0.4846	0.8815

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.5000	A
Sitta canadensis (skin)	1	1.4600	A
Sitta canadensis	4	0.7750	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.7250	0.03294	22.01	0.0000
Sitta canadensis (skin)	0.6850	0.04822	14.21	0.0001

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.04000	0.04980	-0.8032	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.5000	A
Sitta canadensis (skin)	1	1.4600	A
Sitta canadensis	4	0.7750	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.7250	0.03294	22.01	0.0000
Sitta canadensis (skin)	0.6850	0.04822	14.21	0.0001

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.04000	0.04980	-0.8032	0.7175

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.2067	A
Sitta canadensis (skin)	1	1.1200	A
Sitta canadensis	4	0.6800	B

```
Means that do not share a letter are significantly different.

Name = Sitta canadensis  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Sitta canadensis (alcohol)      0.5267     0.02830    18.61     0.0000
Sitta canadensis (skin)         0.4400     0.04143    10.62     0.0004


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Sitta canadensis (skin)    -0.08667     0.04279   -2.025     0.2961


Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name                        N    Mean  Grouping
Sitta canadensis (alcohol)  3  1.2067  A
Sitta canadensis (skin)     1  1.1200  A
Sitta canadensis            4  0.6800    B

Means that do not share a letter are significantly different.

Name = Sitta canadensis  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Sitta canadensis (alcohol)      0.5267     0.02830    18.61     0.0000
Sitta canadensis (skin)         0.4400     0.04143    10.62     0.0003


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of            Adjusted
Name                       of Means  Difference  T-Value    P-Value
Sitta canadensis (skin)    -0.08667     0.04279   -2.025     0.2012


Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint
     IV

Name                        N    Mean  Grouping
Sitta canadensis (alcohol)  3  1.1833  A
Sitta canadensis (skin)     1  1.0500    B
Sitta canadensis            4  0.6225      C

Means that do not share a letter are significantly different.

Name = Sitta canadensis  subtracted from:

                            Difference       SE of            Adjusted
Name                          of Means  Difference  T-Value    P-Value
Sitta canadensis (alcohol)      0.5608     0.01341    41.82     0.0000
Sitta canadensis (skin)         0.4275     0.01963    21.78     0.0000


Name = Sitta canadensis (alcohol)  subtracted from:

                         Difference       SE of            Adjusted
```

Name	of Means	Difference	T-Value	P-Value
Sitta canadensis (skin)	-0.1333	0.02028	-6.576	0.0037

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	1.1833	A
Sitta canadensis (skin)	1	1.0500	B
Sitta canadensis	4	0.6225	C

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5608	0.01341	41.82	0.0000
Sitta canadensis (skin)	0.4275	0.01963	21.78	0.0000

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.1333	0.02028	-6.576	0.0029

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Sitta canadensis	4	3.2400	A
Sitta canadensis (skin)	1	1.2000	B
Sitta canadensis (alcohol)	3	1.1333	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-2.107	0.07504	-28.07	0.0000
Sitta canadensis (skin)	-2.040	0.10985	-18.57	0.0000

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.06667	0.1135	0.5876	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Sitta canadensis	4	3.2400	A
Sitta canadensis (skin)	1	1.2000	B
Sitta canadensis (alcohol)	3	1.1333	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-2.107	0.07504	-28.07	0.0000
Sitta canadensis (skin)	-2.040	0.10985	-18.57	0.0000

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.06667	0.1135	0.5876	0.8325

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	5.3400	A
Sitta canadensis (alcohol)	3	5.0900	A
Sitta canadensis	4	3.7075	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.382	0.2783	4.968	0.0127
Sitta canadensis (skin)	1.633	0.4074	4.007	0.0308

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2500	0.4208	0.5942	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	5.3400	A
Sitta canadensis (alcohol)	3	5.0900	A
Sitta canadensis	4	3.7075	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.382	0.2783	4.968	0.0097
Sitta canadensis (skin)	1.633	0.4074	4.007	0.0232

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2500	0.4208	0.5942	0.8292

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Sitta canadensis	4	3.4900	A
Sitta canadensis (skin)	1	2.4100	A
Sitta canadensis (alcohol)	3	0.6433	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-2.847	0.2592	-10.98	0.0003
Sitta canadensis (skin)	-1.080	0.3794	-2.85	0.1079

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	1.767	0.3918	4.509	0.0190

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping
Sitta canadensis	4	3.4900	A
Sitta canadensis (skin)	1	2.4100	A
Sitta canadensis (alcohol)	3	0.6433	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-2.847	0.2592	-10.98	0.0003
Sitta canadensis (skin)	-1.080	0.3794	-2.85	0.0781

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	1.767	0.3918	4.509	0.0145

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	3.9633	A
Sitta canadensis	4	3.7050	A
Sitta canadensis (skin)	1	1.8400	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.258	0.2458	1.051	1.0000
Sitta canadensis (skin)	-1.865	0.3598	-5.183	0.0106

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-2.123	0.3717	-5.713	0.0069

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	3.9633	A
Sitta canadensis	4	3.7050	A
Sitta canadensis (skin)	1	1.8400	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.258	0.2458	1.051	0.5806
Sitta canadensis (skin)	-1.865	0.3598	-5.183	0.0081

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-2.123	0.3717	-5.713	0.0053

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	7.1067	A
Sitta canadensis (skin)	1	6.2300	B
Sitta canadensis	4	4.4375	C

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.669	0.1431	18.651	0.0000
Sitta canadensis (skin)	1.793	0.2095	8.557	0.0011

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.8767	0.2164	-4.052	0.0294

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	7.1067	A
Sitta canadensis (skin)	1	6.2300	B
Sitta canadensis	4	4.4375	C

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.669	0.1431	18.651	0.0000
Sitta canadensis (skin)	1.793	0.2095	8.557	0.0008

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.8767	0.2164	-4.052	0.0222

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Sitta canadensis	4	2.3525	A
Sitta canadensis (skin)	1	0.8700	B
Sitta canadensis (alcohol)	3	0.6000	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-1.753	0.2111	-8.301	0.0012
Sitta canadensis (skin)	-1.483	0.3091	-4.797	0.0147

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2700	0.3192	0.8459	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Sitta canadensis	4	2.3525	A
Sitta canadensis (skin)	1	0.8700	B
Sitta canadensis (alcohol)	3	0.6000	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-1.753	0.2111	-8.301	0.0010
Sitta canadensis (skin)	-1.483	0.3091	-4.797	0.0112

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value

Sitta canadensis (skin)	0.2700	0.3192	0.8459	0.6937

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Sitta canadensis	4	1.8700	A
Sitta canadensis (skin)	1	1.6100	B
Sitta canadensis (alcohol)	3	1.3233	C

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-0.5467	0.02479	-22.05	0.0000
Sitta canadensis (skin)	-0.2600	0.03629	-7.17	0.0025

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2867	0.03748	7.649	0.0018

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name	N	Mean	Grouping
Sitta canadensis	4	1.8700	A
Sitta canadensis (skin)	1	1.6100	B
Sitta canadensis (alcohol)	3	1.3233	C

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-0.5467	0.02479	-22.05	0.0000
Sitta canadensis (skin)	-0.2600	0.03629	-7.17	0.0019

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2867	0.03748	7.649	0.0014

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Sitta canadensis	4	2.2450	A
Sitta canadensis (alcohol)	3	2.0633	A
Sitta canadensis (skin)	1	1.6100	A

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-0.1817	0.2539	-0.716	1.0000
Sitta canadensis (skin)	-0.6350	0.3716	-1.709	0.4446

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.4533	0.3838	-1.181	0.8719

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Sitta canadensis	4	2.2450	A
Sitta canadensis (alcohol)	3	2.0633	A
Sitta canadensis (skin)	1	1.6100	A

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	-0.1817	0.2539	-0.716	0.7656
Sitta canadensis (skin)	-0.6350	0.3716	-1.709	0.2900

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.4533	0.3838	-1.181	0.5123

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	4.8600	A
Sitta canadensis (alcohol)	3	4.8467	A
Sitta canadensis	4	3.0850	B

Means that do not share a letter are significantly different.

All Pairwise Comparisons among Levels of Name
Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.762	0.1624	10.850	0.0003
Sitta canadensis (skin)	1.775	0.2377	7.468	0.0020

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.01333	0.2455	0.05432	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	4.8600	A
Sitta canadensis (alcohol)	3	4.8467	A
Sitta canadensis	4	3.0850	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.762	0.1624	10.850	0.0003
Sitta canadensis (skin)	1.775	0.2377	7.468	0.0016

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.01333	0.2455	0.05432	0.9984

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	15.6000	A B
Sitta canadensis (alcohol)	3	15.3400	A
Sitta canadensis	4	12.9100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.430	0.5417	4.486	0.0194
Sitta canadensis (skin)	2.690	0.7929	3.392	0.0582

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2600	0.8189	0.3175	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	15.6000	A
Sitta canadensis (alcohol)	3	15.3400	A
Sitta canadensis	4	12.9100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	2.430	0.5417	4.486	0.0148
Sitta canadensis (skin)	2.690	0.7929	3.392	0.0432

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.2600	0.8189	0.3175	0.9465

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	22.3000	A
Sitta canadensis (alcohol)	3	17.6767	A B
Sitta canadensis	4	15.8100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.867	1.064	1.754	0.4195
Sitta canadensis (skin)	6.490	1.558	4.165	0.0263

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	4.623	1.609	2.873	0.1046

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	22.3000	A
Sitta canadensis (alcohol)	3	17.6767	A B
Sitta canadensis	4	15.8100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.867	1.064	1.754	0.2755
Sitta canadensis (skin)	6.490	1.558	4.165	0.0199

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	4.623	1.609	2.873	0.0759

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	2.6900	A
Sitta canadensis	4	2.1150	B

Sitta canadensis (skin)	1	1.8100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5750	0.09917	5.798	0.0065
Sitta canadensis (skin)	-0.3050	0.14517	-2.101	0.2689

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.8800	0.1499	-5.869	0.0061

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Sitta canadensis (alcohol)	3	2.6900	A
Sitta canadensis	4	2.1150	B
Sitta canadensis (skin)	1	1.8100	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	0.5750	0.09917	5.798	0.0050
Sitta canadensis (skin)	-0.3050	0.14517	-2.101	0.1842

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	-0.8800	0.1499	-5.869	0.0047

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	3.7500	A
Sitta canadensis (alcohol)	3	3.5633	A
Sitta canadensis	4	1.6025	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.961	0.1794	10.928	0.0003
Sitta canadensis (skin)	2.148	0.2627	8.176	0.0013

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.1867	0.2713	0.6881	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Sitta canadensis (skin)	1	3.7500	A
Sitta canadensis (alcohol)	3	3.5633	A
Sitta canadensis	4	1.6025	B

Means that do not share a letter are significantly different.

Name = Sitta canadensis subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (alcohol)	1.961	0.1794	10.928	0.0003
Sitta canadensis (skin)	2.148	0.2627	8.176	0.0011

Name = Sitta canadensis (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Sitta canadensis (skin)	0.1867	0.2713	0.6881	0.7803

General Linear Model: LoDI, LoDII, ... versus Name

Factor	Type	Levels	Values
Name	fixed	3	Turdus migratorius, Turdus migratorius (alcohol), Turdus migratorius (skin)

Analysis of Variance for LoDI, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	5.9092	5.9092	2.9546	4.12	0.088
Error	5	3.5895	3.5895	0.7179		
Total	7	9.4987				

S = 0.847290   R-Sq = 62.21%   R-Sq(adj) = 47.09%

Unusual Observations for LoDI

Obs	LoDI	Fit	SE Fit	Residual	St Resid
5	11.0800	11.0800	0.8473	-0.0000	* X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoDII, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	2.3453	2.3453	1.1727	2.33	0.193
Error	5	2.5191	2.5191	0.5038		
Total	7	4.8645				

```
S = 0.709809   R-Sq = 48.21%   R-Sq(adj) = 27.50%


Unusual Observations for LoDII

                                           St
Obs    LoDII      Fit  SE Fit  Residual  Resid
  5  11.0200  11.0200  0.7098    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIII, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  18.4865  18.4865  9.2433  24.70  0.003
Error    5   1.8714   1.8714  0.3743
Total    7  20.3579


S = 0.611779   R-Sq = 90.81%   R-Sq(adj) = 87.13%


Unusual Observations for LoDIII

                                           St
Obs   LoDIII      Fit  SE Fit  Residual  Resid
  5  16.1200  16.1200  0.6118   -0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoDIV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  12.1396  12.1396  6.0698  10.44  0.016
Error    5   2.9079   2.9079  0.5816
Total    7  15.0475


S = 0.762611   R-Sq = 80.68%   R-Sq(adj) = 72.95%


Unusual Observations for LoDIV

                                         St
Obs   LoDIV     Fit  SE Fit  Residual  Resid
  5  9.7200  9.7200  0.7626    0.0000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint II, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS     F      P
Name     2  0.91885  0.91885  0.45942  9.21  0.021
Error    5  0.24934  0.24934  0.04987
Total    7  1.16819


S = 0.223312   R-Sq = 78.66%   R-Sq(adj) = 70.12%
```

```
Unusual Observations for W@Pjoint II

                                                  St
Obs  W@Pjoint II      Fit   SE Fit  Residual  Resid
  5      1.91000  1.91000  0.22331  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@Pjoint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  1.30412  1.30412  0.65206  30.39  0.002
Error    5  0.10727  0.10727  0.02145
Total    7  1.41139


S = 0.146470   R-Sq = 92.40%   R-Sq(adj) = 89.36%


Unusual Observations for W@Pjoint III

     W@Pjoint
Obs       III      Fit   SE Fit  Residual  St Resid
  5   2.46000  2.46000  0.14647  -0.00000         * X
  7   2.21000  2.45667  0.08456  -0.24667     -2.06 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.95769  0.95769  0.47884  41.28  0.001
Error    5  0.05800  0.05800  0.01160
Total    7  1.01569


S = 0.107703   R-Sq = 94.29%   R-Sq(adj) = 92.01%


Unusual Observations for W@2joint III

     W@2joint                               St
Obs       III      Fit   SE Fit  Residual  Resid
  5   2.40000  2.40000  0.10770  -0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for W@2joint IV, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS   Adj MS      F      P
Name     2  0.68355  0.68355  0.34177  13.23  0.010
Error    5  0.12914  0.12914  0.02583
Total    7  0.81269


S = 0.160712   R-Sq = 84.11%   R-Sq(adj) = 77.75%
```

Unusual Observations for W@2joint IV

Obs	W@2joint IV	Fit	SE Fit	Residual	St Resid	
5	2.04000	2.04000	0.16071	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for W@3joint IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.46325	0.46325	0.23162	44.99	0.001
Error	5	0.02574	0.02574	0.00515		
Total	7	0.48899				

S = 0.0717519   R-Sq = 94.74%   R-Sq(adj) = 92.63%

Unusual Observations for W@3joint IV

Obs	W@3joint IV	Fit	SE Fit	Residual	St Resid	
5	1.75000	1.75000	0.07175	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhI,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	22.852	22.852	11.426	20.49	0.004
Error	5	2.789	2.789	0.558		
Total	7	25.640				

S = 0.746820   R-Sq = 89.12%   R-Sq(adj) = 84.77%

Unusual Observations for LoPhI,II

Obs	LoPhI,II	Fit	SE Fit	Residual	St Resid	
5	2.78000	2.78000	0.74682	0.00000	*	X
6	4.08000	2.84000	0.43118	1.24000	2.03	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhII,II, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	7.8221	7.8221	3.9111	88.62	0.000
Error	5	0.2207	0.2207	0.0441		
Total	7	8.0428				

S = 0.210079   R-Sq = 97.26%   R-Sq(adj) = 96.16%

Unusual Observations for LoPhII,II

```
                                                St
Obs  LoPhII,II      Fit   SE Fit  Residual  Resid
  5    4.52000  4.52000  0.21008   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,III, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS       F      P
Name     2  54.338  54.338  27.169  238.68  0.000
Error    5   0.569   0.569   0.114
Total    7  54.907


S = 0.337385   R-Sq = 98.96%   R-Sq(adj) = 98.55%


Unusual Observations for LoPhI,III

                                                St
Obs  LoPhI,III      Fit   SE Fit  Residual  Resid
  5    2.53000  2.53000  0.33738   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS      F      P
Name     2  10.2565  10.2565  5.1283  31.28  0.001
Error    5   0.8197   0.8197  0.1639
Total    7  11.0763


S = 0.404905   R-Sq = 92.60%   R-Sq(adj) = 89.64%


Unusual Observations for LoPhII,III

                                                 St
Obs  LoPhII,III      Fit   SE Fit  Residual  Resid
  5     4.23000  4.23000  0.40491   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,III, using Adjusted SS for Tests

Source  DF   Seq SS   Adj SS  Adj MS       F      P
Name     2  14.0389  14.0389  7.0194  155.37  0.000
Error    5   0.2259   0.2259  0.0452
Total    7  14.2648


S = 0.212556   R-Sq = 98.42%   R-Sq(adj) = 97.78%


Unusual Observations for LoPhIII,III

                                                  St
Obs  LoPhIII,III      Fit   SE Fit  Residual  Resid
```

```
  5      6.05000  6.05000  0.21256   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhI,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS      F      P
Name     2  8.7853  8.7853  4.3927  22.42  0.003
Error    5  0.9795  0.9795  0.1959
Total    7  9.7648


S = 0.442598   R-Sq = 89.97%   R-Sq(adj) = 85.96%


Unusual Observations for LoPhI,IV

                                              St
Obs  LoPhI,IV      Fit   SE Fit  Residual  Resid
  5   2.38000  2.38000  0.44260   0.00000      * X

X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  4.3351  4.3351  2.1676  9.93  0.018
Error    5  1.0919  1.0919  0.2184
Total    7  5.4271


S = 0.467320   R-Sq = 79.88%   R-Sq(adj) = 71.83%


Unusual Observations for LoPhII,IV

Obs  LoPhII,IV      Fit   SE Fit  Residual  St Resid
  3    4.74000  3.89250  0.23366   0.84750      2.09 R
  5    2.57000  2.57000  0.46732   0.00000         * X

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.


Analysis of Variance for LoPhIII,IV, using Adjusted SS for Tests

Source  DF  Seq SS  Adj SS  Adj MS     F      P
Name     2  1.2985  1.2985  0.6492  3.76  0.101
Error    5  0.8635  0.8635  0.1727
Total    7  2.1620


S = 0.415582   R-Sq = 60.06%   R-Sq(adj) = 44.08%


Unusual Observations for LoPhIII,IV

Obs  LoPhIII,IV      Fit   SE Fit  Residual  St Resid
  1     2.65000  3.40750  0.20779  -0.75750     -2.10 R
  5     2.56000  2.56000  0.41558   0.00000         * X
```

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for LoPhIV,IV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	9.7589	9.7589	4.8794	15.21	0.007
Error	5	1.6041	1.6041	0.3208		
Total	7	11.3630				

S = 0.566410   R-Sq = 85.88%   R-Sq(adj) = 80.24%

Unusual Observations for LoPhIV,IV

Obs	LoPhIV,IV	Fit	SE Fit	Residual	St Resid	
5	3.08000	3.08000	0.56641	-0.00000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Foot Length, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	19.7098	19.7098	9.8549	17.24	0.006
Error	5	2.8586	2.8586	0.5717		
Total	7	22.5684				

S = 0.756117   R-Sq = 87.33%   R-Sq(adj) = 82.27%

Unusual Observations for Foot Length

Obs	Foot Length	Fit	SE Fit	Residual	St Resid	
5	18.7700	18.7700	0.7561	0.0000	*	X

X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Lotmt, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.22	0.22	0.11	0.01	0.993
Error	5	81.36	81.36	16.27		
Total	7	81.58				

S = 4.03388   R-Sq = 0.27%   R-Sq(adj) = 0.00%

Unusual Observations for Lotmt

Obs	Lotmt	Fit	SE Fit	Residual	St Resid	
5	32.8000	32.8000	4.0339	0.0000	*	X
8	26.0600	33.2133	2.3290	-7.1533	-2.17	R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@prox, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.2386	0.2386	0.1193	0.73	0.526
Error	5	0.8147	0.8147	0.1629		
Total	7	1.0534				

S = 0.403669   R-Sq = 22.66%   R-Sq(adj) = 0.00%

Unusual Observations for Wotmt@prox

Obs	Wotmt@prox	Fit	SE Fit	Residual	St Resid
5	4.76000	4.76000	0.40367	-0.00000	* X
8	3.60000	4.26667	0.23306	-0.66667	-2.02 R

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Analysis of Variance for Wotmt@cond, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
Name	2	0.7841	0.7841	0.3920	1.74	0.267
Error	5	1.1267	1.1267	0.2253		
Total	7	1.9108				

S = 0.474700   R-Sq = 41.03%   R-Sq(adj) = 17.45%

Unusual Observations for Wotmt@cond

Obs	Wotmt@cond	Fit	SE Fit	Residual	St Resid
3	4.68000	3.79500	0.23735	0.88500	2.15 R
5	4.50000	4.50000	0.47470	-0.00000	* X

R denotes an observation with a large standardized residual.
X denotes an observation whose X value gives it large leverage.

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDI

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	11.570	A
Turdus migratorius (skin)	1	11.080	A
Turdus migratorius	4	9.755	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.815	0.6471	2.805	0.1134
Turdus migratorius (skin)	1.325	0.9473	1.399	0.6623

Name = Turdus migratorius (alcohol) subtracted from:

```
                           Difference       SE of           Adjusted
Name                         of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)     -0.4900      0.9784  -0.5008     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for LoDI

Name                          N    Mean  Grouping
Turdus migratorius (alcohol)  3  11.570  A
Turdus migratorius (skin)     1  11.080  A
Turdus migratorius            4   9.755  A

Means that do not share a letter are significantly different.

Name = Turdus migratorius  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Turdus migratorius (alcohol)       1.815      0.6471    2.805    0.0819
Turdus migratorius (skin)          1.325      0.9473    1.399    0.4091


Name = Turdus migratorius (alcohol)  subtracted from:

                           Difference       SE of           Adjusted
Name                         of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)     -0.4900      0.9784  -0.5008    0.8741


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDII

Name                          N    Mean  Grouping
Turdus migratorius (alcohol)  3  12.787  A
Turdus migratorius            4  12.297  A
Turdus migratorius (skin)     1  11.020  A

Means that do not share a letter are significantly different.

Name = Turdus migratorius  subtracted from:

                              Difference       SE of           Adjusted
Name                            of Means  Difference  T-Value   P-Value
Turdus migratorius (alcohol)       0.489      0.5421    0.902    1.0000
Turdus migratorius (skin)         -1.278      0.7936   -1.610    0.5051


Name = Turdus migratorius (alcohol)  subtracted from:

                           Difference       SE of           Adjusted
Name                         of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)      -1.767      0.8196   -2.155    0.2510


Grouping Information Using Tukey Method and 95.0% Confidence for LoDII

Name                          N    Mean  Grouping
Turdus migratorius (alcohol)  3  12.787  A
Turdus migratorius            4  12.297  A
Turdus migratorius (skin)     1  11.020  A

Means that do not share a letter are significantly different.

Name = Turdus migratorius  subtracted from:
```

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.489	0.5421	0.902	0.6623
Turdus migratorius (skin)	-1.278	0.7936	-1.610	0.3244

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-1.767	0.8196	-2.155	0.1729

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	21.083	A
Turdus migratorius	4	19.915	A
Turdus migratorius (skin)	1	16.120	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.168	0.4673	2.500	0.1634
Turdus migratorius (skin)	-3.795	0.6840	-5.548	0.0078

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-4.963	0.7064	-7.026	0.0027

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIII

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	21.083	A
Turdus migratorius	4	19.915	A
Turdus migratorius (skin)	1	16.120	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.168	0.4673	2.500	0.1158
Turdus migratorius (skin)	-3.795	0.6840	-5.548	0.0061

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-4.963	0.7064	-7.026	0.0021

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Turdus migratorius	4	13.463	A
Turdus migratorius (alcohol)	3	13.420	A
Turdus migratorius (skin)	1	9.720	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.043	0.5825	-0.073	1.0000
Turdus migratorius (skin)	-3.743	0.8526	-4.389	0.0213

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.700	0.8806	-4.202	0.0254

Grouping Information Using Tukey Method and 95.0% Confidence for LoDIV

Name	N	Mean	Grouping
Turdus migratorius	4	13.463	A
Turdus migratorius (alcohol)	3	13.420	A
Turdus migratorius (skin)	1	9.720	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.043	0.5825	-0.073	0.9971
Turdus migratorius (skin)	-3.743	0.8526	-4.389	0.0162

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.700	0.8806	-4.202	0.0193

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	1.943	A
Turdus migratorius (skin)	1	1.910	A B
Turdus migratorius	4	1.258	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.6858	0.1706	4.021	0.0303
Turdus migratorius (skin)	0.6525	0.2497	2.613	0.1424

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.03333	0.2579	-0.1293	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint II

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	1.943	A
Turdus migratorius (skin)	1	1.910	A B
Turdus migratorius	4	1.258	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.6858	0.1706	4.021	0.0229
Turdus migratorius (skin)	0.6525	0.2497	2.613	0.1017

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.03333	0.2579	-0.1293	0.9908

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.460	A
Turdus migratorius (alcohol)	3	2.457	A
Turdus migratorius	4	1.650	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.8067	0.1119	7.211	0.0024
Turdus migratorius (skin)	0.8100	0.1638	4.946	0.0129

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.003333	0.1691	0.01971	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@Pjoint III

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.460	A
Turdus migratorius (alcohol)	3	2.457	A

Turdus migratorius	4	1.650	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.8067	0.1119	7.211	0.0019
Turdus migratorius (skin)	0.8100	0.1638	4.946	0.0099

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.003333	0.1691	0.01971	0.9998

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.400	A
Turdus migratorius (alcohol)	3	2.170	A
Turdus migratorius	4	1.550	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.6200	0.08226	7.537	0.0020
Turdus migratorius (skin)	0.8500	0.12042	7.059	0.0026

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.2300	0.1244	1.849	0.3709

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint III

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.400	A
Turdus migratorius (alcohol)	3	2.170	A
Turdus migratorius	4	1.550	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.6200	0.08226	7.537	0.0015
Turdus migratorius (skin)	0.8500	0.12042	7.059	0.0021

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.2300	0.1244	1.849	0.2468

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.040	A
Turdus migratorius (alcohol)	3	1.847	A
Turdus migratorius	4	1.322	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.5242	0.1227	4.270	0.0238
Turdus migratorius (skin)	0.7175	0.1797	3.993	0.0312

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1933	0.1856	1.042	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for W@2joint IV

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	2.040	A
Turdus migratorius (alcohol)	3	1.847	A
Turdus migratorius	4	1.322	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.5242	0.1227	4.270	0.0181
Turdus migratorius (skin)	0.7175	0.1797	3.993	0.0235

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1933	0.1856	1.042	0.5855

Grouping Information Using Bonferroni Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	1.750	A
Turdus migratorius (alcohol)	3	1.563	A
Turdus migratorius	4	1.143	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.4208	0.05480	7.679	0.0018
Turdus migratorius (skin)	0.6075	0.08022	7.573	0.0019

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1867	0.08285	2.253	0.2220

Grouping Information Using Tukey Method and 95.0% Confidence for W@3joint IV

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	1.750	A
Turdus migratorius (alcohol)	3	1.563	A
Turdus migratorius	4	1.143	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.4208	0.05480	7.679	0.0014
Turdus migratorius (skin)	0.6075	0.08022	7.573	0.0015

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1867	0.08285	2.253	0.1543

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Turdus migratorius	4	6.205	A
Turdus migratorius (alcohol)	3	2.840	B
Turdus migratorius (skin)	1	2.780	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-3.365	0.5704	-5.899	0.0060
Turdus migratorius (skin)	-3.425	0.8350	-4.102	0.0280

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.06000	0.8624	-0.06958	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,II

Name	N	Mean	Grouping
Turdus migratorius	4	6.205	A
Turdus migratorius (alcohol)	3	2.840	B
Turdus migratorius (skin)	1	2.780	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-3.365	0.5704	-5.899	0.0046
Turdus migratorius (skin)	-3.425	0.8350	-4.102	0.0212

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.06000	0.8624	-0.06958	0.9973

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	7.587	A
Turdus migratorius	4	6.200	B
Turdus migratorius (skin)	1	4.520	C

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.387	0.1605	8.642	0.0010
Turdus migratorius (skin)	-1.680	0.2349	-7.153	0.0025

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.067	0.2426	-12.64	0.0002

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,II

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	7.587	A
Turdus migratorius	4	6.200	B
Turdus migratorius (skin)	1	4.520	C

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.387	0.1605	8.642	0.0008

Turdus migratorius (skin)	-1.680	0.2349	-7.153	0.0019

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.067	0.2426	-12.64	0.0001

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping	
Turdus migratorius	4	6.718	A	
Turdus migratorius (skin)	1	2.530		B
Turdus migratorius (alcohol)	3	1.243		B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-5.474	0.2577	-21.24	0.0000
Turdus migratorius (skin)	-4.188	0.3772	-11.10	0.0003

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	1.287	0.3896	3.303	0.0642

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,III

Name	N	Mean	Grouping		
Turdus migratorius	4	6.718	A		
Turdus migratorius (skin)	1	2.530		B	
Turdus migratorius (alcohol)	3	1.243			C

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-5.474	0.2577	-21.24	0.0000
Turdus migratorius (skin)	-4.188	0.3772	-11.10	0.0003

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	1.287	0.3896	3.303	0.0475

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Turdus migratorius	4	7.098	A

Turdus migratorius (alcohol)	3	5.123	B
Turdus migratorius (skin)	1	4.230	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-1.974	0.3093	-6.384	0.0042
Turdus migratorius (skin)	-2.868	0.4527	-6.334	0.0043

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.8933	0.4675	-1.911	0.3429

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,III

Name	N	Mean	Grouping
Turdus migratorius	4	7.098	A
Turdus migratorius (alcohol)	3	5.123	B
Turdus migratorius (skin)	1	4.230	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-1.974	0.3093	-6.384	0.0033
Turdus migratorius (skin)	-2.868	0.4527	-6.334	0.0034

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.8933	0.4675	-1.911	0.2299

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	9.700	A
Turdus migratorius	4	7.365	B
Turdus migratorius (skin)	1	6.050	C

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	2.335	0.1623	14.383	0.0001
Turdus migratorius (skin)	-1.315	0.2376	-5.533	0.0079

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.650	0.2454	-14.87	0.0001

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,III

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	9.700	A
Turdus migratorius	4	7.365	B
Turdus migratorius (skin)	1	6.050	C

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	2.335	0.1623	14.383	0.0001
Turdus migratorius (skin)	-1.315	0.2376	-5.533	0.0061

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-3.650	0.2454	-14.87	0.0001

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Turdus migratorius	4	3.650	A
Turdus migratorius (skin)	1	2.380	A B
Turdus migratorius (alcohol)	3	1.397	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-2.253	0.3380	-6.666	0.0034
Turdus migratorius (skin)	-1.270	0.4948	-2.566	0.1507

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.9833	0.5111	1.924	0.3370

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhI,IV

Name	N	Mean	Grouping
Turdus migratorius	4	3.650	A
Turdus migratorius (skin)	1	2.380	A B
Turdus migratorius (alcohol)	3	1.397	B

Means that do not share a letter are significantly different.

```
Name = Turdus migratorius  subtracted from:

                              Difference       SE of            Adjusted
Name                           of Means  Difference  T-Value   P-Value
Turdus migratorius (alcohol)      -2.253      0.3380   -6.666    0.0027
Turdus migratorius (skin)         -1.270      0.4948   -2.566    0.1073


Name = Turdus migratorius (alcohol)  subtracted from:

                           Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)      0.9833      0.5111    1.924    0.2264


Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhII,IV

Name                          N   Mean  Grouping
Turdus migratorius            4  3.893  A
Turdus migratorius (skin)     1  2.570  A B
Turdus migratorius (alcohol)  3  2.377    B

Means that do not share a letter are significantly different.

Name = Turdus migratorius  subtracted from:

                              Difference       SE of            Adjusted
Name                           of Means  Difference  T-Value   P-Value
Turdus migratorius (alcohol)      -1.516      0.3569   -4.247    0.0243
Turdus migratorius (skin)         -1.323      0.5225   -2.531    0.1574


Name = Turdus migratorius (alcohol)  subtracted from:

                           Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)      0.1933      0.5396   0.3583     1.000


Grouping Information Using Tukey Method and 95.0% Confidence for LoPhII,IV

Name                          N   Mean  Grouping
Turdus migratorius            4  3.893  A
Turdus migratorius (skin)     1  2.570  A B
Turdus migratorius (alcohol)  3  2.377    B

Means that do not share a letter are significantly different.

Name = Turdus migratorius  subtracted from:

                              Difference       SE of            Adjusted
Name                           of Means  Difference  T-Value   P-Value
Turdus migratorius (alcohol)      -1.516      0.3569   -4.247    0.0185
Turdus migratorius (skin)         -1.323      0.5225   -2.531    0.1118


Name = Turdus migratorius (alcohol)  subtracted from:

                           Difference       SE of            Adjusted
Name                        of Means  Difference  T-Value   P-Value
Turdus migratorius (skin)      0.1933      0.5396   0.3583    0.9326
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Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Turdus migratorius	4	3.407	A
Turdus migratorius (alcohol)	3	2.617	A
Turdus migratorius (skin)	1	2.560	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.7908	0.3174	-2.492	0.1652
Turdus migratorius (skin)	-0.8475	0.4646	-1.824	0.3832

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.05667	0.4799	-0.1181	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIII,IV

Name	N	Mean	Grouping
Turdus migratorius	4	3.407	A
Turdus migratorius (alcohol)	3	2.617	A
Turdus migratorius (skin)	1	2.560	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.7908	0.3174	-2.492	0.1170
Turdus migratorius (skin)	-0.8475	0.4646	-1.824	0.2541

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.05667	0.4799	-0.1181	0.9924

Grouping Information Using Bonferroni Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	5.670	A
Turdus migratorius	4	3.485	B
Turdus migratorius (skin)	1	3.080	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	2.1850	0.4326	5.0508	0.0118

Turdus migratorius (skin)	-0.4050	0.6333	-0.6395	1.0000

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-2.590	0.6540	-3.960	0.0322

Grouping Information Using Tukey Method and 95.0% Confidence for LoPhIV,IV

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	5.670	A
Turdus migratorius	4	3.485	B
Turdus migratorius (skin)	1	3.080	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	2.1850	0.4326	5.0508	0.0091
Turdus migratorius (skin)	-0.4050	0.6333	-0.6395	0.8060

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-2.590	0.6540	-3.960	0.0243

Grouping Information Using Bonferroni Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	23.877	A
Turdus migratorius	4	22.325	A
Turdus migratorius (skin)	1	18.770	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.552	0.5775	2.687	0.1304
Turdus migratorius (skin)	-3.555	0.8454	-4.205	0.0253

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-5.107	0.8731	-5.849	0.0062

Grouping Information Using Tukey Method and 95.0% Confidence for Foot Length

Name	N	Mean	Grouping
Turdus migratorius (alcohol)	3	23.877	A

Turdus migratorius	4	22.325	A
Turdus migratorius (skin)	1	18.770	B

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	1.552	0.5775	2.687	0.0936
Turdus migratorius (skin)	-3.555	0.8454	-4.205	0.0192

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-5.107	0.8731	-5.849	0.0048

Grouping Information Using Bonferroni Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Turdus migratorius	4	33.325	A
Turdus migratorius (alcohol)	3	33.213	A
Turdus migratorius (skin)	1	32.800	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.1117	3.081	-0.0362	1.000
Turdus migratorius (skin)	-0.5250	4.510	-0.1164	1.000

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.4133	4.658	-0.08874	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Lotmt

Name	N	Mean	Grouping
Turdus migratorius	4	33.325	A
Turdus migratorius (alcohol)	3	33.213	A
Turdus migratorius (skin)	1	32.800	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	-0.1117	3.081	-0.0362	0.9993
Turdus migratorius (skin)	-0.5250	4.510	-0.1164	0.9926

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	-0.4133	4.658	-0.08874	0.9957

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	4.760	A
Turdus migratorius (alcohol)	3	4.267	A
Turdus migratorius	4	4.223	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.04417	0.3083	0.1433	1.0000
Turdus migratorius (skin)	0.53750	0.4513	1.1910	0.8614

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.4933	0.4661	1.058	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@prox

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	4.760	A
Turdus migratorius (alcohol)	3	4.267	A
Turdus migratorius	4	4.223	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.04417	0.3083	0.1433	0.9888
Turdus migratorius (skin)	0.53750	0.4513	1.1910	0.5074

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.4933	0.4661	1.058	0.5766

Grouping Information Using Bonferroni Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	4.500	A
Turdus migratorius (alcohol)	3	4.390	A
Turdus migratorius	4	3.795	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.5950	0.3626	1.641	0.4851
Turdus migratorius (skin)	0.7050	0.5307	1.328	0.7244

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1100	0.5481	0.2007	1.000

Grouping Information Using Tukey Method and 95.0% Confidence for Wotmt@cond

Name	N	Mean	Grouping
Turdus migratorius (skin)	1	4.500	A
Turdus migratorius (alcohol)	3	4.390	A
Turdus migratorius	4	3.795	A

Means that do not share a letter are significantly different.

Name = Turdus migratorius subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (alcohol)	0.5950	0.3626	1.641	0.3132
Turdus migratorius (skin)	0.7050	0.5307	1.328	0.4408

Name = Turdus migratorius (alcohol) subtracted from:

Name	Difference of Means	SE of Difference	T-Value	Adjusted P-Value
Turdus migratorius (skin)	0.1100	0.5481	0.2007	0.9781

Appendix IV

Number	IVPP V 10918	IVPP V 6862	IVPP V 12330	IVPP V 12374	IVPP V 12430	IVPP V 12698	IVPP V 13353	IVPP V 127213
Genus	*Confuciusornis*	*Gansus*	*Microraptor z*	*Jeholornis*	*Caudipteryx*	*Sapeornis*	*Jeholornis*	*Pedopenna*
LoDI	7.76	8.73	4.58	N/A	13.4		9.2	7.96
w/claw	N/A	13.16	7.99	N/A	N/A		16.66	12.54
LoDII	N/A	20.66	7.95	24.67	38.11		20.96	26.32
w/claw	N/A	25.01	14.17	35.78	54.79		30.34	33.77
LoDIII	N/A	27.75	16.3		52.96		32.8	42.69
w/claw	N/A	32.14	20.48	N/A	71.61		40.71	51.33
LoDIV	N/A	34.82	13.11		31.22		29.98	N/A
w/claw	N/A	37.6	16.83	N/A	44.3		37.26	N/A
W@Pjoint II	N/A	N/A	N/A	4.23	8.8		3.59	N/A
W@Pjoint III	N/A	N/A	N/A	4.85	8.14		3.34	N/A
W@Pjoint IV	2.16	N/A	N/A	3.82	7.53		3.48	N/A
W@2joint III	N/A	N/A	N/A	3.22	7.11		3.25	N/A
W@2joint IV	N/A	2.22	N/A	3.3	6.78		2.98	N/A
W@3joint IV	N/A	1.83	N/A	2.63	6.05		2.91	N/A
LoPhI, II	8.41	10.39	5.49	11.98	23.93		10.42	13.75
LoPhII, II	N/A	11.27	2.42	14.13	16.91		11.65	13.23
LoPhI, III	9.05	11.73	6.89	15.14	24.87		13.09	21.37
LoPhII, III	N/A	10.6	5.1	13.25	19.75		10.34	10.83
LoPhIII, III	N/A	8.16	5.31	13.92	14.62		9.5	9.72
LoPhI, IV	5.39	11.08	4.93	7.81	13.18		10.29	N/A
LoPhII, IV	7.3	8.29	4.47	8.42	9.42		7.24	N/A
LoPhIII, IV	N/A	8.98	2.59	7.91	8.56		5.61	N/A
LoPhIV, IV	N/A	7.36	3.6	12.06	7.79		8.69	N/A
WoPhI, II	N/A	N/A	N/A	2.63	7.48		2.14	N/A
WoPhII, II	N/A	N/A	N/A	2.63	N/A		1.78	N/A
WoPhI, III	N/A	N/A	N/A	2.88	5.11		2.61	N/A
WoPhII, III	N/A	N/A	N/A	2.29	4.33		2.04	N/A
WoPhIII, III	N/A	N/A	N/A	1.83	4.45		1.65	N/A
WoPhI, IV	2.22	1.7	N/A	2.89	5.96		2.43	N/A
WoPhII, IV	2.11	1.27	N/A	2.73	6.37		2.09	N/A
WoPhIII, IV	N/A	1.13	N/A	2.21	6.01		1.94	N/A

Number	IVPP V 10918	IVPP V 6862	IVPP V 12330	IVPP V 12374	IVPP V 12430	IVPP V 12698	IVPP V 13353	IVPP V 127213
Genus	*Confuciusornis*	*Gansus*	*Microraptor z*	*Jeholornis*	*Caudipteryx*	*Sapeornis*	*Jeholornis*	*Pedopenna*
WoPhIV, IV	N/A	1.15	N/A	1.65	5.49		1.22	N/A
Foot length	N/A	34.02	22.03	N/A	N/A		38.15	50.51
LoUng I	N/A	4.82	3.44	10.61	11.32		9.39	4.34
w/sheath	N/A	N/A	N/A	13.95	N/A		10.79	N/A
LoUng II	N/A	5.25	7.38	15.88	18.25		12.42	12.9
w/sheath	N/A	N/A	9.24	19.27	N/A		14.72	N/A
LoUng III	N/A	4.75	5.84	12.09	19.69		12.1	10.77
w/sheath	N/A	N/A	8.1	16.14	N/A		13.92	N/A
LoUng IV	N/A	4.52	5.31	11.7	14.07		9.9	N/A
w/sheath	N/A	N/A	6.7	16.06	N/A		N/A	N/A
Lotmt	30.05	31.87	34.5	48.89 (est)	112.92	44.58	39.6	56.96
Lott	N/A	N/A	67.93	96.9	192.2	83.3	78.28	N/A
Lofem	N/A	N/A	51.92	70.5	148.91	80.26	62.3	N/A
Wotmt@prox	N/A	N/A	5.09	11.35	34.17	12.23	12.05	8.79
Wotmt@cond	N/A	N/A	4.35	N/A	28.63	10.64*	10.34	N/A
Wott@prox	N/A	N/A	N/A	10.94	24.3	13.22	13.11	N/A
Wott@mid	N/A	N/A	N/A	6.71	21.72	7.84	7.26	8.98
Wott@cond	N/A	N/A	N/A	12.84	29.83	10.98	7.46	N/A
Wofem@cond	N/A	N/A	N/A	10.6	26.57	8.77	9.25	N/A
LoHum	50.98	N/A	N/A	109.41	69.64	126.39	88.03	N/A
LoRad	45.17	N/A	32.24	100.94	59.06	132.1	84.2	N/A
LoUln	41.15	N/A	34.54	107.85	61.09	132.19	87.28	N/A
LoCarp	23.56	N/A	N/A	57.07	27.54	61.91	40.47	N/A
LoBeak	22.98	N/A	N/A	N/A	49.41	N/A	N/A	N/A
WoBeak	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Number	IVPP V 13275	IVPP V 13276	IVPP V 11370	IVPP V 10919	IVPP V 13156	IVPP V 11372	IVPP V 11795	IVPP V 9769
Genus	*Sapeornis*	*Sapeornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Cathayornis*
LoDI	15.14	15.87	7.44	7.57	7.38	5.4	N/A	N/A
w/claw	27.08	27.95	15.54	N/A	15.72	9.4	N/A	N/A
LoDII	N/A	18.09	20.25	17.63	16.44	13.6	11.06	N/A
w/claw	N/A	32.75	31.67	27.26	21.19	26	16.07	N/A
LoDIII	N/A	33.11	25.38	25.1	23.97	21.21	14.26	N/A
w/claw	N/A	41.78	33.96	35.33	36.1	28.79	20.72	N/A
LoDIV	N/A	N/A	22.36	21.55	21.08	18.89	N/A	N/A
w/claw	N/A	N/A	31.3	32.89	30.52	26.32	N/A	N/A
W@Pjoint II	N/A	N/A	3.68	N/A	3.87	2.62	N/A	N/A
W@Pjoint III	4.88	N/A	3.16	N/A	3.44	2.77	N/A	N/A
W@Pjoint IV	N/A	N/A	3.02	N/A	2.93	2.13	N/A	N/A
W@2joint III	N/A	N/A	3.43	N/A	2.4	2.31	N/A	N/A
W@2joint IV	N/A	N/A	2.86	N/A	2.51	2.14	N/A	N/A
W@3joint IV	N/A	N/A	2.58	N/A	2.45	2.1	1.55	N/A
LoPhI, II	N/A	7.43	9.95	10.37	7.88	6.37	4.86	N/A
LoPhII, II	N/A	11.59	10.69	6.68	10.01	7.27	6.12	N/A
LoPhI, III	11.8	11.95	8.46	5.23	9.28	9.54	5.17	N/A
LoPhII, III	10.59	10.75	8.04	10.18	7.68	5.73	4.85	N/A
LoPhIII, III	N/A	11.46	8.25	8.32	7.78	6.49	4.84	N/A
LoPhI, IV	5.34	N/A	6.5	6.14	5.95	4.33	N/A	N/A
LoPhII, IV	6.25	N/A	5.25	5.58	4.24	6.12	N/A	N/A
LoPhIII, IV	6.65	N/A	4.78	3.92	4.34	3.55	2.95	N/A
LoPhIV, IV	8.87	N/A	6.15	6.72	6.41	5.15	4.19	N/A
WoPhI, II	N/A	2.11	2.54	N/A	2.81	1.48	N/A	N/A
WoPhII, II	N/A	N/A	2.54	N/A	2.37	1.4	N/A	N/A
WoPhI, III	3.12	N/A	2.4	N/A	2.49	1.57	N/A	N/A
WoPhII, III	2.39	N/A	2.29	N/A	1.87	1.75	N/A	N/A
WoPhIII, III	N/A	N/A	1.81	N/A	N/A	1.44	N/A	N/A
WoPhI, IV	N/A	N/A	2.35	N/A	2.03	1.54	N/A	N/A
WoPhII, IV	N/A	N/A	1.68	N/A	1.82	N/A	N/A	N/A
WoPhIII, IV	N/A	N/A	1.99	N/A	1.7	1.48	1.18	N/A

Number	IVPP V 13275	IVPP V 13276	IVPP V 11370	IVPP V 10919	IVPP V 13156	IVPP V 11372	IVPP V 11795	IVPP V 9769
Genus	*Sapeornis*	*Sapeornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Cathayornis*
WoPhIV, IV	N/A	N/A	1.49	N/A	1.13	1.24	0.88	N/A
Foot length	N/A	39.51	33.27	29.2	30.26	28.23	N/A	N/A
LoUng I	15.02	14.35	8.55	N/A	9.09	7.23	6.06	N/A
w/sheath	N/A	15.98	10.09	N/A	10.85	9.24	N/A	N/A
LoUng II	13.64	11.7	10.3	12.24	13.45	8.43	6.1	N/A
w/sheath	16.06	15.87	16.7	14.57	18.71	12.19	N/A	N/A
LoUng III	11.33	15.77	13.35	11.34	12.02	7.63	7.52	N/A
w/sheath	N/A	25.1	20.34	15.65	16.84	10.84	N/A	N/A
LoUng IV	13.44	N/A	13.94	10.77	9.12	6.85	5.49	N/A
w/sheath	16.37	N/A	17.22	13.59	14.14	9.83	N/A	N/A
Lotmt	42.64	40.69	34.43	29.82	30.42	N/A	N/A	N/A
Lott	81.82	85.46	69.85	N/A	60.66	51.57	41.48	29.58
Lofem	70.59	72.18	58.61	N/A	53.41	43.97	33.73	22.91
Wotmt@prox	11.7	11.5	9.82	7.53	7.78	6.65	5.71	N/A
Wotmt@cond	12.14	9.19	7.92	7.02	9.37	6.96	N/A	N/A
Wott@prox	12.26	12.86	9.69	N/A	8.36	7.96	N/A	3.47
Wott@mid	6.79	N/A	4.33	N/A	5.82	3.76	N/A	1.79
Wott@cond	11.69	N/A	9.1	N/A	7.93	6.4	N/A	N/A
Wofem@cond	15.04	11.36	9.93	N/A	7.94	N/A	N/A	3.21
LoHum	121.97	119.57	68.46	N/A	62.23	52.09	44.85	26.9
LoRad	118.68	121.8	54.64	N/A	46.96	41.92	36.03	25.93
LoUln	120.14	123.67	58.99	N/A	55.2	43.88	40.79	27.32
LoCarp	52.63	49.54	33.37	N/A	30.93	27.82	N/A	13.5
LoBeak	N/A	N/A	37.08	N/A	35.04	35.11	N/A	N/A
WoBeak	N/A	N/A	12.42	N/A	12.16	11.21	N/A	N/A

Number	IVPP V 10531	IVPP V 10530	IVPP V 10916	IVPP V 10897	IVPP V 11794	IVPP V 14412	IVPP V 11640	IVPP V 14533
Genus	*Longirostrornis*	*Longchengornis*	*Eocathayornis*	*Cuspirostriornis*	*Confuciusornis*	*Jinzhouornis*	*Confuciusornis*	*Hongshanornis*
LoDI	N/A	4.87	N/A	4.78	6.87	5.75	6.57	4.89
w/claw	N/A	8.31	N/A	10.18	13.91	11.61	15.62	7.18
LoDII	N/A	N/A	N/A		17.59	20.83	16.47	12.65
w/claw	N/A	N/A	N/A		28.66	30.23	25.12	15.82
LoDIII	N/A		N/A		23.68	18	22.17	16.93
w/claw	N/A	N/A	N/A		33.94	26.25	22.81	19.67
LoDIV	N/A	N/A	N/A	N/A	20.9	14.51	17.45	15.95
w/claw	N/A	N/A	N/A	N/A	29.99	21.88	22.95	18.81
W@Pjoint II	N/A	N/A	N/A	N/A	3.4	1.94	3.56	1.16
W@Pjoint III	N/A	N/A	N/A	N/A	3.15	2.1	3.68	1.6
W@Pjoint IV	N/A	N/A	N/A	N/A	2.69	1.67	2.89	1.39
W@2joint III	N/A	N/A	N/A	N/A	3.13	2.18	N/A	1.26
W@2joint IV	N/A	N/A	N/A	N/A	2.14	1.56	3.01	1.2
W@3joint IV	N/A	N/A	N/A	N/A	2.55	1.68	N/A	1.16
LoPhI, II	7.08?	N/A	N/A	4.42	7.96	7.3	7.97	7.17
LoPhII, II	5.66?	3.86?	N/A	5.51	9.46	7.28	9.92	5.13
LoPhI, III	5.95	4.39	N/A	5.75	9.17	7.81	9.22	6.5
LoPhII, III	5.08	4.33	N/A	4.99	7.57	5.71	8.73	6
LoPhIII, III	5.55	5.29	N/A	5.49	7.54	6.74	7.83	4.99
LoPhI, IV	3.76	4.15	N/A	2.92?	5.86	4.68	6.19	4.9
LoPhII, IV	N/A	3.94	N/A	N/A	4.64	3.85	4.99	4.27
LoPhIII, IV	N/A	N/A	N/A	N/A	4.89	3.69	4.59	3.88
LoPhIV, IV	N/A	N/A	N/A	N/A	5.71	5.65	6.05	3.92
WoPhI, II	N/A	N/A	N/A	N/A	1.82	1.15	2.37	0.71
WoPhII, II	N/A	N/A	N/A	1.14	N/A	1.11	N/A	N/A
WoPhI, III	1.02	N/A	N/A	0.85	2.49	1.13	N/A	0.9
WoPhII, III	0.92	N/A	N/A	N/A	2.07	1.3	2.01	0.74
WoPhIII, III	N/A	N/A	N/A	0.68	1.54	1	N/A	N/A
WoPhI, IV	0.67	1.13	N/A	N/A	1.78	1.06	1.96	0.86
WoPhII, IV	N/A	0.73	N/A	N/A	1.62	1.28	1.75	0.77
WoPhIII, IV	N/A	N/A	N/A	N/A	1.72	1.14	N/A	0.79

Number	IVPP V 10531	IVPP V 10530	IVPP V 10916	IVPP V 10897	IVPP V 11794	IVPP V 14412	IVPP V 11640	IVPP V 14533
Genus	*Longirostrornis*	*Longchengornis*	*Eocathayornis*	*Cuspirostriornis*	*Confuciusornis*	*Jinzhouornis*	*Confuciusornis*	*Hongshanornis*
WoPhIV, IV	N/A	N/A	N/A	N/A	1.27	0.87	N/A	N/A
Foot length	N/A	N/A	N/A	N/A	30.1	26.53	33.15	19.24
LoUng I	4.45	6	N/A	6.2	8.78	5.53	10.81	2.87
w/sheath	N/A	N/A	N/A	7.11	11.34	N/A	N/A	N/A
LoUng II	5.89	6.02	N/A	6.26	13.6	6.92	11.64	3.75
w/sheath	6.39	N/A	N/A	7.7	18.28	N/A	15.95	N/A
LoUng III	6.24	5.12	N/A	5.6	9.67	7.96	12.83	4.25
w/sheath	8.5	7.38	N/A	7.21	N/A	N/A	15.56	N/A
LoUng IV	4.63	N/A	N/A	4.49	9.88	7.11	10.11	2.93
w/sheath	5.84	N/A	N/A	5.68	14.13	N/A	13.8	N/A
Lotmt	18.64	17.84	N/A	18.67	30.18	26.69	31.14	20.59
Lott	32.3	31.63	N/A	32.23	65.81	45.47	63.98	38
Lofem	27.66	20.85	N/A	26.69	55.22	36.35	55.25	21.67
Wotmt@prox	3.93	3.62	N/A	3.88	8.24	5.46	8.05	3.94
Wotmt@cond	4.61	3.15	N/A	4.47	7.78	5.61	9.22	4.79
Wott@prox	4.4	3.28	N/A	3.91	9.14	5.72	10.18	3.71
Wott@mid	1.98	2.2	N/A	N/A	6.01	N/A	5.64	1.88
Wott@cond	4.31	2.93	N/A	4.3	7.41	5.86	10.55	3.52
Wofem@cond	3.21	N/A	N/A	3.74	N/A	N/A	8.22	N/A
LoHum	28.23	31.95	23.35	29.28	N/A	45.95	64.29	26.68
LoRad	N/A	27.64	23.86	28.9	53.7	N/A	54.26	23.13
LoUln	N/A	30.31	25.7	30.68	54.56	N/A	54.93	26.13
LoCarp	N/A	13.81	9.72	13.6	33.58	N/A	30.53	13.74
LoBeak	13.47	N/A	N/A	N/A	N/A	19.12	31.67	14.12
WoBeak	5.03	N/A	N/A	N/A	N/A	N/A	12.09	N/A

Number	IVPP V 15900	IVPP V 13313	IVPP V 9934	IVPP V 11537	IVPP V 10896	IVPP V 10904	IVPP V 17972	IVPP V 13358
Genus	*Zhangjiangorn*	*Confuciusornis*	*Chaoyangia*	*Eoenantiornis*	*Cathayornis*	*Cathayornis*	*Microraptor gui*	*Yanornis*
LoDI	7.52	N/A	N/A	4.62	4.57	N/A	N/A	7.86
w/claw	11.46	N/A	N/A	N/A	7.82	N/A	N/A	12.39
LoDII	14.26	13.76	N/A	8.88	N/A	N/A	17.42	19.89
w/claw	19.59	20.57	N/A	N/A	N/A	N/A	31.52	N/A
LoDIII	22.33	19.26	N/A	N/A	N/A	N/A	33.79	30.67
w/claw	26.93	27.21	N/A	N/A	N/A	N/A	45.12	36.17
LoDIV	23.14	17.37	N/A	N/A	N/A	N/A	33.99	26.46
w/claw	27.94	22.72	N/A	N/A	N/A	N/A	40.76	30.3
W@Pjoint II	2.28	2.54	N/A	1.72	N/A	N/A	N/A	N/A
W@Pjoint III	2.15	2.18	N/A	N/A	N/A	N/A	N/A	N/A
W@Pjoint IV	2.53	1.79	N/A	N/A	N/A	N/A	N/A	2.88
W@2joint III	2.4	2.17	N/A	N/A	N/A	N/A	N/A	N/A
W@2joint IV	N/A	1.75	N/A	N/A	N/A	N/A	N/A	2.67
W@3joint IV	N/A	1.99	N/A	N/A	N/A	N/A	N/A	2.44
LoPhI, II	9.25	6.88	N/A	3.93	N/A	N/A	7.72	12.41
LoPhII, II	7.43	7.82	N/A	5.02	N/A	N/A	10.14	11.63
LoPhI, III	7.39	6.72	N/A	3.57	N/A	N/A	13.73	13.12
LoPhII, III	9.19	6.02	N/A	N/A	N/A	N/A	11.39	9.64
LoPhIII, III	9.14	6.21	N/A	N/A	N/A	N/A	9.57	9.87
LoPhI, IV	6.53	5.38	N/A	N/A	N/A	N/A	10.93	9.44
LoPhII, IV	4.6	3.38	N/A	N/A	N/A	N/A	9.92	7.51
LoPhIII, IV	5.65	3.74	N/A	?2.28	N/A	N/A	7.75	6.75
LoPhIV, IV	5.73	5.42	N/A	?2.89	N/A	N/A	5.57	6.19
WoPhI, II	1.62	1.35	N/A	0.85	N/A	N/A	N/A	1.59
WoPhII, II	1.34	N/A	N/A	N/A	N/A	N/A	N/A	N/A
WoPhI, III	1.84	1.27	N/A	N/A	N/A	N/A	N/A	N/A
WoPhII, III	1.55	1.44	N/A	N/A	N/A	N/A	N/A	N/A
WoPhIII, III	1.36	1.16	N/A	N/A	N/A	N/A	N/A	N/A
WoPhI, IV	1.5	1.26	N/A	N/A	N/A	N/A	N/A	N/A
WoPhII, IV	1.57	1.15	N/A	N/A	N/A	N/A	N/A	N/A
WoPhIII, IV	N/A	1.15	N/A	?0.48	N/A	N/A	N/A	1.58

Number	IVPP V 15900	IVPP V 13313	IVPP V 9934	IVPP V 11537	IVPP V 10896	IVPP V 10904	IVPP V 17972	IVPP V 13358
Genus	*Zhangjiangorn*	*Confuciusornis*	*Chaoyangia*	*Eoenantiornis*	*Cathayornis*	*Cathayornis*	*Microraptor g*	*Yanornis*
WoPhIV, IV	N/A	N/A	N/A	N/A	N/A	N/A	N/A	1.62
Foot length	25.77	26.12	N/A	N/A	N/A	N/A	39.15	37.51
LoUng I	8.04	N/A	N/A	4.98	6.81	N/A	N/A	4.24
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
LoUng II	9.72	8.23	N/A	5.84	N/A	N/A	22.9	8.71
w/sheath	N/A	N/A	N/A	7	N/A	N/A	N/A	N/A
LoUng III	8.17	8.61	N/A	N/A	N/A	N/A	14.8	8.08
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
LoUng IV	9.21	6.64	N/A	4.6	N/A	N/A	13.36	5.73
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
Lotmt	27.73	21.53	N/A	19.67	16.65	17.8	69.41	37.08
Lott	63.47	51.96	N/A	32.26	33.67	33.55	141.64	70.79
Lofem	45.89	44.1	43.93	26.61	N/A	N/A	N/A	57.66
Wotmt@prox	8.03	7.35	N/A	4.59	4.19	3.41	13.22	7.84
Wotmt@cond	7.07	5.52	N/A	3.85	4.08	3.57	11.41	6.84
Wott@prox	9.84	5.95	9.75	4.76	3.57	5.16	12.14	11.58
Wott@mid	5.42	4.2	3.47	1.88	2.14	2.29	6.64	N/A
Wott@cond	8.22	7.16	N/A	N/A	3.87	3.24	N/A	8.39
Wofem@cond	N/A	7.18	6.41	N/A	N/A	N/A	N/A	N/A
LoHum	71.31	54.2	N/A	28.98	30.36	N/A	87.9	75.3
LoRad	74.43	43.39	N/A	29.12	27.94	N/A	76.31	67.56
LoUln	74.83	46.36	N/A	31.71	31.04	N/A	79.13	74.62
LoCarp	31.85	28.1	N/A	10.13	12.7	N/A	42.73	34.52
LoBeak	27.99	21.82	N/A	N/A	N/A	N/A	N/A	25.28
WoBeak	5.46	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Number	IVPP V 9770	IVPP V 13259	IVPP V 12631	IVPP V 11303	IVPP V 13476	IVPP V 12444	IVPP V 15471	IVPP V13352
Genus	*Boluochia*	*Yanornis*	*Yixianornis*	*Liaoningornis*	*Microraptor g*	*Yanornis*	*Epidexipteryx*	*Microraptor gui*
LoDI	N/A	9.73	7.78	5.47	N/A	8.83	6.74	N/A
w/claw	N/A	15.1	12.86	N/A	N/A	N/A	N/A	N/A
LoDII	N/A		21.21	10.34	17.99		N/A	18.9
w/claw	N/A	N/A	29.07	N/A	32.9	N/A	N/A	29.9
LoDIII	N/A	34.34	33.76		32.18		N/A	32
w/claw	N/A	N/A	39.8	N/A	42.14	N/A	N/A	N/A
LoDIV	N/A		27.66		N/A		N/A	23.58
w/claw	N/A	N/A	32.5	N/A	N/A	N/A	N/A	N/A
W@Pjoint II	N/A	2.83	2.31	N/A	N/A	2.92	N/A	N/A
W@Pjoint III	N/A	3.88	1.69	N/A	N/A	N/A	N/A	N/A
W@Pjoint IV	N/A	3.55	1.89	N/A	N/A	3.59	N/A	N/A
W@2joint III	N/A	3.46	N/A	N/A	N/A	N/A	N/A	N/A
W@2joint IV	N/A	2.77	1.89	N/A	N/A	3.17	N/A	N/A
W@3joint IV	N/A	3.02	1.54	N/A	N/A	N/A	N/A	2.02
LoPhI, II	N/A	13.24	11.7	4.96	9.55	14.05	N/A	9.39
LoPhII, II	N/A	12	9.33	5.25	7.88	11.57	N/A	9.62
LoPhI, III	N/A	14.9	11.56	6.13	13.7	14.69	N/A	13.63
LoPhII, III	N/A	10.08	9.14	5.58	9.45	11.29	N/A	10.09
LoPhIII, III	N/A	9.97	9.24	5.85	9.31	10.34	N/A	8.29
LoPhI, IV	N/A	9.75	7.26	3.17	N/A	11.4	N/A	11.32
LoPhII, IV	N/A	8.07	6.18	3.07	7.31	7.78	N/A	7.6
LoPhIII, IV	N/A	6.58	5.74	2.85	N/A	7.28	N/A	6.08
LoPhIV, IV	N/A	7.39	6.39	N/A	7.38	8.03	N/A	6.72
WoPhI, II	N/A	2.21	1.27	N/A	6.08	2.17	N/A	N/A
WoPhII, II	N/A	1.87	0.83	N/A	6.96	N/A	N/A	N/A
WoPhI, III	N/A	1.49	1.68	N/A	N/A	N/A	N/A	N/A
WoPhII, III	N/A	2.44	1.5	N/A	N/A	N/A	N/A	2.43
WoPhIII, III	N/A	2.06	0.82	N/A	N/A	N/A	N/A	N/A
WoPhI, IV	N/A	2.54	1.1	N/A	N/A	N/A	N/A	N/A
WoPhII, IV	N/A	1.93	1.49	N/A	N/A	N/A	N/A	2.36
WoPhIII, IV	N/A	1.81	0.94	N/A	N/A	1.78	N/A	2.22

Number	IVPP V 9770	IVPP V 13259	IVPP V 12631	IVPP V 11303	IVPP V 13476	IVPP V 12444	IVPP V 15471	IVPP V13352
Genus	*Boluochia*	*Yanornis*	*Yixianornis*	*Liaoningornis*	*Microraptor g*	*Yanornis*	*Epidexipteryx*	*Microraptor gui*
WoPhIV, IV	N/A	1.55	0.79	N/A	N/A	1.63	N/A	1.77
Foot length	N/A	45.68	38.37	N/A	39.23	N/A	N/A	N/A
LoUng I	N/A	6.41	5.47	4.58	6.62	N/A	N/A	N/A
w/sheath	N/A	N/A	N/A	N/A	8.71	N/A	N/A	N/A
LoUng II	N/A	7.53	6.19	4.96	17.75	6.75	N/A	18.81
w/sheath	N/A	N/A	N/A	N/A	20.91	N/A	N/A	N/A
LoUng III	N/A	7.66	6.43	5.2	13.01	7.91	N/A	N/A
w/sheath	N/A	N/A	N/A	N/A	16.76	N/A	N/A	N/A
LoUng IV	N/A	6.51	4.72	3.96	11.72	5.8	N/A	N/A
w/sheath	N/A	N/A	N/A	N/A	15.06	N/A	N/A	N/A
Lotmt	17.41	37.73	26.85	15.44	61.68	38.5	28.73	70.11
Lott	36.88	69.76	53.77	32.83	N/A	77.39	63.77	126.18
Lofem	N/A	49.87	40.87	26.6	N/A	57.09	45.08	85.44
Wotmt@prox	4	9.35	6.44	3.59	10.81	7.32	5.64	N/A
Wotmt@cond	4.25	8.06	6.11	3.76	N/A	10.17	N/A	10.73
Wott@prox	4.68	10.85	7.59	4.83	N/A	11.94	10.32	9.69
Wott@mid	N/A	4.82	3.77	2.21	N/A	N/A	4.7	6.35
Wott@cond	3.65	7.8	6.36	4.07	12.22	N/A	8.54	N/A
Wofem@cond	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
LoHum	N/A	68.44	49.7	N/A	N/A	73.52	50.7	73.1
LoRad	N/A	72.57	48.15	N/A	N/A	72.3	N/A	71.1
LoUln	N/A	76.02	50.15	N/A	N/A	76.25	N/A	71.5
LoCarp	N/A	35.37	25.34	N/A	N/A	36.38	N/A	45.5
LoBeak	N/A	N/A	20.28	N/A	N/A	N/A	N/A	N/A
WoBeak	N/A	N/A	5.09	N/A	N/A	N/A	N/A	N/A

Number	IVPP V 13350	IVPP V 13396	IVPP V 10996	IVPP V 12811	IVPP V 11374	IVPP V 11375	IVPP V 11553	N/A
Genus	*Jeholornis*	*Sapeornis*	*Yanornis*	*Sinornithosaurus*	*Confuciusornis*	*Confucuisornis*	*Confucuisornis*	*Gansus*
LoDI	8.88	11.94	N/A	11.05	5.66	5.57	3.59	N/A
w/claw	13.81	21.26	N/A	N/A	12.63	13.27	7.53	N/A
LoDII	19.44	17.03	24.02		13.57	14.18	11.43	N/A
w/claw	27.8	27.13	N/A	N/A	20.93	25.34	16.57	N/A
LoDIII	30.94	28.22	N/A	54.65	20.27	19.22	14.98	N/A
w/claw	37.63	37.21	N/A	69.18	23.21	32.19	20.59	N/A
LoDIV	28.71	22.35	N/A	49.89	18.6	17.86	11.99	N/A
w/claw	33.89	32.27	N/A	65.25	20.22	27.59	17.26	N/A
W@Pjoint II	2.29	2.15	13.95	N/A	2.48	2.49	N/A	N/A
W@Pjoint III	N/A	3.23	10.17	N/A	2.77	2.52	1.39	N/A
W@Pjoint IV	N/A	N/A	N/A	N/A	2.1	2.21	1.35	N/A
W@2joint III	N/A	N/A	N/A	N/A	N/A	2.58	1.5	N/A
W@2joint IV	N/A	N/A	N/A	N/A	2.31	1.93	1.16	N/A
W@3joint IV	N/A	N/A	N/A	N/A	1.8	N/A	N/A	N/A
LoPhI, II	9.12	9.14	N/A	14.6	6.7	6.86	6.07	14.78
LoPhII, II	10.32	9.94	N/A	16.66	8.4	8.43	6.08	N/A
LoPhI, III	11.07	10.83	N/A	24.4	8.29	7.5	5.16	12.52
LoPhII, III	10.24	8.58	N/A	16.33	6.66	6.3	4.88	N/A
LoPhIII, III	10.91	9.2	N/A	16.04	6.77	7.35	5.43	N/A
LoPhI, IV	9.49	7.02	N/A	19.12	5.24	4.51	4.14	N/A
LoPhII, IV	6.5	4.92	N/A	13.25	4.31	4.31	2.25	N/A
LoPhIII, IV	4.95	5.31	N/A	10.15	4	4.39	2.3	N/A
LoPhIV, IV	7.57	7.22	N/A	10.11	5.65	6.01	4.08	N/A
WoPhI, II	2.17	1.6	2.03	4.38	1.95	2.17	N/A	N/A
WoPhII, II	1.86	1.08	N/A	N/A	N/A	1.69	N/A	N/A
WoPhI, III	2.19	2.51	N/A	N/A	2.12	2.33	1.15	N/A
WoPhII, III	N/A	1.99	N/A	N/A	N/A	1.95	1.17	N/A
WoPhIII, III	N/A	N/A	N/A	N/A	N/A	1.7	0.72	N/A
WoPhI, IV	N/A	N/A	N/A	N/A	N/A	1.63	1.16	N/A
WoPhII, IV	N/A	N/A	N/A	N/A	1.57	1.55	1.14	N/A
WoPhIII, IV	N/A	N/A	N/A	N/A	1.71	1.49	1.07	N/A

Number	IVPP V 13350	IVPP V 13396	IVPP V 10996	IVPP V 12811	IVPP V 11374	IVPP V 11375	IVPP V 11553	N/A
Genus	*Jeholornis*	*Sapeornis*	*Yanornis*	*Sinornithosaurus*	*Confuciusornis*	*Confucuisornis*	*Confucuisornis*	*Gansus*
WoPhIV, IV	N/A	N/A	N/A	N/A	1.13	1.45	N/A	N/A
Foot length	42.78	35.54	N/A	N/A	21.18	28.2	19.04	N/A
LoUng I	7.41	10.22	N/A	10.95	7.7	6.67	5.24	N/A
w/sheath	8.8	13.03	N/A	N/A	N/A	9.43	5.8	N/A
LoUng II	11.37	8.98	N/A	N/A	8.2	8.68	6.15	N/A
w/sheath	12.47	12.65	N/A	N/A	11.65	12.02	N/A	N/A
LoUng III	11.4	9.26	N/A	16.75	9.74	8.58	6.26	N/A
w/sheath	11.74	13.39	N/A	N/A	12.72	12.1	N/A	N/A
LoUng IV	10.83	8.1	N/A	15.65	8.7	8.36	5.71	N/A
w/sheath	11.62	12.7	N/A	N/A	11.45	12.18	N/A	N/A
Lotmt	37.61	32.32	29.16	93.99	26.11	26.22	20.01	31.02
Lott	69.61	65.7	75.4	N/A	54.08	53.94	40.48	N/A
Lofem	58.38	55.31	57.4	N/A	46.47	45.69	32.01	N/A
Wotmt@prox	9.28	9.64	8.41	20.53	7.03	7.04	5.39	5.95
Wotmt@cond	9.73	8.61	9.22	N/A	7.84	7.52	5.42	5.99
Wott@prox	9.92	9.82	10.71	13.73	7.25	8.81	N/A	N/A
Wott@mid	5.72	6.28	4.71	N/A	4.87	5.44	2.75	N/A
Wott@cond	9.85	8.91	7.69	15.43	8.01	6.69	4.77	N/A
Wofem@cond	N/A	N/A	N/A	N/A	6.95	7.46	N/A	N/A
LoHum	N/A	91.07	76.08	N/A	53.19	52.63	41.67	N/A
LoRad	N/A	87.55	76.95	N/A	45.68	45.79	36.7	N/A
LoUln	N/A	88.54	79.49	N/A	45.63	44.87	35.44	N/A
LoCarp	N/A	38.73	38.78	N/A	24.9	20.43	19.08	N/A
LoBeak	28.34	N/A	N/A	N/A	21.5	28.99	16.07	N/A
WoBeak	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

Number	IVPP V 15074	IVPP V 15080	IVPP V 15084	IVPP V 15083	IVPP V 15077	N/A Cast	IVPP V 11307	IVPP V 13175A
Genus	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Confucuisornis*	*Confucuisornis*
LoDI	6.5	8.23	6.92	6.64	8.07	7.38	4.02	6.34
w/claw	N/A	12.51	11.33	9.83	1.77	11.32	9.71	12.52
LoDII	19.47	24.94	20.23	21.62	N/A	27.35	11.39	19.08
w/claw	N/A	29.44	23.24	N/A	N/A	N/A	16.84	N/A
LoDIII	N/A	N/A	26.11	27.78	N/A	32.55	15.33	24.79
w/claw	N/A	N/A	30.16	N/A	N/A	N/A	20.43	N/A
LoDIV	28.43	N/A	23.55	30.41	N/A	38.3	13.52	23.04
w/claw	N/A	N/A	26.88	N/A	N/A	N/A	18.2	N/A
W@Pjoint II	1.87	2.17	N/A	N/A	2.47	2.16	2.16	3.28
W@Pjoint III	N/A	3.49	N/A	N/A	N/A	N/A	2.07	3.23
W@Pjoint IV	2.01	2.07	N/A	N/A	N/A	N/A	1.9	N/A
W@2joint III	1.95	N/A	N/A	N/A	N/A	2.01	1.94	2.6
W@2joint IV	1.93	N/A	1.71	N/A	N/A	1.51	1.73	2.17
W@3joint IV	1.45	N/A	1.7	N/A	N/A	1.78	1.69	2.37
LoPhI, II	11.77	13.64	9.53	11.53	13.96	14.59	5.21	8.44
LoPhII, II	8.12	12.06	9.88	10.09	12.63	12.76	6	10.64
LoPhI, III	N/A	12.9	11.76	11.88	N/A	14.36	5.42	9.23
LoPhII, III	N/A	N/A	7.93	8.54	10.71	9.45	5.09	7.99
LoPhIII, III	9.75	N/A	6.82	7.36	9.18	8.74	5.68	7.97
LoPhI, IV	8.97	11.08	8.99	9.17	N/A	11.35	3.83	6.01
LoPhII, IV	7.55	8.83	6.19	7.47	7.92	9.43	3.03	5.4
LoPhIII, IV	6.96	N/A	4.89	6.85	8.7	8.84	3.35	5.2
LoPhIV, IV	6.97	N/A	4.76	6.92	N/A	8.68	4.34	6.43
WoPhI, II	1.49	N/A	N/A	N/A	N/A	N/A	1.65	3.03
WoPhII, II	1.16	1.18	N/A	N/A	1.31	1.58	1.03	N/A
WoPhI, III	N/A	1.93	N/A	N/A	N/A	N/A	1.37	2.75
WoPhII, III	N/A	N/A	N/A	N/A	N/A	1.36	1.29	2.53
WoPhIII, III	0.96	N/A	N/A	N/A	N/A	1.15	1.17	N/A
WoPhI, IV	1.66	1.21	N/A	N/A	N/A	N/A	1.44	N/A
WoPhII, IV	1.36	1.19	N/A	N/A	N/A	N/A	1.34	1.98
WoPhIII, IV	1.28	N/A	1.11	N/A	N/A	1.16	1.15	1.75

Number	IVPP V 15074	IVPP V 15080	IVPP V 15084	IVPP V 15083	IVPP V 15077	N/A Cast	IVPP V 11307	IVPP V 13175A
Genus	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Gansus*	*Confucuisornis*	*Confucuisornis*
WoPhIV, IV	0.84	N/A	N/A	N/A	N/A	0.93	N/A	1.48
Foot length	N/A	N/A	31.59	34.21	N/A	41.03	19.34	N/A
LoUng I	N/A	4.25	4.69	3.16	4.11	3.63	5.08	9.57
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	7.13	N/A
LoUng II	3.94	5.05	4.38	4.33	5.11	4.75	4.91	14.14
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	7.5	17.16
LoUng III	4.19	N/A	4.82	3.83	N/A	4.17	5.66	11.93
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	8.56	N/A
LoUng IV	3.39	N/A	3.58	3.56	N/A	3.89	5.81	8.54
w/sheath	N/A	N/A	N/A	N/A	N/A	N/A	8.52	12.68
Lotmt	28.08	29.88	36.36	29.13	38.35	36.73	19.8	31.22
Lott	N/A	52.72	N/A	N/A	N/A	55.26	41.36	62.93
Lofem	N/A	31.62	30.52	N/A	N/A	N/A	35.67	54.58
Wotmt@prox	N/A	N/A	N/A	N/A	N/A	N/A	5.91	9.71
Wotmt@cond	N/A	6.85	N/A	N/A	N/A	N/A	4.67	10.11
Wott@prox	N/A	N/A	N/A	N/A	5.72	N/A	N/A	8.84
Wott@mid	N/A	N/A	N/A	N/A	N/A	N/A	4.27	5.38
Wott@cond	4.35	N/A	N/A	N/A	N/A	N/A	4.98	8.27
Wofem@cond	N/A	N/A	N/A	N/A	5.3	N/A	4.78	N/A
LoHum	N/A	N/A	N/A	N/A	N/A	N/A	45.1	59.61
LoRad	N/A	N/A	N/A	N/A	N/A	N/A	37.04	52.7
LoUln	N/A	N/A	N/A	N/A	N/A	N/A	38.82	56.42
LoCarp	N/A	N/A	N/A	N/A	N/A	N/A	26.16	31.76
LoBeak	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
WoBeak	N/A	N/A	N/A	N/A	N/A	N/A	N/A	13.53

Number	IVPP V 13175B	IVPP V 12325	IVPP V 13168
Genus	*Confucuisornis*	*Longipteryx*	*Confucuisornis*
LoDI	8.66	5.77	5.5
w/claw	17.75	N/A	N/A
LoDII	19.17	8.34	14.56
w/claw	N/A	N/A	N/A
LoDIII	24.37	N/A	20.53
w/claw	33.8	N/A	N/A
LoDIV	23.25	N/A	16.99
w/claw	N/A	N/A	23.24
W@Pjoint II	N/A	1.91	2.74
W@Pjoint III	3.19	1.93	2.73
W@Pjoint IV	3.04	1.71	N/A
W@2joint III	N/A	N/A	2.29
W@2joint IV	2.74	N/A	N/A
W@3joint IV	2.6	N/A	N/A
LoPhI, II	8.64	3.68	6.85
LoPhII, II	10.53	4.89	7.71
LoPhI, III	9.21	3.98	7.65
LoPhII, III	8.64	4.83	6.67
LoPhIII, III	8.89	N/A	6.21
LoPhI, IV	6.56	3.36	4.78
LoPhII, IV	5.86	3.23	4.27
LoPhIII, IV	5.52	N/A	3.73
LoPhIV, IV	7.1	N/A	5.35
WoPhI, II	N/A	1.44	1.83
WoPhII, II	N/A	N/A	N/A
WoPhI, III	2.6	1.19	2.22
WoPhII, III	N/A	0.97	1.98
WoPhIII, III	N/A	N/A	N/A
WoPhI, IV	2.28	N/A	1.6
WoPhII, IV	1.71	1.15	N/A
WoPhIII, IV	1.97	N/A	N/A

Number	IVPP V 13175B	IVPP V 12325	IVPP V 13168
Genus	*Confucuisornis*	*Longipteryx*	*Confucuisornis*
WoPhIV, IV	1.62	N/A	N/A
Foot length	N/A	N/A	N/A
LoUng I	9.35	N/A	N/A
w/sheath	12.76	N/A	N/A
LoUng II	13.33	N/A	9.35
w/sheath	17.29	N/A	11.95
LoUng III	11.32	N/A	8.81
w/sheath	14.38	N/A	11.96
LoUng IV	9.87	N/A	7.45
w/sheath	13.15	N/A	9.96
Lotmt	31.29	19.99	27.26
Lott	67.24	31.43	52.48
Lofem	55.39	27.68	44.33
Wotmt@prox	8.84	4.44	6.99
Wotmt@cond	9.59	4.83	7.25
Wott@prox	N/A	4.8	N/A
Wott@mid	6.87	3.02	N/A
Wott@cond	9.21	N/A	N/A
Wofem@cond	10.98	N/A	7.92
LoHum	67.69	44.3	51.9
LoRad	56.41	42.3	43.03
LoUln	59.46	45.04	44.56
LoCarp	36.23	15.3	26.95
LoBeak	32.51	31.57	26.12
WoBeak	N/A	N/A	N/A

Number	PMOL-AB0003	PMOL-AB00017	PMOL-AB00016	PMOL-AB00041A-B	PMOL-AB00114	PMOL-AB00019
Genus	Enantiornithine	Enantiornithine	Enantiornithine	Enantiornithine	*Confuciusornis jianchangensis*	*Alaeoalaornis*
LoDI	3.96	3.32	4.05	4.43	4.78	4.88
LoDII	8.21	7.55	8.59	6.82	11.27	N/A
LoDIII	12.29	11.99	13.86	11.26	16.63	13.86
LoDIV	8.88	9.79	9.75	9.15	13.81	N/A
W@Pjoint II	1.61	1.39	1.95	1.44	2.32	N/A
W@Pjoint III	0	1.56	N/A	N/A	N/A	N/A
W@Pjoint IV	1.56	N/A	N/A	N/A	1.67	N/A
W@2joint III	1.42	1.41	N/A	N/A	N/A	N/A
W@2joint IV	1.17	N/A	N/A	N/A	N/A	N/A
W@3joint IV	1.16	N/A	N/A	N/A	N/A	N/A
LoPhI, II	3.67	3.46	4.71	3.39	6.53	N/A
LoPhII, II	4.87	4.11	4.69	3.98	6.47	3.29
LoPhI, III	4.42	5.1	5.05	4.45	6.92	4.49
LoPhII, III	3.74	3.57	3.96	3.78	5.44	4.61
LoPhIII, III	4.82	4.01	4.39	3.62	5.66	5.83
LoPhI, IV	3.52	2.3	2.56	2.47	3.4	3.79
LoPhII, IV	2.14	2.82	2.17	2.26	3.04	2.49
LoPhIII, IV	0	2.05	2.31	2.44	2.88	N/A
LoPhIV, IV	3	2.47	3.09	2.73	4.16	3.46
WoPhI, II	0.75	0.9	1.47	0.95	N/A	N/A
WoPhII, II	0	0.79	1.43	0.77	1.16	N/A
WoPhI, III	0.95	0.87	N/A	N/A	N/A	N/A
WoPhII, III	0.71	0.91	N/A	N/A	N/A	N/A
WoPhIII, III	0.67	0.76	N/A	N/A	N/A	N/A

Number	PMOL-AB0003	PMOL-AB00017	PMOL-AB00016	PMOL-AB00041A-B	PMOL-AB00114	PMOL-AB00019
Genus	Enantiornithine	Enantiornithine	Enantiornithine	Enantiornithine	*Confuciusornis jianchangensis*	*Alaeoalaornis*
WoPhI, IV	0	N/A	N/A	N/A	1.53	N/A
WoPhII, IV	0	N/A	N/A	N/A	1.15	0.79
WoPhIII, IV	0	N/A	N/A	N/A	N/A	N/A
WoPhIV, IV	0	N/A	N/A	N/A	N/A	N/A
Foot length	14.12	12.06	16.58	11.49	20.2	14.94
Lotmt	14.61	14.14	16.02	13.9	20.92	18.11
Lott	26.97	28.13	32	25.57	48.15	35.24
Lofem	23.48	19.55	24.65	19.95	42	26.14
Wotmt@prox	4.18	3.23	4.21	2.9	5.18	3.91
Wotmt@cond	2.88	3.25	4.34	2.94	5.21	3.76
Wott@prox	3.83	4.01	5.37	4.08	5.88	N/A
Wott@mid	0	N/A	N/A	N/A	N/A	N/A
Wott@cond	2.59	2.98	3.44	2.69	5.36	4.07
Wofem@cond	3.13	N/A	2.95	2.83	N/A	N/A

PMOL-AB00027	PMOL-AB00018	PMOL-AB00125	PMOL-AB00122	PMOL-AB00149	PMOL-AB00150
Dapingfengornis	*Shenshiornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*
3.74	13.48	5.12	6.84	6.01	6.88
7.19	17.11	15.26	15.6	21.25	17.72
12.24	27.32	19.63	23.13	23.22	24.48
9.73	N/A	18.25	23.71	20.39	20.57
1.62	N/A	2.58	N/A	N/A	3.89
1.2	N/A	2.5	N/A	3.55	3.16
1.23	N/A	2.57	N/A	2.67	2.92
N/A	N/A	2.09	N/A	3.85	2.92
N/A	N/A	2.51	N/A	2.88	2.53
N/A	N/A	1.98	N/A	2.63	2.59
3.82	11.38	6.47	9.01	10.87	7.64
4.14	5.92	7.89	10.72	9.26	9.82
4.83	9.2	7.05	9.25	8.8	9.07
4.19	9.24	6.69	7.89	6.48	7.53
5.03	8.39	5.95	7.25	8.08	8.15
2.58	5.62	6.6	6.26	5.72	5.68
2.58	N/A	4.46	4.8	5.12	4.64
2.17	N/A	4.35	5.31	4.47	3.25
3	N/A	4.96	6.39	6.7	5.01
1.17	N/A	2.38	N/A	N/A	2.58
0.93	N/A	2.16	N/A	N/A	2.48
0.8	1.94	1.92	N/A	2.66	2.32
N/A	1.48	2.08	N/A	2.42	2.2
N/A	1.37	1.37	N/A	2.14	1.96

PMOL-AB00027	PMOL-AB00018	PMOL-AB00125	PMOL-AB00122	PMOL-AB00149	PMOL-AB00150
Dapingfengornis	*Shenshiornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*	*Confuciusornis*
0.85	2.04	1.51	N/A	2.37	2.13
N/A	N/A	2.14	N/A	2.43	1.98
N/A	N/A	1.46	N/A	2.7	1.71
N/A	N/A	1.14	N/A	2.05	1.19
14.33	31.95	22.81	28.92	30.45	34.12
15.38	30.94	25.41	28.59	31.07	28.94
27.67	64.29	53.84	68.27	67.92	60.19
20.07	60.73	43.11	53.53	52.49	51.37
2.87	9.12	7.47	7.52	10.23	N/A
3.18	9.25	7.04	7.75	10.98	9.35
4.21	6.88	9.06	11.66	8.7	12.04
N/A	N/A	4.3	N/A	5.13	5.36
2.31	9.34	7.96	N/A	8.67	6.8
3.4	8.71	4.5	8.82	8.6	10.56

Number	DNHM D2455	DNHM D2126	DNHM D1878	DNHM D2522	DNHM D2139	D2452
Genus	*Zhongornis*	*Houshanornis*	*Shanweiniao*	*Rapanaxavis*	*Dalianraptor*	*Confuciusornis*
LoDI	1.76	3.77	4.18	4.51	7.03	7.97
LoDII	6.22	5.23	7.5	7.31	18.8	18.5
LoDIII	8.93	10.88	9.04	8.44	24.76	24.05
LoDIV	7.3	7.33	9.1	8.15	23.15	23.31
W@Pjoint II	1.16	N/A	1.21	1.1	N/A	2.77
W@Pjoint III	1.14	N/A	0.9	0.97	N/A	N/A
W@Pjoint IV	0.8	N/A	N/A	1.15	N/A	1.81
W@2joint III	0.86	N/A	1.17	0.83	N/A	N/A
W@2joint IV	0.82	N/A	0.94	0.85	N/A	N/A
W@3joint IV	0.53	N/A	0.7	0.77	N/A	N/A
LoPhI, II	2.71	3.43	3.39	2.86	9.19	9.61
LoPhII, II	3.25	2.67	4.44	5.1	9.51	10.81
LoPhI, III	3.21	4.44	3.03	2.66	9.59	9.73
LoPhII, III	3.06	4.5	2.7	2.39	7.63	8.67
LoPhIII, III	3.01	4.52	3.99	4.02	10.71	8.65
LoPhI, IV	1.69	N/A	N/A	1.71	N/A	6.77
LoPhII, IV	1.65	2.38	3.32	1.57	N/A	5.56
LoPhIII, IV	1.5	2.45	2.45	1.74	N/A	N/A
LoPhIV, IV	2.26	3.01	4.03	3.74	9.52	6.68
WoPhI, II	0.38	N/A	0.83	0.78	N/A	1.75
WoPhII, II	0.58	N/A	0.78	0.78	N/A	1.53
WoPhI, III	0.87	N/A	0.79	0.78	N/A	N/A
WoPhII, III	0.71	N/A	0.68	0.61	N/A	N/A
WoPhIII, III	0.51	N/A	1.14	0.59	N/A	N/A

Number	DNHM D2455	DNHM D2126	DNHM D1878	DNHM D2522	DNHM D2139	D2452
Genus	*Zhongornis*	*Houshanornis*	*Shanweiniao*	*Rapanaxavis*	*Dalianraptor*	*Confuciusornis*
WoPhI, IV	0.67	N/A	N/A	0.8	N/A	1.79
WoPhII, IV	0.75	N/A	0.83	0.86	N/A	1.56
WoPhIII, IV	0.61	N/A	1	0.62	N/A	N/A
WoPhIV, IV	0.59	N/A	0.74	0.49	N/A	N/A
Foot length	11.05	N/A	10.2	10.74	37.35	29.64
Lotmt	9.91	15.53	11.31	13.12	30.69	31.32
Lott	18.23	26.01	22.85	24.49	62.68	71.67
Lofem	16.44	20.73	14.9	18.77	62.86	58.45
Wotmt@prox	3.28	3.07	3.08	3.18	N/A	7.73
Wotmt@cond	2.75	3.14	2.75	2.21	N/A	8.68
Wott@prox	2.87	N/A	3.58	2.66	N/A	9.22
Wott@mid	1.26	N/A	1.56	1.59	6	5.62
Wott@cond	2.99	N/A	2.78	3.46	6.55	8.62