# Integrating ecology and evolution in deep time: using Ecological Niche <br> Modeling to study species' evolutionary responses to climate from the Pliocene to the present-day biodiversity crisis 

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Integrating ecology and evolution in deep time: using Ecological Niche Modeling to study species' evolutionary responses to climate from the Pliocene to the present-day biodiversity crisis

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#### Abstract

The aim of my dissertation was to elucidate how environmental changes have influenced evolutionary and distributional patterns in the near-shore molluscan fauna of the Atlantic Coastal Plain (southeastern U.S.) over the past three million years. Disentangling the long-term evolutionary responses of species to environmental change is important for understanding the mechanisms controlling evolutionary processes and for assessing how current and future climate changes will impact Earth's biodiversity. My dissertation was comprised of three chapters that integrated both paleontological and neontological data to study the molluscan record of the Atlantic Coastal Plain. The first study in my dissertation focused on 14 extant marine mollusk species and their potential responses to future climate changes over the next $\sim 100$ years. Two hypotheses were tested: that suitable areas will shift northwards for these species, and that they will show varied responses to future climate change based on species-specific niche attributes. I found that species were not predicted to shift pole-ward, but rather showed varied responses to future warming. Many of the studied species will be hard hit by future climate changes, such that over $20 \%$ of their suitable area will disappear by the end of this century. The second study statistically analyzed whether the niches of mollusk species remained stable across three million years of profound environmental changes. Prior to this research, the long-term evolutionary dynamics of species' niches to differing climatic regimes remained uncertain, even though the question is vital to understanding the fate of biodiversity in a rapidly changing world. I found that species' tolerances were statistically similar from the Pliocene to the present-day, which suggest that species will respond to current and future warming by altering distributions to track suitable habitat, or, if the pace of change is too rapid, by going extinct. The last study tested whether niche breadth and/or geographic range size was a better predictor of extinction selectivity for mollusk species from the Pliocene. I hypothesized that species that went


extinct post Pliocene would have smaller geographic ranges and smaller niche breadths compared with those species that are still extant. I found that only realized niche breadth (i.e., the breadth of the environment actually occupied by a species) and geographic range size, rather than fundamental niche breadth, are inversely related to extinction probability. This finding has implications for assessing which species are more at risk as a consequence of current and future climate changes, and helps to sharpen our understanding of which macroevolutionary processes shape patterns of diversity over evolutionary time scales. Together, these studies indicated that abiotic, environmental factors play a fundamental role in governing species' distributions in deep time. More specifically, species did not seem to rapidly evolve in response to new environmental conditions, but tracked preferred habitat or faced extirpation if conditions exceeded their tolerance limits. These findings can be used to ensure that paleobiology does not become the biology of the future.

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## Introduction

My research interests are focused on gaining deeper insight into macroevolutionary patterns and processes preserved in the fossil record. The aim of my dissertation is to elucidate how environmental changes have influenced evolutionary and distributional patterns in the near-shore molluscan fauna of the Atlantic Coastal Plain (southeastern U.S.) over the past three million years. Disentangling the long-term evolutionary responses of species to environmental change is important for understanding the mechanisms controlling evolutionary processes (Ross \& Allmon, 1990; Gould, 2002; Parmesan, 2006; Wiley \& Lieberman, 2011) and for assessing how current and future climate changes (IPCC, 2007) will impact Earth's biodiversity (Burrows et al., 1991; Araújo \& Rahbek, 2006; Harley et al., 2006). Whereas modern biological inquiry can examine only a snapshot of a species' lifetime, the paleontological record provides a ledger of species' responses to constantly changing environments over millions of years (Roy et al., 1996; Patzkowsky \& Holland, 2012). Therefore, to fully understand the evolutionary and conservation implications of current climate changes, we must look to similar episodes of environmental change in the past using the entire duration of species' lifetimes (Jablonski, 1991; McKinney, 1997; Dietl \& Flessa, 2011). Here, I consider the Pliocene fossil record, which was the most recent period in Earth history when temperatures were sustained at levels expected at the end of this century (Robinson \& Dowsett, 2008).

## Study system

My dissertation is comprised of three chapters that integrate both paleontological and neontological data to study the molluscan record of the Atlantic Coastal Plain (Dietl \& Flessa,

2011; Fritz et al., 2013). The past three million years of molluscan evolution in the Atlantic Coastal Plain provide an excellent record in which to study implications of climate change for two reasons. First, remains of fossil and recent mollusks are extremely abundant ((Allmon et al., 1993; Campbell, 1993; Hendricks, 2009) and present interesting diversity patterns (Todd et al., 2002; Vermeij, 2005). Overall diversity in the region has remained relatively unchanged since the Pliocene, despite $\sim 70 \%$ extinction, indicating that extinctions were balanced by originations (Allmon et al., 1993).

Second, the Atlantic Coastal Plain experienced significant environmental disturbances, from the closing of the Isthmus of Panama about three million years ago to numerous Pleistocene glacial/interglacial cycles (Krantz, 1990; Toscano \& York, 1992; Cronin \& Dowsett, 1996). These environmental changes can be divided into three major intervals: (i) the early Pliocene, when sea surface temperatures were generally cooler than today; (ii) the 'mid-Pliocene warm period' (mPWP), $\sim 3.3-3 \mathrm{Ma}$, when temperatures were generally warmer than today, reflecting closure of the Isthmus of Panama and reorientation of the Gulf Stream along the eastern coast of North America (Dowsett \& Cronin, 1990); and (iii) a cooling period associated with the onset of Northern Hemisphere glaciations around 2.5-2.4 Ma and continuing to the present-day (Williams et al., 2009). Isotopic and biotic evidence suggests that there was reduced seasonality and warmer conditions along the eastern seaboard of the USA during the mPWP, with winter water conditions generally $3-5^{\circ} \mathrm{C}$ warmer than today in the Carolinas and Virginias (Dowsett \& Wiggs, 1992; Knowles et al., 2009; Williams et al., 2009). These environmental changes provide the perfect backdrop to analyze how species are affected by abiotic changes over geological time scales.


Table 0.1 Ten core extant species that served as the link across all three chapters, some of which are economically important.

## Research chapters

I used the above-described system to investigate over 100 bivalve and gastropod species that occur in the Neogene record of the Atlantic Coastal Plain. My goal was to uncover general patterns for how species respond to environmental change, and thus I utilized taxa that were both ecologically and phylogenetically distinct. Ten core extant species served as a link across all three chapters, some of which are economically important (Table 0.1); remaining species were classified within 50 bivalve and 16 gastropod genera. I personally vetted and compiled an extensive database of species' occurrences spanning over three million years and covering the entirety of the Atlantic Coastal Plain. These data were derived from visits to several natural history collections and from detailed analyses of the literature. In order to ensure appropriate stratigraphic context and age controls for these occurrences, I assembled a stratigraphic database for all Pliocene-Recent geologic units of the Atlantic Coastal Plain (Appendix S2.2). Correlations and unit ages were determined by literature survey and use of various stratigraphic databases.

The first study in my dissertation focused on 14 extant marine mollusk species and their potential responses to future climate changes over the next $\sim 100$ years. Two hypotheses were tested: that suitable areas will shift northwards for these species, and that they will show varied responses to future climate change based on species-specific niche attributes (Saupe et al., 2014, in press). Ecological niche models (ENMs) were used to forecast potential distributions according to three scenarios of future change for three time slices using climate data from the Hadley Climate Centre (UK). Contrary to my hypothesis, I did not find a coherent pattern of areas with suitable environments expanding at high-latitude range boundaries, with simultaneous contraction at their low-latitude boundaries. These results contrast with previously-documented trends among terrestrial and other marine species, which are rapidly shifting their ranges to higher latitudes. Furthermore, although one might
expect that warming would benefit tropical species, I found that many of the studied species will lose significant portions of their suitable habitat and may even face extirpation by the end of this century. Alternatively, my second hypothesis was supported in that species were predicted to have differing responses to future warming, which depended upon the particulars of their niche characteristics. The species-specific nature of responses to climate change is consistent with those observed in the fossil record during past episodes of climate change.

The second study focused on ten fossil species and statistically analyzed whether their niches remained stable across three million years of profound environmental changes (Saupe et al., in review). Prior to this research, the long-term evolutionary dynamics of species' niches to differing climatic regimes remained uncertain, even though the question is vital to understanding the fate of biodiversity in a rapidly changing world. I found that the environmental preferences of species remained stable across three million years. My results suggest that species will respond to current and future warming by altering distributions to track suitable habitat, or, if the pace of change is too rapid, by going extinct. My research also supports the use of methods that project species' present-day environmental requirements to future climatic landscapes to assess conservation risks (e.g., (Peterson et al., 2002; Thuiller et al., 2005; Saupe et al., 2014, in press). At the macroevolutionary scale, this research provides evidence that species' distributions are structured by environmental factors.

The last study tested whether niche breadth and/or geographic range size were better predictors of extinction selectivity for mollusk species from the Pliocene. Small geographic range sizes have often been associated with increased risk of extinction in both neontological (Schwartz et al., 2006; Fritz et al., 2009; Boulangeat et al., 2012) and paleontological (Jablonski \& Hunt, 2006; Payne \& Finnegan, 2007; Harnik, 2011) studies, while theory suggests that specialist species should be at higher risk during times of environmental change (Eldredge, 1979; Vrba, 1980; McKinney, 1997; Devictor et al., 2008; Colles et al., 2009; Myers \& Saupe, 2013). Using ENM and paleoclimatic data, I was able to quantify niche
breadth for Pliocene species that (i) have survived to the present-day and (ii) have since gone extinct. I hypothesized that species that went extinct post Pliocene would have smaller geographic ranges and smaller niche breadths compared with those species that are still extant. However, contrary to my hypothesis, I found that only realized niche breadth (i.e., the breadth of the environment actually occupied by a species) and geographic range size, rather than fundamental niche breadth, are inversely related to extinction probability. This finding has implications for assessing which species are more at risk as a consequence of current and future climate changes (Mace et al., 2008), and helps to sharpen our understanding of which macroevolutionary processes shape patterns of diversity over millions of years (Lieberman \& Vrba, 1995; Myers \& Saupe, 2013).

The results of these studies highlight the importance of integrating neontological and paleontological data to study macroevolutionary patterns through time. My research indicates that abiotic, environmental factors play a fundamental role in governing species' distributions across millions of years. More specifically, species do not seem to rapidly evolve in response to new environmental conditions, but rather they track preferred habitat or face extirpation if conditions exceed tolerance limits. The lack of evolution in niche attributes potentially provides a mechanism explaining patterns of morphological stasis observed in the fossil record (Eldredge \& Gould, 1972; Eldredge et al., 2005). I also discovered that the breadth of the fundamental niche (i.e., whether a species is an environmental specialist or generalist) is not a major factor controlling extinction probability. Indeed, the actual amount of niche space occupied by the species (i.e., the realized niche) and geographic range size seem to be the main factors impacting survivorship. The future models I constructed for these mollusks predict that they will be hard hit by climate changes, particularly since the pace of future change may exceed past rates. Thus, even though they survived conditions in the Pliocene similar to those predicted for the end of this century, the speed at which we approach these changes may be too rapid for species to keep pace.

At the heart of it, I am fascinated by Earth's biodiversity, both past and present. As a child, I would marvel at the red-eyed tree frogs, pangolins, tarsiers, fennec foxes, and jumping spiders that would peer at me from the pages of nature magazines. I began a journey to study this biodiversity because I want to understand how and why it evolved, and ultimately by doing so, I hope to better protect it for generations to come. With respect to my dissertation, human-induced climate changes will have critical implications for biodiversity in general and for commercial mollusks, since near shore environments provide over \$US14 trillion/year in ecosystem goods and services (Costanza et al., 1997). However, protecting diversity is not only vital for our economy and for maintaining our food and medicine reserves (Chapin et al., 2000; Parmesan and Yohe, 2003), but for preserving the sense of awe we receive from our flora and fauna-for ensuring that beauty remains in this world. I hope that my dissertation, with a look towards the past, can inform our future-let us not make paleobiology the biology of the future.

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## Chapter 1. Climate change and marine mollusks of the western North Atlantic: future prospects and perils



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#### Abstract

Numerous studies have examined potential responses of terrestrial biotas to future climate change, but fewer have considered marine realms. We forecast how marine molluscan faunas of the Atlantic Coastal Plain might respond to environmental change over the remainder of this century. We test the hypotheses that suitable areas will shift northwards for studied species, and that species will show varied responses to future climate change. We generated ecological niche models (in GARP and MAXENT) for 14 ecologically, economically and potentially medically important mollusk species, using present-day summaries and future forecasts of climate from the Hadley Centre and known species occurrence data from natural history collections. Niche models were used to forecast potential distributions according to three scenarios of future change for three time slices. Northern extremes of suitability are predicted to shift northwards for only three (GARP) or four (MAXENT) of the 14 species, whereas the southern edge of suitability is predicted to shift southwards for seven (GARP) and one (MAXENT) of the 14 species. When changes in the geographical centroids of suitability are considered, no significant poleward shifts are anticipated for individual species. Instead, half of the study species (many economically important) experience substantial ( $>20 \%$ ) loss of suitable environmental area, even under the lowest-emission future climate scenario. Furthermore, the direction and magnitude of the response to predicted climate change is species-specific. We do not find a coherent pattern of areas with suitable environments expanding at high-latitude range boundaries, with simultaneous contraction at their low-latitude boundaries. Tropical marine mollusks may thus show varied responses as average temperatures warm. These results contrast with trends among terrestrial and other marine species, which are rapidly shifting their ranges to higher latitudes. Conversely, the differing responses of these species to future warming are consistent with responses of species to past episodes of change, as observed in the fossil


record.

## Introduction

Predicting the impacts of future climate change on Earth's biodiversity is critical to preserving biological resources and for understanding evolutionary processes (Thomas et al., 2004; Chen et al., 2011). The advent of ecological niche models (ENMs) has facilitated these types of predictions, being the standard framework used to project species' abiotic requirements onto future climate landscapes, in order to assess likely changes in distributional potential. ENM analyses, however, have focused primarily on terrestrial species, leaving the predicted responses of marine taxa understudied to date. This imbalance reflects the difficulty of obtaining representative datasets for marine species' occurrences and environmental parameters, and of studying marine processes (Richardson \& Poloczanska, 2008; Dambach \& Rödder, 2011; Robinson et al., 2011). Recently, however, new marineorientated data resources have allowed for rapid developments in the study of marine species, from present-day patterns of suitability (e.g. Lima et al., 2007; Pauly et al., 2011; Reiss et al., 2011; Tyberghein et al., 2012; Yesson et al., 2012) to predicting species' responses to changing climate (e.g. Clark et al., 2003; Cheung et al., 2009; Dambach \& Rödder, 2011; Lenoir et al., 2011; Russell et al., 2012; Jones et al., 2013).

Here, we use novel present-day summaries and modeled future climates from the Met Office Hadley Centre (Jones et al., 2011) to study 14 abundant, well-sampled, ecologically and phylogenetically diverse marine mollusk species (Table 1.1) from the near-shore continental shelf of the western North Atlantic. Three of these species are commercially important: the Atlantic oyster, Crassostrea virginica (Gmelin, 1791); the southern hard-shell clam, Mercenaria campechiensis (Gmelin, 1791); and the giant Atlantic cockle, Dinocardium robustum (Lightfoot, 1786). We also include Crepidula fornicata (Linnaeus, 1758), an invasive species detrimental to aquaculture in Europe, and Conus spp., which have
biomedical potential (Alonso et al., 2003).
We test two hypotheses regarding the likely responses of these mollusks to future changes: (1) that they will respond to changing climate by shifting their distributions polewards, and (2) that they will respond to changing climate as a function of speciesspecific niche attributes, not congruently as an assemblage. Previous research supports the first hypothesis, because marine ectotherms tend to occupy the full extent of latitudes within their thermal limits (Pörtner \& Knust, 2007; Tewksbury et al., 2008; Sunday et al., 2012). Consequently, ectotherms should shift northwards in response to warming, because temperatures outside their thermal envelopes decrease their capacity to perform aerobically, and detrimentally impact other physiological processes (Somero, 2002; Pörtner \& Knust, 2007).

Poleward range shifts have formed the dominant observed (Jones et al., 2010; Sorte et al., 2010) and anticipated (Cheung et al., 2009; Albouy et al., 2013) response by marine species to climate change, but recent research indicates that this focus underestimates the impacts of climate change on species' distributions. Evidence suggests that multidirectional distributional shifts are probably due to complexity of the species' niches. VanDerWal et al. (2013) propose that multidirectional shifts might be more pronounced for tropical or subtropical species than for temperate species, but this hypothesis remains relatively untested because of the prevailing focus on temperate species. Thus, our study, which focuses on both temperate and tropical species, may shed light on these response dynamics (see Table S1.1.1 in Appendix S1.1).

We also test whether the focal species are likely to respond to changing climate independently and idiosyncratically, with differing distributional shifts. Based on species' responses to longer-term climate oscillations (e.g. Foster et al., 1990) and previous studies (e.g. Edwards \& Richardson, 2004; Pörtner \& Knust, 2007; Peterson et al., 2008a; Drinkwater et al., 2010; VanDerWal et al., 2013), we anticipate diverse responses to
changing climate that are related to the unique climatic envelope of each species. If noncongruent responses were identified, assemblage composition and community structure could be affected (Harley et al., 2006; Worm et al., 2006).

## Materials and Methods

## Study area.

We trained models for each species in an area generated by buffering distributional data by $10.5^{\circ}$ and dissolving buffered areas to create a continuous region. This buffered region represented a simple hypothesis of distributional potential for these species, tempered by sampling effort. We excluded areas that were not adequately sampled (e.g. South America), because the inclusion of undersampled areas may result in false absences during model calibration. Isolated occurrence points were also excluded from the training region for this reason, and because we deemed them potentially unreliable. In effect, we sought to focus on the union of the area sampled by researchers and that most likely accessible to the species sensu Phillips et al. (2009), VanDerWal et al. (2009) and Peterson et al. (2011). Models were calibrated on these circumscribed areas (Barve et al., 2011) and projected to the entire study region, which comprised the eastern seaboard of North America, the Gulf Coast, the Caribbean and part of South America, from $28^{\circ} \mathrm{S}$ to $56^{\circ} \mathrm{N}$ and from $110^{\circ} \mathrm{W}$ to $33^{\circ} \mathrm{W}$. All spatial analyses were conducted within these bounds (Fig. 1.1).


Figure 1.1 Distributional data for all 14 marine mollusk species within the western North Atlantic. For individual maps, see Figs S1.1.1-1.1.4 in Appendix S1.1.

## Distributional data.

Presence-only distributional data were obtained from the Florida Museum of Natural History (FLMNH), the Academy of Natural Sciences of Drexel University, the University of Michigan Museum of Zoology, the Natuurhistorisch Museum Rotterdam and the U.S.

National Museum of Natural History (Fig. 1.1, Table 1.1, Figs S1.1.1-S1.1.4 in Appendix S1.1). The data obtained were representative of the known distributions of these species (Table S1.1.1), the majority of which occupy depths from c. 0 to 70 m , and are subtropical to tropical (see Table S1.1.1 for details). Only adult forms (benthic) were considered in this study; as such, potential variation in the environmental preferences of larval stages was not captured [most species considered here have planktotrophic larvae, except Conus anabathrum Crosse, 1865, Melongena corona (Gmelin, 1791), Terebra dislocata (Say, 1822) and Lucina pensylvanica (Linnaeus, 1758)]. Although assessing heterogeneity in environmental preferences through ontogeny was of interest, it would have been difficult to implement for marine species whose planktonic or free-swimming larval forms lack distributional records (Hiddink, 2003; Robinson et al., 2011).

We georeferenced distributional data following the point-radius method (Wieczorek et al., 2004) using either Google Earth 6.0 combined with the MANIS Georeferencing Calculator (Wieczorek et al., 2001) or BioGeomancer (Guralnick et al., 2006). The exact protocols depended upon the particular locality string and followed standard georeferencing guidelines (Chapman \& Wieczorek, 2006). Only distributional data with spatial uncertainty less than 6.5 km were retained, totalling 1334 records across the 14 species (Table 1.1). These minor levels of uncertainty in the data should not influence model performance (Graham et al., 2008), given that they were finer than the spatial resolution of our environmental data $\left(1^{\circ} \times 1^{\circ}\right)$. We subsampled the occurrence data to leave one record per environmental pixel, to account for sampling biases (Royle et al., 2012; Yackulic et al., 2013).

Table 1.1 Model evaluation results for 14 mollusk species from the western North Atlantic. The second column indicates number of spatially unique points used to calibrate each model. The following columns report $P$-values and area under the curve ratios from the partial receiver operating characteristic analyses (partial ROC), designed to assess model significance. A similar number of external occurrence points were used in partial ROC analyses. The ' $\%$ pts omitted' column specifies the proportion of external testing points omitted by binary present-day models at a $5 \%$ omission threshold.

|  | No. of <br> spatially <br> unique <br> training <br> points |  | $P$ | MAXENT <br> AUC <br> ratio | $\%$ pts <br> omitted | $P$ | GURP <br> ratio |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Bivalvia |  |  |  |  |  |  |  |
| \% pts |  |  |  |  |  |  |  |
| Anomia simplex | 24 | 0.0112 | 1.36 | $6.1 \%$ | 0.0284 | 1.43 | $20.4 \%$ |
| Crassostrea virginica | 22 | 0.0000 | 1.64 | $27.6 \%$ | 0.0000 | 1.70 | $0.0 \%$ |
| Dinocardium robustum | 21 | 0.0000 | 1.67 | $5.4 \%$ | 0.0000 | 1.63 | $2.7 \%$ |
| Lucina pensylvanica | 17 | 0.0000 | 1.44 | $7.5 \%$ | 0.0641 | 1.24 | $20.0 \%$ |
| Mercenaria campechiensis | 15 | 0.0000 | 1.72 | $28.6 \%$ | 0.1196 | 1.13 | $34.3 \%$ |
| Gastropoda |  |  |  |  |  | 0.0000 | 1.54 |
| Bulla occidentalis | 47 | 0.0000 | 1.59 | $3.1 \%$ | $3.1 \%$ |  |  |
| Conus anabathrum | 17 | 0.0000 | 1.51 | $5.6 \%$ | 0.0043 | 1.30 | $11.1 \%$ |
| Conus spurius | 24 | 0.0000 | 1.56 | $6.5 \%$ | 0.0000 | 1.51 | $8.7 \%$ |
| Crepidula fornicata | 29 | 0.0000 | 1.48 | $11.5 \%$ | 0.0096 | 1.45 | $7.7 \%$ |
| Melongena corona | 19 | 0.0478 | 1.32 | $14.7 \%$ | 0.0161 | 1.48 | $12.0 \%$ |
| Neverita duplicata | 23 | 0.022 | 1.63 | $9.1 \%$ | 0.0066 | 1.57 | $13.6 \%$ |
| Oliva sayana | 19 | 0.0000 | 1.85 | $32.5 \%$ | 0.0000 | 1.70 | $5.0 \%$ |
| Strombus alatus | 19 | 0.0001 | 1.64 | $5.0 \%$ | 0.0054 | 1.58 | $7.5 \%$ |
| Terebra dislocata | 18 | 0.0002 | 1.61 | $6.7 \%$ | 0.0473 | 1.46 | $8.9 \%$ |

## Environmental data

Niche models for present-day distributions were constructed using eight surface-level environmental variables from the Ocean Cycle model (Diat-HadOCC) component of the Hadley Centre Global Environmental Model version 2 with Earth System components (HadGEM2-ES; Moss et al., 2010; Collins et al., 2011; Martin et al., 2011) and a world bathymetry layer (Amante \& Eakins, 2009). The eight Diat-HadOCC variables represented modeled averages for 1991-2010 at $1^{\circ} \times 1^{\circ}$ resolution: dissolved inorganic carbon (DIC); diatom phytoplankton concentration; non-diatom phytoplankton concentration; zooplankton; sea-surface temperature (SST); sea-surface salinity (SSS); total alkalinity; and nitrogen concentration. The bathymetry grid was resampled from $2^{\prime}$ resolution to $1^{\circ}$ using the naturalneighbour interpolation function in ArcGIS 10 (Sibson, 1981). These data provided a rich environmental characterization with which to assess how species may respond to
environmental change. Although temperature and salinity have been reported to constrain the distributions of other marine invertebrates (e.g. Jones et al., 2009; Tunnell et al., 2010; Russell et al., 2012), the additional parameters were potentially important in determining the suitability of environments for marine mollusks (Talmage \& Gobler, 2009).

Future environmental parameters were derived from HadGEM2-ES under the new Intergovernmental Panel on Climate Change (IPCC) 5th Assessment Report Representative Concentration Pathways (RCP) 2.6, 4.5 and 8.5 emission scenarios (Moss et al., 2010), representing least to greatest estimated greenhouse gas emissions, respectively; these scenarios allowed us to understand and assess variation among possible future climates. We evaluated RCP scenarios for 2021-2040, 2041-2060 and 2081-2100. Future projections for depth changes in the ocean were not available, so present-day bathymetry was used. Keeping bathymetry at present-day conditions should not affect our analyses, given the resolution of our study and the fact that sea level is predicted to rise only $c .20-65 \mathrm{~cm}$ over this interval (IPCC, 2007).

## Modeling algorithms.

GARP (Genetic Algorithm for Rule-Set Prediction) provides an evolutionary computing algorithm for building ENMs based on non-random associations between known occurrence points for a species and sets of environmental coverages (Stockwell \& Peters, 1999). We used DESKTOPGARP 1.1.3 (available at: http://www.lifemapper.org/desktopgarp/) with an internal testing feature (i.e. a random $50 \%$ of input data held back to evaluate model quality), resulting in 100 models for each species, with a 0.01 convergence limit and maximum of 1000 iterations. The 'best subsets' procedure was implemented (Anderson et al., 2003), wherein the ten best models were summed in ArcGIS 10 (ESRI, Redlands, CA, USA) to create a map of model agreement, with pixel values ranging from 0 to 10 . We changed the values of two peripheral pixels from each environmental layer, because

DESKTOPGARP rescales predictor variable values to the range $0-254$. This ensured that the lowest and highest values from projection regions and time slices were also present in calibration regions, producing consistent projections in GARP.

MAXENT (version 3.1.1) minimizes the relative entropy between two probability densities (one from the distributional data and one from the background or study area) defined in covariate space (Elith et al., 2011). We used the default parameters, including logistic output, random test percentage 0 , regularization multiplier 1 , and 10,000 background points. Linear, quadratic, product, threshold and hinge feature types were enabled, and we removed duplicate presences. We also ran MAXENT with extrapolation disabled, which truncates the model response curves outside values found in the calibration region and elicits a response curve closer to that of GARP (Owens et al., 2013).

## Model analysis and verification.

## Post-processing of ENMs.

Maps of projected ENMs were initially converted into integer grids, retaining three significant digits, and reclassified as either 0 (unsuitable area) or 1 (suitable area) for ease of comparison (Liu et al., 2005) using threshold values that allowed a maximum of $5 \%$ omission error based on the calibration data. A certain percentage of occurrence data was accepted as omission error in model predictions, because error may exist in the dataset (Peterson et al., 2011). Although the choice of threshold may affect analyses (Nenzen \& Araújo, 2011; Jones et al., 2013), the raw model results exhibited patterns similar to those obtained using thresholds. Calculations of the area predicted to be suitable within the study region were performed by projecting grids onto a global cylindrical equal-area projection, and summing the areas in ARCMAP. Once the maps were reclassified, we calculated the potential cumulative area lost and gained from the present to the three future time slices sensu Cheung et al. (2009) and Thuiller et al. (2005). These maps were not representative of distribution sensu stricto, but rather areas of predicted environmental suitability. The
assumption was that species would track and fill suitable areas. Hence, the cumulative environmental suitability maps potentially misrepresented diversity in the present (i.e. subject to assumptions regarding which areas were accessible to the species; Barve et al., 2011) and for the future (Aranda \& Lobo, 2011). Our analysis, however, aimed to characterize potential new area gained and lost across species. To visualize cumulative suitable area lost/gained as a function of latitude, we tabulated the distributions of values across particular latitudes in R 2.15.0 (R Core Team, 2012), and standardized based on numbers of pixels available (Fig. 1.2).

Latitudinal range shifts through time were calculated using gCentroid in the RGEOS package in R 2.15.0 (Bivand \& Rundel, 2011). First, present-day and future binary suitability maps were converted to polygons in ARCGIS 10. These (often non-contiguous) polygons were then imported into R to find the 'centre of mass' or true centroid of areas presenting suitable conditions for each time slice.

## Model quality metrics.

We assessed present-day model quality using three approaches (Table 1.1, Table S1.1.1). The first two analyses relied on external testing data ( $50 \%$ of occurrence points) set aside for each species (i.e. not used in model calibration). First, we calculated omission error rates, with false negatives defined as distributional data points falling at sites identified (wrongly) as unsuitable by the models (Anderson et al., 2003). Second, we tested model predictions via partial receiver operating characteristic analyses (partial ROC; Peterson et al., 2008b). We used a Visual Basic routine developed by N. Barve (University of Kansas, Lawrence, KS; http://hdl.handle.net/1808/10059), using an expected error rate of $E=5 \%$ (Peterson et al., 2008b). We performed 1000 bootstrap iterations by resampling $50 \%$ of test points with replacement. Third, we compared our models qualitatively with previously published distributions (see Table S1.1.1 for references). We found few map-based depictions of these species distributions in the literature, so we compared our models to
textual descriptions of species' ranges. We assessed the correspondence of our models with published distributional summaries, with regard to omission error rather than commission error, because species may often be absent from suitable regions owing to biological or historical constraints, or may not be sampled (Peterson et al., 2011).

## Model extrapolation.

When transferring models to different situations, conditions outside the range of values of environmental variables in the calibration region may be encountered, leading to extrapolation. MAXENT identifies areas of potential strict extrapolation via clamping and multivariate environmental similarity surfaces (MESS; Elith et al., 2011). We used Mobility Oriented Parity (MOP), a modification of MESS, to (1) assess where strict extrapolation may occur, and to (2) calculate environmental similarity from a given pixel in a transfer time/region to those within the calibration region (Owens et al., 2013). We compared environmental similarity using the closest $10 \%$ of pixels in the environmental space of the study area to a given pixel, in both the present-day projection and the RCP 8.5 2081-2100 time slice within R (Owens et al., 2013). We chose the RCP 8.5 2081-2100 time slice for visualization of extrapolation because these environmental parameters deviated most from present-day parameters.

The above approach focused on ranges of values for environmental variables independently, but novel combinations of values for these predictors should also be considered (combinational extrapolation). Zurrell et al. (2012) extended the MESS concept to identify parts of environmental space within sampled ranges of individual univariate predictors, but representing new multivariate combinations of variables (combinational extrapolation). These new combinations could pose the same extrapolation problems to a model. We ran the R script of Zurrell et al. (2012) to detect such areas, creating environmental overlap masks for present-day projections and the RCP 2.6 2081-2100 and RCP 8.5 2081-2100 time slices.

## Sensitivity tests on predictor data.

We performed sensitivity tests to assess how the inclusion of environmental predictors might affect our modeling results. First, we excluded bathymetry from analyses, because it may provide only indirect information on a species' physiology, and indirect variables should be avoided when transferring models in space and time (Peterson et al., 2011). Similarly, we assessed whether numbers of variables and correlations among them (tested using 'cor’ in R 2.15.0; see Fig. 1.2.1 in Appendix S1.2) artificially induced declines in suitable areas anticipated under future climate-change scenarios. That is, we repeated the exercise using a less-correlated subset of predictor variables (i.e. only bathymetry, diatom phytoplankton concentration, nitrogen concentration, SST and SSS). Because results of these exercises were closely similar and we had no reason to exclude particular variables, we present only those results derived from the full analysis (Table S1.2.1 in Appendix S1.2).

To ascertain which variables drove the predicted broad-scale future changes, we reprojected future models holding each temporally varying variable constant (i.e. using the present-day value for that variable and future values for all other variables), totalling eight iterations per species. These jackknifed simulations were compared to the original projected future distributions to assess how changes in a particular variable influenced future projections, thereby identifying the variable(s) that cause the changes. We performed the reverse analysis to assess congruence between the approaches, wherein we held variables at present-day conditions except for one variable set to future values. This process was repeated for all variables for each species, but rather than being compared to original future projections, the latter simulations were compared to present-day models. The above analyses were undertaken using MAXENT for the 2081-2100 time slice of the RCP 2.6 and RCP 8.5 scenarios to illustrate generalities of the system's behaviour (see Tables S1.2.2 \& S1.2.3 in Appendix S1.2).

## Results

We present the lowest scenario for greenhouse gas emissions (RCP 2.6) - that is, the best-case scenario - unless otherwise noted (the more extreme scenarios are documented in Appendix S1.1, with results mirroring those from the conservative scenario, albeit with greater reductions in suitable area predicted for all species). Results for MAXENT represent those under the default settings, which produced fewer overall changes in suitability, unless otherwise noted.

## Model analysis and verification.

## Model quality metrics.

Model evaluation exercises suggest satisfactory model performance, with the possible exceptions of Lucina pensylvanica and Mercenaria campechiensis. Omission error rates are generally low: $78 \%$ of models have $<15 \%$ omission error (Table 1.1). Partial ROC tests are statistically significant, except for the GARP models for L. pensylvanica and
M. campechiensis (Table 1.1). Finally, our models accord well with published distributions (Table S1.1.1 and Figs S1.1.5-S1.1.8 in Appendix S1.1): only one (M. campechiensis) omits large regions known to be inhabited. Errors occur along the northern extreme of the species' range, where records document $M$. campechiensis in waters off New Jersey, but models predict suitable areas only as far north as Georgia and South Carolina. Less severe omission errors occur in MaXent models for Oliva sayana Ravenel, 1834 and Strombus alatus Gmelin, 1791, where small suitable areas are again missing from northern reaches of these species' ranges.

## Model extrapolation.

Novel environments occur in areas that do not intersect with model predictions for either the present-day or the RCP 8.5 2081-2100 projection (Fig. S1.3.1 and Table S1.3.1 in Appendix S1.3). Environmental overlap masks indicate that the present-day projections are largely unaffected by novel combinations of environmental parameters, except for regions off
the coast of Brazil. Conversely, future time slices show large numbers of pixels presenting novel environmental combinations (Fig. S1.3.2 in Appendix S1.3).

Figure 1.2 Cumulative suitable area lost/gained for all 14 marine mollusk species in the western North Atlantic for Representative Concentration Pathways (RCP) 2.6 emission scenario, tabulated across latitudes and standardized for the available area per latitude.

## Future suitability patterns.

Poleward range shifts.
Northern and southern extremes of suitability for most species are predicted to remain relatively constant through the remainder of this century, even when allowing for model extrapolation. Northern extremes of suitability are predicted to shift northward for only three (GARP; Bulla occidentalis Adams, 1850, Crassostrea virginica and Crepidula fornicata) or four (MAXENT; plus Conus spurius Gmelin, 1791) of the 14 species, whereas the southern edge of suitability is predicted to shift southwards for seven (GARP; Conus anabathrum, Conus spurius, Crassostrea virginica, Melongena corona, Mercenaria campechiensis, Lucina pensylvanica and Terebra dislocata) and one (MAXENT; Melongena corona) of the 14 species (Fig. 1.3). When changes in the geographical centroid of suitability are considered, no significant poleward shifts in suitable conditions are observed for individual species (Fig. 1.3). Across all species, the average change in centroid position from now to the end of century is only $1.4^{\circ}$ (MAXENT) or $5.1^{\circ}$ (GARP), but this shift occurs towards the equator, not polewards (see Table 1.2 and Figs S1.1.10 \& S1.1.11 in Appendix S1.1 for other RCP scenarios). The centroid of suitable conditions shifts northwards for some species (e.g. Crepidula fornicata and Crassostrea virginica) and southwards for others (e.g. Mercenaria campechiensis and Terebra dislocata).

Table 1.2 Average change in centroid position across all 14 marine mollusk species from the present to 2081-2100 for each IPCC Representative Concentration Pathways (RCP) emission scenario, expressed in degrees latitude.

| RCP scenario | MAXENT | GARP |
| :--- | :--- | :--- |
| 2.6 | -1.43 | -5.14 |
| 4.5 | -3.46 | -4.14 |
| 8.5 | -4.37 | -3.70 |
| Mean | -3.09 | -4.33 |

Species-specific versus assemblage responses.
Most species are predicted to exhibit declines in available suitable area. Ten (MAXENT) or 12 (GARP) of the 14 species show a contraction of suitable area (Figs $1.4 \&$ 1.5), including the medically or economically important species Conus anabathrum, Dinocardium robustum and Mercenaria campechiensis. Even so, the amount of decline and regions affected vary among species considered, as the centroid analyses indicate (Fig. 1.3).

Half of species show reductions in suitable area of more than $20 \%$ by 2080 (Anomia simplex d'Orbigny, 1853, Conus anabathrum, Dinocardium robustum, Mercenaria campechiensis, Oliva sayana, Strombus alatus and Terebra dislocata). GARP estimates reductions in suitable conditions of around $60 \%$ for four of these taxa (Conus anabathrum, Dinocardium robustum, Mercenaria campechiensis and Terebra dislocata), whereas MAXENT predicts less dramatic, but still substantial (25-47\%), losses for the same species. Running MAXENT without extrapolation suggests declines in suitable area similar to those under default settings for most species. Even closely related taxa are predicted to respond to warming differently: Conus spurius gains area (MAXENT) or has minor retractions (GARP and non-extrapolation version of MAXENT), unlike
C. anabathrum, which is anticipated to undergo dramatic reductions in suitable area.

Figure 1.3 Latitudinal extent (light shading) and change in centroid of suitable conditions (dark line) for each of the 14 marine mollusk species in the western North Atlantic from the present (P) to each time slice (2021-2040, 2041-2060 and 20812100) for IPCC Representative Concentration Pathways (RCP) 2.6 emission scenario. Note that both the absolute extent and centroid of suitable conditions remains fairly stable through time. Some species (e.g. Crassostrea virginica and Crepidula fornicata) have extents and centroids that shift slightly north, while others have extents and centroids that shift slightly south (e.g. Mercenaria campechiensis and Terebra dislocata). This variability highlights the species-specific nature of the predicted responses to future climate change.



Figure 1.4 Histograms depicting the number of marine mollusk species that gained or lost suitable area in the western North Atlantic per time slice, algorithm and RCP emission scenario compared to present-day models. Darker colours indicate gains in suitable area, whereas lighter colours indicate loss of suitable area.

Across the full set of species, the loss of suitable conditions generally increases with time. Declines in suitable conditions are common across the study area, particularly at latitudes $10-15^{\circ} \mathrm{N}$ (Fig. 1.2). Some regions may become unsuitable for many of the species considered: e.g. the Lesser Antilles, Bay of Campeche, the Atlantic seaboard south of South Carolina, and the Bahamas (Figs S1.1.9, S1.1.12 \& S1.1.13 in Appendix S1.1).

Few species are predicted to see newly suitable area or an overall expansion in distributional potential. For instance, Bulla occidentalis and Crassostrea virginica are the only species that see distributional potential increasing under both modeling algorithms.

MAXENT models anticipate relative stasis or increases in available area for Conus spurius and Lucina pensylvanica. Under the non-extrapolative version of MAXENT, however, only L. pensylvanica gains suitable area. Although the loss of distributional area outpaces any absolute gains, predictions for newly suitable areas tend to be concentrated near the equator (Fig. 1.2, Figs S1.1.9, S1.1.12 \& S1.1.13). Despite expected reductions in distributional potential under future climate scenarios, all species are predicted to retain some continuously suitable areas through time (Table 1.3). The average area reconstructed as stable and suitable in all time slices across all species is $61.8 \%$ (MAXENT) and $49.0 \%$ (GARP), expressed as a percentage of the present-day suitable area.







[^0]Table 1.3 Percentage of area predicted to remain suitable for 14 marine mollusk species within the study region according to RCP 2.6, 4.5 and 8.5 emission scenarios. The 'Present' column designates the percentage of present-day suitable area for particular species within the study region. The 'All suitable' column indicates the amount of area that remained continuously suitable geographically throughout all time slices, expressed as a percentage of the present-day suitable area.

| Species | RCP | Maxent |  |  |  |  | GARP |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | $\begin{aligned} & 2021- \\ & 2040 \\ & \hline \end{aligned}$ | $\begin{aligned} & 2041- \\ & 2060 \\ & \hline \end{aligned}$ | $\begin{aligned} & 2081- \\ & 2100 \end{aligned}$ | All suitable | Present | $\begin{aligned} & 2021- \\ & 2040 \\ & \hline \end{aligned}$ | $\begin{aligned} & 2041- \\ & 2060 \\ & \hline \end{aligned}$ | $\begin{aligned} & 2081- \\ & 2100 \\ & \hline \end{aligned}$ | All <br> suitable | Present |
| Bivalvia |  |  |  |  |  |  |  |  |  |  |  |
|  | 2.6 | 55.1 | 52.3 | 52.7 | 46.5 | 5.7 | 37.1 | 50.6 | 51.2 | 43.2 | 4.3 |
| Anomia simplex | 4.5 | 55.9 | 52.0 | 52.0 | 37.5 |  | 53.6 | 51.8 | 51.2 | 7.4 |  |
|  | 8.5 | 55.9 | 52.0 | 52.3 | 20.7 |  | 53.6 | 51.8 | 51.8 | 0.0 |  |
| Crassostrea virginica | 2.6 | 95.9 | 95.6 | 96.9 | 74.2 | 4.6 | 62.8 | 61.5 | 52.6 | 87.3 | 7.4 |
|  | 4.5 | 95.6 | 96.3 | 95.9 | 70.4 |  | 64.1 | 62.8 | 53.2 | 38.0 |  |
|  | 8.5 | 95.6 | 96.3 | 96.3 | 60.8 |  | 64.1 | 62.8 | 53.8 | 11.0 |  |
| Dinocardium robustum | 2.6 | 60.5 | 46.7 | 50.0 | 44.7 | 4.0 | 65.1 | 49.1 | 46.7 | 29.1 | 3.6 |
|  | 4.5 | 57.9 | 46.7 | 50.7 | 19.7 |  | 63.9 | 46.2 | 49.7 | 6.4 |  |
|  | 8.5 | 57.9 | 46.7 | 50.7 | 0.7 |  | 63.9 | 46.2 | 49.7 | 1.4 |  |
| Lucina pensylvanica | 2.6 | 90.1 | 87.8 | 86.4 | 85.8 | 9.0 | 79.3 | 72.6 | 67.7 | 50.2 | 6.1 |
|  | 4.5 | 90.6 | 87.2 | 85.8 | 58.8 |  | 79.3 | 73.8 | 72.6 | 5.4 |  |
|  | 8.5 | 90.6 | 87.2 | 86.6 | 31.0 |  | 79.3 | 72.0 | 71.3 | 0.0 |  |
| Mercenaria campechiensis | 2.6 | 60.7 | 53.6 | 44.0 | 41.7 | 2.2 | 22.4 | 16.0 | 18.6 | 12.9 | 3.6 |
|  | 4.5 | 58.3 | 48.8 | 42.9 | 38.1 |  | 22.4 | 16.3 | 18.6 | 3.6 |  |
|  | 8.5 | 58.3 | 48.8 | 42.9 | 11.9 |  | 22.4 | 16.3 | 18.6 | 0.0 |  |
| Gastropoda |  |  |  |  |  |  |  |  |  |  |  |
| Bulla occidentalis | 2.6 | 95.1 | 93.9 | 95.0 | 91.4 | 16.1 | 91.8 | 89.6 | 85.6 | 95.9 | 13.6 |
|  | 4.5 | 95.1 | 94.1 | 93.9 | 92.2 |  | 91.8 | 88.6 | 87.5 | 71.0 |  |
|  | 8.5 | 95.1 | 94.1 | 94.0 | 87.8 |  | 91.8 | 88.9 | 87.7 | 20.0 |  |
| Conus anabathrum | 2.6 | 80.8 | 67.8 | 56.3 | 55.1 | 6.3 | 25.6 | 19.5 | 11.3 | 14.3 |  |
|  | 4.5 | 80.4 | 66.9 | 57.1 | 67.8 |  | 24.8 | 18.8 | 15.0 | 0.0 | 4.1 |
|  | 8.5 | 80.4 | 66.9 | 57.1 | 29.4 |  | 24.8 | 18.8 | 15.0 | 0.0 |  |
| Conus spurius | 2.6 | 86.5 | 84.6 | 85.9 | 81.0 | 12.1 | 97.3 | 95.0 | 92.1 | 63.8 |  |
|  | 4.5 | 85.3 | 84.4 | 85.7 | 81.6 |  | 97.1 | 94.4 | 93.7 | 5.8 | 10.1 |
|  | 8.5 | 85.3 | 84.4 | 85.7 | 69.4 |  | 97.1 | 94.6 | 93.7 | 0.0 |  |
| Crepidula fornicata | 2.6 | 77.3 | 66.7 | 69.7 | 63.9 | 8.4 | 89.4 | 84.9 | 74.3 | 73.6 | 8.7 |
|  | 4.5 | 73.9 | 67.9 | 67.9 | 49.7 |  | 88.6 | 82.9 | 80.8 | 44.5 |  |
|  | 8.5 | 73.9 | 67.9 | 69.1 | 38.8 |  | 88.6 | 83.3 | 80.8 | 17.8 |  |
| Melongena corona | 2.6 | 72.9 | 68.8 | 56.3 | 50.0 | 1.3 | 43.5 | 27.5 | 24.6 | 33.3 | 2.2 |
|  | 4.5 | 72.9 | 64.6 | 56.3 | 47.9 |  | 42.0 | 27.5 | 26.1 | 19.5 |  |
|  | 8.5 | 72.9 | 64.6 | 56.3 | 16.7 |  | 42.0 | 27.5 | 26.1 | 3.4 |  |
| Neverita duplicata | 2.6 | 79.5 | 73.4 | 72.7 | 66.9 | 5.0 | 84.0 | 68.6 | 59.4 | 83.4 | 6.7 |
|  | 4.5 | 80.9 | 73.4 | 73.0 | 57.0 |  | 73.0 | 67.6 | 64.2 | 60.5 |  |
|  | 8.5 | 80.9 | 73.4 | 74.1 | 43.7 |  | 73.0 | 67.6 | 64.2 | 41.0 |  |
| Oliva sayana | 2.6 | 87.9 | 79.3 | 58.6 | 58.4 | 3.6 | 73.7 | 62.3 | 44.9 | 43.7 | 4.3 |
|  | 4.5 | 86.2 | 79.3 | 62.1 | 38.7 |  | 74.3 | 61.1 | 55.1 | 19.8 |  |
|  | 8.5 | 86.2 | 79.3 | 62.1 | 27.0 |  | 74.3 | 61.7 | 55.1 | 13.8 |  |
| Strombus alatus | 2.6 | 75.5 | 52.9 | 51.5 | 57.7 | 6.6 | 47.6 | 18.4 | 10.9 | 34.7 | 4.4 |
|  | 4.5 | 64.5 | 52.9 | 51.9 | 42.3 |  | 25.6 | 18.1 | 15.0 | 10.6 |  |
|  | 8.5 | 64.5 | 52.9 | 51.9 | 26.1 |  | 25.6 | 18.4 | 15.0 | 0.0 |  |
| Terebra dislocata | 2.6 | 53.8 | 30.7 | 29.7 | 48.6 | 4.5 | 27.7 | 9.6 | 10.2 | 20.0 | 2.1 |
|  | 4.5 | 31.4 | 30.7 | 29.0 | 30.6 |  | 10.9 | 9.6 | 11.3 | 15.3 |  |
|  | 8.5 | 31.4 | 30.7 | 29.0 | 14.5 |  | 10.9 | 8.9 | 10.9 | 3.5 |  |

## Variables responsible for future trends.

Based on jackknife manipulation, changes in single variables do not seem to drive model predictions for most species, although the suitable area typically decreases or remains stable when individual variables are held constant. In fact, the only individual variables that suggest a potential increase in suitable area for several species are non-diatom phytoplankton and SST (Table S1.2.2). Decreases, increases and stasis in suitable area for single species depend on the variable held constant, which is perhaps to be expected given the complexity of the model parameters and abiotic environmental preferences of species. Reverse analyses, with focal variables set to future values and all other variables held at present-day values, produce similar results (Table S1.2.2).

## Discussion

## Poleward range shifts.

Our initial hypothesis that suitable environmental conditions for species will expand at poleward range boundaries, with simultaneous contraction at low-latitude boundaries, is not broadly supported. Species did not present consistent patterns of poleward expansion, and although suitable area is lost near the equator, it is also lost across the entire study area. In fact, newly suitable environmental areas are predicted to become available at low latitudes. These results match aspects of the predictions of Burrows et al. (1991) and VanDerWal et al. (2013), but differ from other analyses of marine taxa (Cheung et al., 2009; Jones et al., 2010; Sorte et al., 2010; Sunday et al., 2012), which suggest that marine species will shift their distributions polewards in response to warming climates. These opposing responses may derive, as suggested by VanDerWal et al. (2013), from having a primary focus on tropical rather than temperate species, with the narrower climatic tolerances of tropical species producing unpredictable distributional shifts under changing climate. Interestingly, however, the temperate-zone species considered here exhibit the same multidirectional distributional
shifts as the entirely subtropical and tropical assemblages.
We suspect that northern waters will remain too cold for tropical and subtropical species to shift northwards, while substantial environmental perturbations in present-day distributional areas will cause the predicted reductions in suitable area for most of our species. Evidence for this hypothesis is twofold. First, temperature is implicated in causing declines in suitable area, and future values for this variable at species' northern range margins appear to remain outside the environmental tolerance limits determined from species' niche models. Tropical species are particularly sensitive to temperature changes, because their upper lethal thermal limits are closer to the maximum habitat temperature than those of temperate species (Compton et al., 2007; Tewksbury et al., 2008; Sunday et al., 2012; Araújo et al., 2013). Second, environmental overlap analyses suggest that there will be significant environmental perturbation, with virtually all regions having novel environmental combinations in the future. Temperature, however, is not the sole driver of losses in suitable area, because future temperature values in present-day distributional areas remain largely within absolute thermal tolerance limits for these species as determined from niche modeling. Consequently, other variables, such as changes in primary productivity, may work in combination with temperature changes to restrict future predicted species' distributions.

## Species-specific responses.

We also find idiosyncratic and species-specific responses to changing climate. The amount and direction of the predicted responses depends upon the niche characteristics of each species (Foster et al., 1990; Peterson et al., 2008a; VanDerWal et al., 2013), with the areas lost and gained varying between taxa. No consistent response is observed when solely tropical, or subtropical or temperate species are considered. Nevertheless, although the predicted responses are species-specific, the dominant signal for the 21 st century is one of severe ( $>20 \%$ ) distributional reductions for most of our study species, and this aspect of our study matches the patterns documented for terrestrial species (Thuiller et al., 2005; Pereira et
al., 2010; Visconti et al., 2011) and some marine species (e.g. Albouy et al., 2013).

## Modeling constraints.

The results from any predictive study that employs modeling must be treated with some caution. For instance, the assumptions inherent in transferring ENMs among time periods have been discussed in detail elsewhere (Pearman et al., 2008; Peterson et al., 2011), including those associated with the supposition that niches remain stable in the face of environmental change (Peterson, 2011). Other limitations include applying a global Earth System model to the continental shelf (see Holt et al., 2009; Collins et al., 2011), where predictor variables are difficult to validate at the spatial scale considered, and in coastal environments. At the moment, however, these environmental data are the best available, particularly for future projections of both biogeochemical and physical parameters. Ideally, as with other recent studies (Fordham et al., 2012a), we would explore the implications of multiple such models, but that was impossible given the current availability of data.

Our environmental data warrant further consideration with respect to their efficacy in characterizing the niches of marine mollusks. For example, some concern exists regarding whether ocean surface data accurately simulate benthic conditions for these taxa. Although potentially problematic, surface data have previously been employed to characterize the distributions of benthic species that live in shallow waters on the continental shelf (e.g. Bentlage et al., 2013), particularly since surface conditions track benthic conditions to some degree at times of the year when mixing occurs (see Noble, 2001; Korty et al., 2008). Additional caveats include the inability to account for substrate type, a factor that affects fine-scale distributional patterns in benthic mollusks. Inclusion of this variable, however, would be impossible at the coarse spatial resolution of our study.

Aside from these abiotic constraints, our application of ENM does not account for dispersal or population dynamics (Anderson et al., 2009; Fordham et al., 2012b, 2013). These finer-scale processes, however, may play second fiddle to environmental gradients at
broad spatial scales, which have been shown to limit the latitudinal ranges of marine ectotherms (Gaines et al., 2007; Tomašových \& Kidwell, 2009; Robinson et al., 2011; Buckley et al., 2012; Sunday et al., 2012).

Another issue worth noting is that we considered commercially-harvested species: Crassostrea virginica, Dinocardium robustum and Mercenaria campechiensis. These species will become increasingly vulnerable to overfishing with changing climate, which could precipitate population declines not visible to most modeling applications. These species may also prove more difficult to model, since present-day and historical harvest pressures affect perceptions of a species' niche via non-detection in abiotically suitable areas (Mellin et al., 2012; Russell et al., 2012). The inclusion of harvest pressure is likely to indicate a more dire (and perhaps more realistic) future for those species.

If our results are generally applicable, though, they suggest far-reaching effects of climate change on marine mollusks, an essential component of marine ecosystems. Our models not only anticipate extensive degradation of conditions for these species, but also some range shifts that will change the composition of local assemblages. Notably, invasion and community re-organization can also precipitate extinction (Harley, 2011; Urban et al., 2012), such that community-level analyses that consider interspecfic interactions would help clarify the fate of these mollusks (Davis et al., 1998; Araújo \& Guisan, 2006). As with changing interspecific interactions, pollution and overharvesting pose similar severe threats to the survival of species (Harley, 2011; Russell et al., 2012). Thus, the already-substantial amount of 21st-century marine biotic degradation predicted by our models is almost surely an underestimate.

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Chapter 2. Macroevolutionary consequences of profound climate change on niche evolution in marine mollusks over the past $\mathbf{3}$ million years



#### Abstract

In order to predict the fate of biodiversity in a rapidly changing world, we must first understand how species adapt to new environmental conditions. The long-term evolutionary dynamics of species' physiological tolerances to differing climatic regimes remains obscure. Here, we unite paleontological and neontological data to analyze whether species' physiological tolerances remain stable across three million years of profound environmental changes using ten phylogenetically, ecologically, and developmentally diverse mollusk species from the Atlantic Coastal Plain, USA. We additionally investigate whether these species' upper and lower thermal tolerances are constrained across this interval. We find that these species' environmental preferences are stable across the duration of their lifetimes, even when faced with significant environmental perturbations. Our results suggest that species will respond to current and future warming by altering distributions to track suitable habitat, or, if the pace of change is too rapid, by going extinct. Our findings support methods that project species' present-day environmental requirements to future climatic landscapes to assess conservation risks. At the macroevolutionary scale, we provide evidence that species' distributions are structured by environmental factors.


## Introduction

Earth's climate is rapidly changing, altering all facets of our planet at an unprecedented rate, from the biosphere, to the hydrosphere, to the atmosphere (IPCC, 2013). Given these changes, debate exists as to whether species can adapt their physiological tolerances to altered environmental conditions (Pearman et al., 2008; Lavergne et al., 2010; Hoffmann \& Sgrò, 2011). Determining whether species' climatic preferences (niches) evolve or remain stable in the face of environmental change over the long term is important for implementing proper conservation measures and mitigating threats posed to biodiversity (Pereira et al., 2010; Dawson et al., 2011; Moritz \& Agudo, 2013), and for shedding light on macroevolutionary dynamics (Eldredge et al., 2005; Roy et al., 2009; Valentine et al., 2012; Jablonski et al., 2013; Romdal et al., 2013).

Here, we unite paleontological and neontological data (Dietl \& Flessa, 2011; Fritz et al., 2013) to test niche stability across three million years of environmental changes using ten phylogenetically, ecologically, and developmentally diverse bivalve and gastropod species from the Atlantic Coastal Plain, USA (Table S2.1.1 in Appendix S2.1). Species' niches were quantified using ecological niche modeling (ENM) (Peterson et al., 2011) for three time periods within the Pliocene-recent molluscan record of the Atlantic Coastal Plain: midPliocene Warm Period (mPWP; 3.264-3.025 Ma), Eemian Last Interglacial Period (LIG; 130 Ka ), and present-day interval (PI). Our null hypothesis is that niches remained stable across this interval. We additionally investigate whether these species' upper and lower thermal tolerances are constrained across millions of years. Recent research suggests that tolerances to heat are largely conserved within terrestrial species, but that tolerances to cold are more variable (Araújo et al., 2013). This asymmetry is thought to diminish in the marine realm, where ectotherms are limited by both cold and warm conditions due to decreased aerobic capacity (Somero, 2002; Pörtner \& Knust, 2007; Sunday et al., 2011). This study is the first
to incorporate both modern and fossil data across millions of years to understand ecological and evolutionary responses of species to changes in their environment, though see (Malizia \& Stigall, 2011; Stigall, 2012) for analyses in deep time. Although characterizing the entirety of a species' fundamental niche (FN) is often difficult (Araújo et al., 2013), we study close approximations here, given that recent biophysical approaches have determined that FNs can be represented by limited sets of parameters like temperature (Kearney et al., 2010; Kearney et al., 2013). This is particularly true for marine ectotherms, which have been shown to closely match range limits within their thermal tolerances (Sunday et al., 2011).

Theoretical (Kawecki, 1995; Holt, 1996) and empirical studies both support (Martínez-Meyer et al., 2004; Martínez-Meyer \& Peterson, 2006; Strubble et al., 2013) and reject niche stability (Broennimann et al., 2007; Rödder \& Lötters, 2009; Malizia \& Stigall, 2011; Stigall, 2012). The debate has even continued at the genetic level, where recent research indicates that genetic reshuffling in Drosophila species can occur in response to climate change (Umina et al., 2005; Balanyá et al., 2006); however, it is still unknown if these genetic changes translate into evolution of actual physiological tolerances. The context in which niche evolution is considered is important with respect to whether change occurred in actual physiological tolerances (i.e., the FN), or whether it occurred because of differences in resource utilization or underlying environmental structure (i.e., changes in the realized niche; RN). Characterizing the entirety of the FN is difficult (Peterson et al., 2011), and studies may incorrectly indicate niche evolution if environmental availability is not considered (Peterson, 2011; Araújo \& Peterson, 2012; Broennimann et al., 2012). The aforementioned studies have contributed much to our understanding of how species' physiological tolerances evolve; however, questions remain as to the dominance of niche evolution versus stability, particularly since most studies lacked a temporal component that would allow for analysis of change across the entire duration of a species' lifetime (i.e., Mys; Eldredge et al., 2005).

The Atlantic Coastal Plain record is ideal for elucidating the coevolution of species' niches and the environment. Not only has the region experienced profound environmental changes from the closure of the Central American Seaway beginning in the Pliocene (Allmon, 2001) to glacial/interglacial cycles (Cronin, 1988; Haug \& Tiedemann, 1998), but these environmental changes have been associated with patterns of extinction, species turnover, and ecological change (Allmon et al., 1993; Todd et al., 2002; Vermeij, 2005; Klaus et al., 2011). The mid-Pliocene Warm Period ( $\sim 3.1 \mathrm{Mys}$ ), included in this study, is considered a climatic analog for conditions expected at the end of this century, and can contribute to how target species may fare under future climate scenarios (Dowsett et al., 2009). Results are vital for proper mitigation of the risks posed by current and future climate changes to Earth's biodiversity (Moritz \& Agudo, 2013; Warren et al., 2013).

## Materials and Methods

## Study area.

All models were calibrated within a region bounded by the Americas and $34^{\circ} \mathrm{W}$ longitude, and $48^{\circ} \mathrm{N}$ and $44^{\circ} \mathrm{S}$ latitude (Fig. 2.1). We sought the union of the area sampled by researchers and that was most likely accessible to the species across spatial and temporal dimensions (Phillips et al., 2009; VanDerWal et al., 2009; Peterson et al., 2011). With the exception of $L$. pensylvanica and $T$. dislocata, which have benthic larvae, target species are capable of dispersing long distances as planktonic larvae on ocean currents.

## Taxa.

We selected ten species that occur in both the modern and fossil (from $\sim 3.1 \mathrm{Ma}$ to recent) records of the Atlantic Coastal Plain, USA. These species were chosen because they have diverse phylogenetic positions, varied ecological habits and developmental modes, and abundant distributional data available from fossil and modern localities (Table S2.1.1 in Appendix S2.1). We used morphological criteria to identify target species. Each taxon is
readily diagnosable, and the unique combinations of apomorphies that these species possess are present in their fossil representatives. All evidence suggests that these lineages represent species that have distinct evolutionary trajectories, a supposition supported by the fact that most invertebrate species have durations of $>3$ million years (Eldredge et al., 2005).

## Distributional data.

## Present-day

Presence-only distributional data were downloaded from five institutions, including the Florida Museum of Natural History (FLMNH), Academy of Natural Sciences of Drexel University, University of Michigan Museum of Zoology, Natuurhistorisch Museum Rotterdam, and U.S. National Museum of Natural History; records are representative of the known, modern-day distributions of these species (Table S2.1.1 and Figs. S2.1.3-S2.1.5 in Appendix S2.1) (Saupe et al., In Press). We assigned latitude and longitude coordinates to distributional data following standard georeferencing protocols (Chapman \& Wieczorek, 2006). Only records with spatial uncertainty $<15 \mathrm{~km}$ were retained, ensuring that they were matched correctly with corresponding environmental data of a coarser spatial resolution (i.e., $1.25 \times 1.25^{\circ}$ ) (Graham et al., 2008). We subsampled distributional data to leave one record per environmental pixel to account for sampling biases, which reduced records from 1,522 to 324 across the ten species (Table S2.1.1 in Appendix S2.1). This process did not affect the resultant overall distribution of the species, but rather prevented certain localities with multiple records from being unduly weighted in the analyses (Royle et al., 2012; Yackulic et al., 2013).

## Fossil.

We considered fossil distributional data from Pliocene ( $\sim 3.264-3.025 \mathrm{Ma}$ ) and Last Interglacial ( $\sim 130 \mathrm{Ka}$ ) strata of the Atlantic Coastal Plain, USA. To ensure distributional data were derived from geologic units of similar ages to our periods of interest, we generated a stratigraphic database for all Pliocene-recent geologic units of the Atlantic Coastal Plain
(Appendix S2.2). Correlations and unit ages were determined by extensive literature survey and use of various stratigraphic databases, resulting in 10 viable formations for the Pliocene and 16 for the LIG (see Appendix S2.2). We note that these formations are not exactly 3.1 Ma and 130 Ka , respectively, but closely approximate the environmental data currently available.

Distributional records were obtained from onsite investigations of collections to ensure proper species identification, including the Florida Museum of Natural History, Paleontological Research Institution, Virginia Museum of Natural History, Academy of Natural Sciences of Drexel University, and Yale Peabody Museum. As with present-day distributional data, we subsampled fossil distributional data to leave one record per environmental pixel, such that Pliocene records were reduced from 1,140 to 104 records across the ten species, and LIG records were reduced from 442 to 110 records (Table S2.1.1 in Appendix S2.1). At least six spatially-explicit distributional records were used for model calibration for any given species/time period; studies have shown this number to be statistically robust for extant species (Hernandez et al., 2006; Pearson et al., 2007).

## Environmental data.

Environmental data were derived from the coupled atmosphere-ocean HadCM3 global climate model (GCM) (Gordon et al., 2000; Pope et al., 2000) for three time slices: mid-Pliocene Warm Period (mPWP; 3.264-3.025 Ma), Eemian Last Interglacial Period (LIG; 130 Ka ), and pre-industrial (PI; $\sim 1850-1890$ ). Ideally, we would use an ensemble-modeling approach that considered multiple GCMs (Fordham et al., 2012); however, model output from the LIG was available to us only from HadCM3. This GCM has been successfully used within a large range of Quaternary and pre-Quaternary modeling studies. Pre-industrial output was chosen for present-day modeling to match the spread of collecting dates for distributional data, which included museum records from the early to mid 1900's. Boundary conditions for the mPWP GCM used the alternate PRISM3D PlioMIP dataset described in
(Haywood et al., 2011). LIG boundary conditions were from (Singarayer \& Valdes, 2010) and (Singarayer et al., 2011). Here, atmospheric gas concentrations were derived from ice core records (Petit et al., 1999; Spahni et al., 2005; Loulergue et al., 2008), and orbital parameters were derived from (Berger \& Loutre, 1991). The pre-industrial experiment was equivalent to (Braconnot et al., 2007). All experiments were run for 500 model years, and environmental parameters were derived from the final 30 years of each experiment at 1.25 x $1.25^{\circ}$ resolution ( $\sim 140 \times 140 \mathrm{~km}$ at the equator). Where ocean data were unavailable (i.e., sites presenting macrofossil data, but where the GCM indicated land), we used an inversedistance weighted algorithm to extrapolate model data.

Monthly salinity and temperature outputs were converted to maximum, minimum and average yearly coverages for both surface and bottom conditions using ArcGIS. From these coverages, we eliminated variables that significantly co-varied (assessed using the 'cor' function in R.15.2; R Core Team, 2012). Ultimately, two bottom variables: yearly average salinity and temperature, and four surface variables: maximum and minimum salinity, and maximum and minimum temperature, were retained. Both maximum and minimum temperature were preserved, since these variables possessed some degree of independent scatter and were deemed biologically important for marine ectotherms (Tomašových \& Kidwell, 2009; Buckley et al., 2012; Sunday et al., 2012).

To avoid inaccurate niche representations due to truncated model response curves (Owens et al., 2013), we assessed peripherality of distributional data with respect to the environment of the calibration region using histograms produced in R.15.2. Results indicated peripherality of data is not a problem, with the potential exception of bottom salinity and temperature variables.

## Modeling algorithm.

Ecological niche models (ENMs) were generated using Maxent v. 3.3.3 (Phillips et al., 2006), a widely employed and popular modeling algorithm (Fig. 2.1 and Figs. S2.1.1-S2.1.2
in Appendix S2.1). Maxent minimizes the relative entropy between two probability densities — one from the distributional data and one from the background or study area - defined in covariate space (Elith et al., 2011). We enabled only quadratic features to simulate realistic bell-shaped response curves that are known from physiological experiments of plants and animals (Austin, 1985; Austin et al., 1994; Hooper et al., 2008; Angilletta, 2009). However, to test model sensitivity, we also enabled all features (i.e., linear, quadratic, product, threshold, and hinge), which produced models similar to those with only quadratic features. We calibrated models using all spatially-explicit data points for each species/time slice, running 100 bootstrap replicates with a ten percent random test percentage. We took the median of the 100 replicates and converted to integer grids, retaining three decimals, in ArcMap v.10.1. The mean value for these grids was used to threshold to binary predictions (Liu et al., 2005; Freeman \& Moisen, 2008). This method is particularly suitable when prevalence data varies among models, as with past and present time slices (Freeman \& Moisen, 2008).

To correct for biases in fossil distributional data, we implemented a bias file within Maxent for past modeling. The bias file describes the probability that an area was sampled; thus, regions with rock outcrop (i.e., areas where species may actually be detected or sampled) were weighted twice as heavily as regions without rock outcrop. Maxent will then factor out this bias during the modeling process (see (Dudík et al., 2005) for details). This method essentially accounts for incomplete knowledge of a species distribution sensu (Svenning et al., 2011).

## Model verification.

Two model validation methods were used, depending on the prevalence of distributional records (Table S2.1.2 in Appendix S2.1). For species/time slices with $<25$ points, we assessed statistical significance using a jackknife procedure under a least training presence threshold (Pearson et al., 2007). This method, however, may produce over-
optimistic estimates of predictive power for sample sizes $>25$, and thus these species/time slices were tested via partial Receiver Operating Characteristic analyses ("partial ROC") (Peterson et al., 2008). Distributional records were divided into five random replicates of $75 \%$ training and $25 \%$ testing points. Maxent models were re-calibrated using these training sets, performing 1000 bootstrap iterations with random test percentage equal to 20 . The median model from these replicates was assessed for statistical significance using testing sets within a Visual Basic routine developed by N. Barve (U. Kansas; http://hdl.handle.net/1808/10059). The error rate was set to $E=1 \%$ (Peterson et al., 2008), and we performed 1,000 bootstrap iterations by resampling $50 \%$ of test points with replacement.

## Niche comparisons.

## Geographic projections.

We used ENMTools v1.3 (Warren et al., 2008; Warren et al., 2010) to quantify similarity of ENMs within each lineage through time (Table 2.1 and Appendix S2.3). ENMTools uses randomization tests to compare observed similarity to that expected under a null hypothesis. The null is rejected if models are more (or less) similar than expected by chance, based on the environment within the geographical regions of interest (Warren et al., 2010). Similarity is quantified using Schoener's $D$ (Schoener, 1968), with values ranging from 0 to 1 , or more to less similar, respectively.

For each of the ten species, we compared observed niches across three different time periods: mPWP, LIG, and PI. Comparisons were made in two directions sensu (Warren et al., 2008; Warren et al., 2010; Broennimann et al., 2012); i.e., the model of time A was compared to the model of time B projected to time A and vice versa. This was done because it is possible for two niches to be more similar than expected based on the environment available for one time slice, but less similar than expected based on the environment available for the other (or some combination thereof). To ensure accurate response curves
when projecting, we disabled clamping and enabled extrapolation within Maxent (Owens et al., 2013). Null distributions consisted of 100 random models generated within Maxent, with model parameters drawn from the study system. Statistical significance was assessed by creating histograms in R : if the observed value fell outside the null distribution to the high end, niches were more similar than expected by chance, whereas if the observed value fell outside the null distribution to the lower end, niches were more different than expected by chance. Observed values that fell within the null distribution did not allow for discrimination of similarity or differences based on the environment available to the entities in question. Note that because the present analysis was aimed at demonstrating the absence of change (null hypothesis), rather than being a 'fishing expedition' looking for any evidence of change, it was not necessary to apply the Bonferroni adjustment for the geographic or environmental comparisons (Perneger, 1998).

## Environmental comparisons.

The quantitative framework provided by (Warren et al., 2008; Warren et al., 2010) has proven a powerful tool for assessing niche similarity; however, this method makes comparisons using the geographical projections of niches, which can introduce error when analyzing niches through time and in different environments (Williams \& Jackson, 2007; Williams et al., 2007). Consequently, we also calculated metrics of niche overlap in gridded environmental space using the methodology of (Broennimann et al., 2012). Here, ordination techniques (Thuiller et al., 2005; Hof et al., 2010) allow for direct comparison of speciesenvironment relationships in environmental space, and corrects observed distributional densities for each region in light of the availability of environmental space using kernel density functions (Table 2.1 and Appendix S2.3). Niche overlap is measured along gradients of a multivariate analysis, and statistical significance is assessed using the same framework employed in ENMTools. Tests of niche equivalency and niche similarity were performed, but
we focused on niche similarity, since niches will rarely, if ever, be absolutely identical (Warren et al., 2008).

We tested for similarity using a principal component analysis (PCA) applied to all six environmental parameters. We also tested for similarity by reducing niche dimensionality to three variables, including surface coverages for maximum salinity, maximum temperature, and minimum temperature. These variables were retained because they explained the most variance in the data and were deemed biologically important (Tewksbury et al., 2008; Jones et al., 2009; Tunnell et al., 2010; Sunday et al., 2012). Analyses performed with this reduced set of variables are potentially more informative, since over-parameterization can constrict niche estimates and lead to approximations closer to the RN, not the FN. Moreover, these additional variables may be uninformative with regards to species' niche attributes, which would add noise to comparisons and contribute to type II errors. PCA analyses were calibrated on both environments (project=false). We used both the PCA-occ and PCA-env functions; the former calibrates the PCA based only on the distributional data, whereas the latter uses data from the entire environmental space of the two study systems; results were equivalent, and thus we present only those from PCA-env. A bin size of 100 was used to characterize the environment, running 1000 replicates for similarity tests. Since prevalence of distributional data varies through time, i.e., past time slices typically contained fewer data points, we generated input data from ENMs, subsampling one point per pixel in binary predictions so that comparisons were unbiased with regard to the amount of input data. This also ensured that comparisons were being made using approximations closer to the FN, rather than the RN .

We also tested similarity in raw variables (Table 2.2 and Appendix S2.3). We used the script of (Broennimann et al., 2012) to analyze each of the six variables individually, and we modified the script to compare raw variables in two dimensions, while still accounting for differences in availability of environments in a given time period. We were interested in
testing for evolution in overall temperature parameters, and thus we assessed similarity using average bottom temperature and maximum surface temperature. Significance was evaluated by generating histograms in R to determine where observed D values fell in relation to the null distributions.

Table 2.1 P-values for multi-dimensional niche comparison tests (1) using a PCA applied to all six environmental variables (Broennimann et al., 2012); (2) using a PCA applied to the three most important environmental variables; (3) using raw average bottom temperature and maximum surface temperature with a modified script of Broennimann et al. (2012); and (4) using ENMTools (Warren et al., 2008, 2010) on projections of ecological niche models. Bold values indicate non-significant results. All significant results ( $\mathrm{P}<0.05$ ) indicate niches are statistically more similar than expected given the environmental background of the time slices, except for the result with the asterisk, which indicates a niche comparison that was statistically dissimilar. Note that it is possible for two niches to be more similar than expected based on the environment available for one time slice, but less similar than expected based on the environment available for the other. See Appendix S2.3 for graphical depictions of

| Species/Comparison | mPWP-LIG | LIG-mPWP | PI-LIG | LIG-PI | mPWP-PI | PI-mPWP |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Environmental comparison: p-values for tests using PCA on all 6 variables |  |  |  |  |  |  |
|  | 0.06 | 0.00 | 0.00 | 0.00 | 0.04 | 0.00 |
|  | 0.05 | 0.01 | 0.00 | 0.00 | 0.03 | 0.00 |
|  | 0.32 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 |
|  | 0.16 | 0.00 | 0.09 | 0.00 | 0.14 | 0.00 |
|  | 0.15 | 0.00 | 0.00 | 0.00 | 0.06 | 0.00 |
|  | 0.11 | 0.00 | 0.00 | 0.00 | 0.16 | 0.00 |
|  | 0.11 | 0.00 | 0.01 | 0.00 | 0.01 | 0.01 |
|  | 0.09 | 0.00 | 0.00 | 0.00 | 0.05 | 0.00 |
|  | 0.12 | 0.00 | 0.00 | 0.00 | 0.03 | 0.00 |
|  | 0.06 | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 |
| Environmental comparison: p-values for tests using PCA on $\mathbf{3}$ most important variables |  |  |  |  |  |  |
|  Anomia simplex <br> .0 Crassostrea virginica <br> $\sum_{0}^{\text {a }}$ Dinocardium robustum <br> .0 Lucina pensylvanica <br>  Mercenaria campechiensis | 0.01 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 |
|  | 0.04 | 0.00 | 0.03 | 0.00 | 0.00 | 0.00 |
|  | 0.01 | 0.00 | 0.00 | 0.02 | 0.09 | 0.00 |
|  | 0.25 | 0.01 | 0.00 | 0.00 | 0.03 | 0.03 |
|  | 0.01 | 0.00 | 0.00 | 0.02 | 0.00 | 0.00 |
| ๘ Bulla occidentalis | 0.34 | 0.54 | 0.10 | 0.29 | 0.31 | 0.20 |
| Crepidula fornicata | 0.03 | 0.00 | 0.02 | 0.00 | 0.29 | 0.58 |
| 은 Neverita duplicata | 0.08 | 0.00 | 0.01 | 0.44 | 0.01 | 0.00 |
| 耑 Oliva sayana | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| $\bigcirc$ Terebra dislocata | 0.02 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 |
| Environmental comparison: p-values for tests using raw temperature variables |  |  |  |  |  |  |
| Anomia simplex | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| . 7 Crassostrea virginica | <0.05 | NS | <0.05 | <0.05 | <0.05 | NS |
| $\frac{2}{N}$ Dinocardium robustum | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| - Lucina pensylvanica | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| Mercenaria campechiensis | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| \% Bulla occidentalis | NS | NS | <0.05 | <0.05 | <0.05 | NS |
| O- Crepidula fornicata | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| 은 Neverita duplicata | $<0.05$ | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| 耑 Oliva sayana | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | NS |
| $\bigcirc$ Terebra dislocata | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
| Geographic comparison: $\mathbf{p}$-values for tests using ecological niche models |  |  |  |  |  |  |
|  | <0.05 | $<0.05$ | <0.05 | <0.05 | <0.05 | <0.05 |
|  | NS | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
|  | <0.05 | $<0.05$ | <0.05 | <0.05 | <0.05 | <0.05 |
|  | $<0.05$ | $<0.05$ | <0.05 | <0.05 | <0.05 | NS |
|  | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
|  | <0.05* | <0.05 | <0.05 | <0.05 | <0.05 | NS |
|  | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
|  | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
|  | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |
|  | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 | <0.05 |

## Results

Model verification exercises suggest that ENMs are statistically significant for each time period and species ( $P<0.05$, see Table S2.1.2 in Appendix S2.1); model depictions are presented in Fig. 2.1 and Figs. S2.1.1-S2.1.2 in Appendix S2.1. Together, the suite of niche comparisons (360 in total) indicates these species' niches are stable across millions of years. Of the ten ecologically diverse species, nine show niche similarity for the majority of the comparisons. Probabilistically, this result would be obtained only $1 \%$ of the time assuming equal likelihood for evolution versus stability. Bulla occidentalis is the only species with non-significant results across the comparisons, such that its niche dynamics cannot be adequately assessed. We obtain evidence of niche similarity for tests on both principle component analyses (PCAs) and raw variables. Moreover, minimum and maximum temperature tolerances are generally conserved through time.

Figure 2.1 Representative ecological niche models for the present, LIG, and mPWP time slices for two species: Anomia simplex and Oliva sayana. Binary and continuous predictions are presented, with binary predictions thresholded using the mean suitability value from the continuous output. For the binary predictions, yellow=suitable and dark blue=unsuitable, whereas for the continuous predictions, darker grays indicate higher suitability. All analyses were conducted within the geographic extent shown. See Fig. S2.1.1-S2.1.2 in Appendix S2.1 for remaining species analyzed.

## Environmental comparisons.

Comparisons on multi-dimensional niches indicate overwhelming signals of niche stability across time slices. Three analyses were performed to this effect: (1) comparisons on the first two axes of a PCA applied to all six environmental variables, (2) comparisons on the first two axes of a PCA applied to the three most important variables (i.e., maximum and minimum surface temperature, and maximum surface salinity), and (3) two-dimensional comparisons of maximum surface temperature and average bottom temperature (see Appendix S2.3). Of these 180 comparisons, 149 indicate significant similarity, and no comparison finds evidence of niche evolution.

Comparisons considering all six environmental variables indicate niches are statistically similar for virtually all species and time slices (46 of 60 comparisons) (Table 2.1). When niche dimensionality was reduced to the most important variables, nine species show statistically similar niches for all comparisons, with the exception of one or two inconclusive tests for C. fornicata, D. robustum, L. pensylvanica, and N. duplicata (49 of 60 comparisons; Fig. 2.2 and Table 2.1). Bulla occidentalis is the only species with non-significant tests across the time slices. Niches also show stability when raw variables are considered. Seven of the ten species have statistically similar niches across all time comparisons (42 of 60 comparisons; Table 2.1 ). Two other species, $O$. sayana and C. virginica, have statistically similar niches with the exception of one or two inconclusive tests, respectively. Quantifying niche similarity for B. occidentalis proves more difficult, as three of six niche comparisons are non-significant.

| Species | mPWP-LIG LIG-mPWP | PI-LIG LIG—PI | mPWP-PI PI-mPWP |
| :---: | :---: | :---: | :---: |
| A. simplex |   |  |  |

[^1]We also tested whether species conserved their upper and lower thermal tolerance limits, an important consideration for marine ectotherms as temperatures warm (Sunday et al., 2011; Araújo et al., 2013). To this effect, we tested whether species exhibited similarity in their maximum and minimum surface temperature preferences across three million years, resulting in 120 comparisons (see Appendix S2.3). Species seem to conserve their upper thermal tolerance limits; however, results are less conclusive for minimum temperature tolerances (Table 2.2). Across the suite of species, the majority of comparisons are statistically more similar with regard to maximum surface temperature, although five species have one or two comparisons that are inconclusive (B. occidentalis, D. robustum, $L$. pensylvanica, N. duplicata, O. sayana, and T. dislocata). There is no apparent pattern as to which tests are inconclusive (Table 2.2). Comparisons are also statistically similar with regard to minimum temperature tolerances. However, the structure of this variable changes significantly through time, making it difficult to quantify similarities or differences. Consequently, many comparisons are statistically insignificant (Table 2.2). For example, all mPWP -LIG comparisons are inconclusive with the exception of $N$. duplicata, and half of the comparisons for B. occidentalis and L. pensylvanica are also inconclusive.

## Geographic comparisons.

We also tested for similarity and differences using the geographic projections of niches, rather than comparing niches entirely in environmental space. Results from these analyses mirror those from the environmental comparisons. Niches are statistically similar for seven of the ten species across all comparisons (42 of 60 comparisons; Table 2.1 and Appendix 2.3). Crassostrea virginica and L. pensylvanica have one comparison that is inconclusive (LIG-mPWP and PI-mPWP, respectively), while the niche of B. occidentalis is significantly dissimilar for the LIG-mPWP comparison and non-significant for the PImPWP comparison.

Table 2.2 P-values for comparison tests on (1) maximum surface temperature tolerances; and (2) minimum surface temperature tolerances. Comparisons were performed using the framework of (Broennimann et al. (2012). Bold values indicate non-significant results. All other comparisons are statistically more similar than expected given the environmental background of the variable in question. See Appendix S2.3 for graphical depictions of similarity tests.

| Species/Comparison | [mPWP-LIG LIG-mPWP |  | PI-LIG | LIG-PI | ImPWP-PI | PI-mPWP |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Environmental comparison: maximum surface temperature |  |  |  |  |  |  |
| Anomia simplex | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| . ${ }^{\frac{0}{3} \text { Crassostrea virginica }}$ | 0.00 | 0.00 | 0.00 | 0.02 | 0.01 | 0.00 |
| $\frac{\square}{7}$ Dinocardium robustum | 0.03 | 0.00 | 0.00 | 0.00 | 0.09 | 0.00 |
| ¢ Lucina pensylvanica | 0.00 | 0.00 | 0.00 | 0.00 | 0.81 | 0.42 |
| Mercenaria campechiensis | 0.01 | 0.00 | 0.00 | 0.03 | 0.00 | 0.00 |
| ก Bulla occidentalis | 0.00 | 0.00 | 0.02 | 0.60 | 0.96 | 0.02 |
| O. Crepidula fornicata | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 |
| 인 Neverita duplicata | 0.01 | 0.00 | 0.00 | 0.06 | 0.00 | 0.00 |
| N Oliva sayana | 0.00 | 0.00 | 0.01 | 0.15 | 0.54 | 0.00 |
| - Terebra dislocata | 0.03 | 0.00 | 0.00 | 0.02 | 0.43 | 0.02 |
| Environmental comparison: minimum surface temperature |  |  |  |  |  |  |
| Anomia simplex | 0.21 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| . ${ }^{\frac{0}{3} \text { Crassostrea virginica }}$ | 0.91 | 0.05 | 0.00 | 0.03 | 0.01 | 0.00 |
| $\frac{\square}{2}$ Dinocardium robustum | 0.11 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ¢ Lucina pensylvanica | 0.68 | 0.00 | 0.00 | 0.00 | 0.77 | 0.22 |
| Mercenaria campechiensis | 0.82 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 |
| ก Bulla occidentalis | 0.66 | 0.00 | 0.09 | 0.10 | 0.85 | 0.10 |
| Orepidula fornicata | 0.17 | 0.00 | 0.01 | 0.00 | 0.44 | 0.00 |
| 인 Neverita duplicata | 0.50 | 0.00 | 0.05 | 0.00 | 0.00 | 0.00 |
| べ Oliva sayana | 0.07 | 0.00 | 0.03 | 0.00 | 0.29 | 0.00 |
| Terebra dislocata | 0.18 | 0.00 | 0.00 | 0.00 | 0.05 | 0.00 |

## Discussion

Our statistical tests find no support for niche evolution. Instead, we observe niche stability across three million years of considerable environmental changes, from extreme warmth during the mPWP to glacial cycles during the Pleistocene (Cronin, 1988; Haug \& Tiedemann, 1998; Dowsett et al., 2009). These species were either shifting their niche preferences in response to changing conditions at scales too rapid to be detected by our analyses, which seems unlikely, or their preferences remained stable across this temporal interval. Taking our results at face value, niche stability has profound implications for understanding conservation priorities and for elucidating macroevolutionary dynamics.

## Implications for survival of taxa during times of change.

These results impact our understanding of how species respond to climate change on both long and short time scales. As climate continues to change, species that are unable to adapt to new conditions face two futures: extinction or shifting distributions to follow suitable areas. Already, both responses have been documented or predicted as a result of current climate changes. Marine and terrestrial species are forecast to experience climatedriven extinctions into the 22nd century (Sinervo et al., 2010; Maclean \& Wilson, 2011; Bijma et al., 2013). Indeed, the niche stability we have documented may doom many marine species to extinction over the next 100+ years, particularly if they live at their thermal tolerance limits (Tewksbury et al., 2008; Sunday et al., 2012) and are unable to alter upper thresholds. The target species considered here are predicted to experience severe distributional reductions by the end of this century when variables other than temperature and salinity are considered (Saupe et al., In Press), but wholesale extinction is unlikely. This prediction is supported by their survival in the Pliocene, albeit in geographically-reduced areas as determined from occurrence data, when conditions were purportedly similar to those expected at the end of this century (Robinson \& Dowsett, 2008). These small areas of suitability - or micro-refugia - are thought to have played an important role in species' survival during past episodes of climate change (Cheddadi et al., 2006; Graham et al., 2006; Willis \& MacDonald, 2011).

If species are able to keep pace with the changing environment, distributional shifts, rather than extinctions, are expected (Warren et al., 2013). Under this scenario, dispersal ability becomes an important parameter predicting species' responses to climate change (Trakhtenbrot et al., 2005). Present-day elevational, latitudinal, and bathymetric shifts (Hickling et al., 2006; Sorte et al., 2010; Chen et al., 2011) have already been observed in response to current warming patterns, and, indeed, the fossil record provides abundant evidence for habitat tracking during rapid Pleistocene climate cycles (Roy et al., 1996; Hof et
al., 2011). In support of the inadaptability of niches, species followed their climate envelopes over great distances during the Pleistocene, often creating non-analog community assemblages (Williams \& Jackson, 2007).

The stability of niches also affords some confidence to the methods used to assess extinction vulnerability and distributional shifts (e.g., ENM or species distribution modeling; SDM) (Peterson et al., 2011). Consequently, concerns over inaccurate forecasts owing to niche adaptation are somewhat alleviated (Pearman et al., 2008; Hoffmann \& Sgrò, 2011). Nevertheless, ENM or SDM methods typically do not account for dispersal limitations or altered biotic interactions (Davis et al., 1998), though see (Fordham et al., 2013), nor do they consider that species can alter their behavior or microhabitat preferences to buffer against environmental changes (Kearney et al., 2009; Lavergne et al., 2010).

## Macroevolutionary implications of stable niches.

We show that species' distributions are structured by environmental changes, and thus species themselves are largely controlled by external, abiotic factors (Valentine \& Moores, 1970; Vrba, 1985; van Dam et al., 2006; Roy et al., 2009; Jablonski et al., 2013). Although species may modify their behavior or resource utilization, large-scale parameters of their niches do not change. The FN places constraints on species' interactions with the environment, which potentially governs speciation and extinction processes over long time scales (Jablonski et al., 2013; Myers \& Saupe, 2013). Some researchers have suggested that niche stability may promote allopatric speciation (Vrba, 1985; Peterson et al., 1999; Wiens \& Graham, 2005; Kozak \& Wiens, 2006); that is, environmental perturbations may separate two populations, with these populations prevented from merging back together because of FN constraints, eventually leading to diversification.

Niche stability also provides a potential mechanism for the morphological stasis observed within species over millions of years (Eldredge et al., 2005). More specifically, niche stability requires species to track preferred habitats as the environment changes,
thereby continuously joining and separating populations on scales $<10,000$ years. In this framework, any localized phenotypic adaptation is unlikely to be fixed across an entire species, such that no overall net changes are observed for the species as a whole, since localized changes may cancel one another out (Eldredge et al., 2005).

## Potential caveats.

Although our analyses are quantitatively robust, our study is not without limitations. First, our models may approximate the potential niche (PN), rather than the FN (Jackson \& Overpeck, 2000; Soberón \& Nakamura, 2009), given that FNs are often difficult to characterize without detailed physiological studies (Peterson et al., 2011; Araújo et al., 2013). However, niche estimates were calculated from time-averaged environmental preferences (Kidwell \& Holland, 2002), which will closely approximate real physiological tolerance limits, particularly since marine ectotherms tend to occupy the full extent of latitudes within their thermal limits (Tewksbury et al., 2008; Sunday et al., 2012). Second, and related to accurately characterizing the FN, estimates of present-day and past niches may not be equivalent and thus not comparable. This, of course, is of lesser concern here since we documented niche stability rather than niche evolution. Third, we acknowledge that recognition of 'species'—especially in the fossil record-is sometimes contentious, and while these species are diagnosably distinct throughout their duration, they may not constitute single evolutionary lineages. Nonetheless, if they represent closely-related species (i.e., species complexes), the fact that we still obtained niche conservatism suggests this pattern is robust even across speciation events. Fourth, we analyzed data from warm time periods, as distributional data do not exist for glacial periods (e.g., the last glacial maximum, $\sim 21 \mathrm{Ka}$ ). Therefore, our analyses may have missed rapid niche evolution that occurred in response to these colder conditions. Although possible, the scenario is unlikely because of the rate at which niche evolution would have had to occur, and because of the paucity of evidence for physiological adaptations both in the fossil record (Foster et al., 1990; Roy et al.,

1996; Hof et al., 2011) and in experimental studies (Araújo et al., 2013). Moreover, environmental conditions at the mPWP, LIG, and PI differ to a significant degree, such that we were still able to discern whether species adapted to new conditions or tracked stable climate envelopes. Finally, and related to this issue, because paleoclimate models were only available for certain key temporal intervals, we could not capture the entire temporal history of these species in the context of an ENM framework.

## Conclusions

Here, niche evolution is analyzed over millions of years in a synthetic context uniting both modern and paleontological marine data and paleoclimatic models. We find that niches remain stable across the duration of species' lifetimes, even within a context of significant environmental perturbations. Given their responses to past environmental changes, our results indicate that species will respond to current and future warming by altering distributions to track suitable habitat, or, if the pace of change is too rapid, by going extinct. We urge continued examination of the threats that climate change poses to biodiversity to ensure proper implementation of conservation measures, and we stress the value of integrating paleontological and neontological data to explore these issues.

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Chapter 3. Estimating extinction risk as a function of niche breadth and geographic range size: a case study using Pliocene—recent Atlantic Coastal Plain mollusks



#### Abstract

Determining which species are more prone to extinction is vital for conserving Earth's biodiversity and for providing insight into macroevolutionary processes over time. Here, we utilized the exceptional record of Pliocene-recent Atlantic Coastal Plain mollusks to test the relative effects of geographic range size and niche breadth on survivorship of species from the Pliocene to the present-day. We assessed the vulnerability of 93 bivalve and gastropod species to extinction as a function of both fundamental and realized niche breadths, and geographic range size. We additionally examined whether extinct species lost more suitable habitat during the Last Glacial Maximum ( $\sim 21 \mathrm{Ka}$ ) than still-extant species. Contrary to our expectations, extant species did not have larger fundamental niche breadths than extinct species. By contrast, the realized niche emerged as a key predictor of extinction risk. Our results reiterate the well-supported idea that geographic range size is a key predictor of extinction risk. Similarly, the degree of suitable area lost during the Last Glacial Maximum predicted survivorship for studied mollusks. A potentially intriguing aspect of these results is that fundamental niche breadth appears to be decoupled from geographic range size with regard to extinction risk. In essence, this suggests that occupied environmental breadth (i.e., the realized niche) provides a greater buffer against extinction than potential tolerance limits (i.e., the fundamental niche), and the degree to which species are able to fill their fundamental niches provides the measure of extinction risk. This information can be used not only to implement proper conservation policies as we face current extinctions, but also to understand the properties promoting or inhibiting extinction -and perhaps speciationacross evolutionary time.


## Introduction

Determining which species are more prone to extinction is vital for conserving Earth's biodiversity (McKinney, 1997; Thuiller et al., 2005; Schwartz et al., 2006; Barnosky et al., 2011; Harnik, 2011; Lee \& Jetz, 2011; Barnosky et al., 2012) and for providing insight into macroevolutionary processes over evolutionary time scales (Eldredge, 1979; Vrba, 1987; Kiessling \& Aberhan, 2007; Payne \& Finnegan, 2007; Jablonski, 2008). Although several traits have been identified as correlating with extinction risk (McKinney, 1997; Mace et al., 2008; Fritz et al., 2009), one of the most robust is geographic range size, with both neontological (Purvis et al., 2000; Thomas et al., 2004; Schwartz et al., 2006; Harris \& Pimm, 2008) and paleontological (Jablonski \& Roy, 2003; Jablonski \& Hunt, 2006; Kiessling \& Aberhan, 2007; Liow, 2007; Payne \& Finnegan, 2007; Foote et al., 2008; Stigall, 2010; Harnik, 2011; Harnik et al., 2012) studies finding that large geographic range size increases species' survivorship (although see Stanley [1986b], Norris [1992], Vermeij [1993], and Myers et al. [2012] for notable exceptions). Fewer studies, however, have focused on species' environmental niche breadths, and the impact this variable has on extinction risk.

Here, we utilize the exceptional record of Pliocene-recent Atlantic Coastal Plain mollusks to test the relative effects of geographic range size and niche breadth on survivorship of species from the Pliocene to the present-day. We assess the vulnerability of 93 diverse bivalve and gastropod species to extinction as a function of both fundamental (FN) and realized ( RN ) niche breadth, as well as geographic range size. We additionally examine whether extinct species lost more suitable habitat during the Last Glacial Maximum (LGM; $\sim 21 \mathrm{Ka}$ ) than still-extant species. We hypothesize that FN breadth determines survivorship to a greater degree than RN breadth and geographic range size, but that extant species have larger values for all of these traits.

The FN is defined as the set of all combinations of abiotic environmental variables in which a species can survive (Soberón \& Nakamura, 2009; Peterson et al., 2011), and has
been posited to be a species-level trait that is stable within and across lineages (MartínezMeyer \& Peterson, 2006; Myers \& Saupe, 2013; Strubble et al., 2013; Saupe et al., in review). As climate changes, we suggest that this suite of tolerances (i.e., the FN) contributes to a species' ability to survive environmental changes. In contrast, the RN is a subset of the FN that a species occupies at a given time, and which can be constrained for reasons relating to resource use, biotic factors such as competition, and/or dispersal barriers (Pearman et al., 2008; Peterson et al., 2011; Araújo \& Peterson, 2012).

The Neogene Atlantic Coastal Plain molluscan record provides a well-characterized system in which to analyze the dynamics of niche breadth and geographic range over time for several reasons. Molluscan remains are abundant and particularly well studied with respect to patterns of extinction, species turnover, and ecological change across this interval (Allmon et al., 1993; Todd et al., 2002; Vermeij, 2005; Klaus et al., 2011). Moreover, both bivalves and gastropods have proven excellent study systems for analyzing diversity dynamics through time (Jablonski \& Hunt, 2006; Crampton et al., 2010; Nürnberg \& Aberhan, 2013). Climatic changes from the Pliocene to the recent have also been well characterized using global climate models (Haywood et al., 2011).

Potential difficulties arise in testing the relative effect of niche breadth and geographic range size on diversity dynamics because their relationship is complex and often not monotonic (Gaston, 2003; Peterson et al., 2011; Myers \& Saupe, 2013). In particular, they frequently co-vary, such that the effects of geographic range are not easily decoupled from those of niche breadth. With that said, species with large geographic range sizes can have small niche breadth if the underlying environment is homogeneous, whereas species with broad niche breadths can have small geographic ranges if they are limited by dispersal, biotic or other geographic barriers (Eldredge, 1979; Gaston, 2003; Araújo \& Peterson, 2012; Myers \& Saupe, 2013).

Niche breadth is often considered an inverse measure of ecological specialization
(Smith, 1982). Indeed, specialist species (stenotopes) have long been thought to be more prone to extinction than generalist species (eurytopes), especially during times of environmental change (Simpson, 1944; Eldredge, 1979; Vrba, 1987; Brown et al., 1995; McKinney, 1997; Fernandez \& Vrba, 2005). To date, both paleontological (Kammer et al., 1997; Keller et al., 1997; Heim \& Peters, 2011; Harnik et al., 2012; Nürnberg \& Aberhan, 2013) and neontological (Thuiller et al., 2005; Broennimann et al., 2006; Colles et al., 2009; Devictor et al., 2010; Boulangeat et al., 2012) studies have examined the influence of RN breadths on extinction probability, with the general conclusion that broader niche breadths increase species' longevity. Here, we use ecological niche modeling (ENM) to compare both FNs and RNs. We acknowledge that accurately estimating FNs without mechanistic studies is difficult (Kearney \& Porter, 2009), and our results may approximate the existing FN (also known as the potential niche), or some version of $>\mathrm{RN}$ (Jackson \& Overpeck, 2000; Peterson et al., 2011). Recent biophysical approaches, however, have suggested that FNs can be represented by limited sets of parameters like temperature (Kearney et al., 2010; Kearney et al., 2013), and we additionally use model parameters that match known physiological response curves of species (Austin, 1985; Austin et al., 1994; Hooper et al., 2008; Angilletta, 2009). Thus, obtained estimates may at least be congruent with species' potential suitable area.

Ultimately, identification of the traits that promote or inhibit extinction provides insight into the causal mechanisms generating patterns of diversity over evolutionary time scales (Eldredge, 1989; Stanley, 1990; Kammer et al., 1997; Jablonski, 2008). The fossil record provides a ledger of such evolutionary winners and losers, which can be used to generate a list of threat factors leading to species' extinctions. These rule sets are important, because of the time-intensive nature of estimating extinction risk for individual species and populations, and because of the rising concerns over the future of marine ecosystems and biodiversity (Worm et al., 2006; Hendriks et al., 2010; Russell et al., 2012; Jones et al.,

2013; Saupe et al., 2014).

## Material and Methods

## Study extent.

All analyses were conducted within the Atlantic Coastal Plain. Models were calibrated within a region bounded by the Americas and $34^{\circ} \mathrm{W}$ longitude, and $48^{\circ} \mathrm{N}$ and $44^{\circ} \mathrm{S}$ latitude. We sought the union of the area sampled by researchers and which was most likely accessible to the species during the Pliocene (Phillips et al., 2009; VanDerWal et al., 2009; Peterson et al., 2011).

## Taxa.

We selected target taxa from 30 genera of gastropods classified within eight families (Bursidae, Conidae, Fasciolariidae, Muricidae, Personidae, Ranellidae, Strombidae, and Tonnidae) and 71 genera of bivalves classified within six families (Arcidae, Cariidae, Carditidae, Lucinidae, Tellinidae, and Veneridae) in the Digital Atlas of Neogene Life (Hendricks et al., 2013). We utilized all species having Pliocene presences in the Digital Atlas, with the exception of those with poor sampling, extreme micro-endemism, or poor model quality, detailed below. We eliminated species with very restricted distributions to account for potential artifacts that might arise from sampling bias by using a two-step process: we retained species with $\geq$ four spatially unique occurrence points at 2.5 arc-minute ( $\sim 4.5 \mathrm{~km}$ ) resolution; and we also excluded species with only one spatially unique occurrence point at $1.25^{\circ}$ resolution (i.e., the scale of the environmental data). This procedure ensured that poorly sampled species were removed from niche estimations. A total of 47 extinct (of 80) and 46 extant (of 65) species remained after eliminating poorly sampled species as well as those with non-significant niche models (see niche modeling sections below for details), resulting in a total of 16 gastropod genera and 50 bivalve genera. Many extant species have fossil records that extend into the Pliocene ( $\sim 3.1 \mathrm{Ma}$ ), as most marine invertebrates have durations > 3 million years (Stanley, 1979; Eldredge et al., 2005; Patzkowsky \& Holland,
2012). Pliocene records for these extant species were verified by examination of museum collections and literature survey.

## Distributional data.

We considered fossil distributional data from Pliocene ( $\sim 3.264-3.025 \mathrm{Ma}$ ) strata of the Atlantic Coastal Plain, USA. Distributional records were primarily obtained from the Florida Museum of Natural History (FLMNH), with additional records from the Academy of Natural Sciences of Drexel University, Paleontological Research Institution, Yale Peabody Museum, and Virginia Museum of Natural History, for ten viable stratigraphic units identified using the database of Saupe et al. (in review) (Table 3.2). The holdings of the FLMNH represent the largest collection of Neogene Atlantic Coastal Plain mollusks, with extensive distributional coverage for hundreds of species across the eastern seaboard (Fig. 3.1). For each species, we subsampled distributional data to leave one record per environmental pixel (Tables 3.1.1 and 3.1.2). This was done to prevent certain localities with multiple records from being unduly weighted in niche modeling analyses (Royle et al., 2012; Yackulic et al., 2013), and did not affect the resultant overall distribution of the species. The spatial resolution of the environmental data $\left(1.25 \times 1.25^{\circ}\right.$, described below) limited the number of spatially unique occurrence points available per species. We retained species with $\geq$ two spatially unique occurrence points at $1.25^{\circ}$ resolution whose models were significant and congruent with those constructed using more occurrence data (Tables 3.1.1 and 3.1.2). Moreover, all species possessed at least four spatially unique occurrence points at 2.5 arcminute resolution, a number shown to be statistically robust for modern species (Hernandez et al., 2006; Pearson et al., 2007). The frequency distribution of occurrences per species retained in the analyses was right-skewed on a normal plot (Fig. 3.2), a pattern found for many other extant terrestrial and marine taxa (Gaston, 1998; Gaston \& He, 2002). This indicates our data are commensurate with neontological data, which are presumably unbiased
with regard to sampling. Additional corrections for potential sampling biases are described in ecological niche modeling protocols.

| Family | Genus | Species | Author | Extinction status | \# of pts 2.5 arc-minute | \# of pts $1.25^{\circ}$ | P-value |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Anomiidae | Anomia | simplex | d'Orbigny, 1853 | Extant | 48 | 12 | <0.001 |
| Arcidae | Anadara | megarata | Olsson \& Harbison, 1953 | Extinct | 5 | 2 | NA |
| Arcidae | Anadara | notoflorida | Vokes, 1969 | Extinct | 6 | 2 | NA |
| Arcidae | Anadara | idonea | Conrad, 1832 | Extinct | 6 | 2 | NA |
| Arcidae | Arca | wagneriana | Dall, 1898 | Extinct | 18 | 3 | <0.001 |
| Arcidae | Barbatia | irregularis | Dall, 1898 | Extinct | 5 | 2 | NA |
| Arcidae | Scapharca | scalarina | Heilprin, 1886 | Extinct | 21 | 6 | <0.001 |
| Cardiidae | Acrosterigma | dalli | Heilprin, 1886 | Extinct | 4 | 2 | NA |
| Cardiidae | Dallocardia | muricata | Linnaeus, 1758 | Extinct | 31 | 9 | <0.001 |
| Cardiidae | Dinocardium | robustum | Lightfoot, 1786 | Extant | 22 | 7 | <0.001 |
| Cardiidae | Laevicardium | mortoni | Conrad, 1831 | Extant | 110 | 19 | <0.001 |
| Cardiidae | Papyridea | semisulcata | Gray, 1825 | Extant | 4 | 3 | 0.025 |
| Cardiidae | Planicardium | virginianum | Conrad, 1839 | Extinct | 6 | 3 | 0.033 |
| Cardiidae | Planicardium | acutilaqueatum | Conrad, 1839 | Extinct | 13 | 6 | <0.001 |
| Cardiidae | Trachycardium | egmontianum | Shuttleworth, 1853 | Extant | 12 | 4 | <0.001 |
| Cardiidae | Trachycardium | evergladeensis | Mansfield, 1931 | Extinct | 7 | 3 | 0.026 |
| Cardiidae | Trachycardium | oedalium | Dall, 1900 | Extinct | 11 | 5 | <0.001 |
| Cardiidae | Trigoniocardia | willcoxi | Dall, 1900 | Extinct | 13 | 3 | <0.001 |
| Carditidae | Cardita | olga | Mansfield, 1939 | Extinct | 7 | 2 | NA |
| Carditidae | Carditamera | tamiamiensis | Mansfield, 1931 | Extinct | 5 | 3 | <0.001 |
| Carditidae | Carditamera | dasytes | Olsson, 1967 | Extinct | 8 | 3 | <0.001 |
| Carditidae | Carditamera | floridana | Conrad, 1838 | Extant | 4 | 4 | <0.001 |
| Carditidae | Carditamera | arata | Conrad, 1832 | Extinct | 29 | 11 | <0.001 |
| Carditidae | Cyclocardia | granulata | Say, 1824 | Extinct | 29 | 11 | <0.001 |
| Carditidae | Pleuromeris | tridentata | Say, 1826 | Extant | 22 | 9 | <0.001 |
| Carditidae | Pteromeris | perplana | Conrad, 1841 | Extant | 18 | 8 | <0.001 |
| Carditidae | Pteromeris | abbreviata | Conrad, 1841 | Extinct | 10 | 7 | <0.001 |
| Lucinidae | Anodontia | schrammi | Crosse, 1876 | Extant | 7 | 4 | <0.001 |
| Lucinidae | Anodontia | alba | Link, 1807 | Extant | 25 | 5 | <0.001 |
| Lucinidae | Armimiltha | disciformis | Heilprin, 1886 | Extinct | 15 | 3 | <0.001 |
| Lucinidae | Callucina | keenae | Chavan, 1971 | Extant | 24 | 11 | <0.001 |
| Lucinidae | Cavilinga | blanda | Dall, 1901 | Extant | 17 | 8 | <0.001 |
| Lucinidae | Codakia | orbicularis | Linnaeus, 1758 | Extant | 19 | 4 | <0.001 |
| Lucinidae | Ctena | orbiculata | Montagu, 1808 | Extant | 10 | 3 | <0.001 |
| Lucinidae | Divalinga | quadrisulcata | d'Orbigny, 1846 | Extant | 23 | 12 | <0.001 |
| Lucinidae | Lucina | pensylvanica | Linnaeus, 1758 | Extant | 37 | 6 | <0.001 |
| Lucinidae | Lucinisca | nassula | Conrad, 1846 | Extant | 16 | 7 | <0.001 |
| Lucinidae | Miltha | caloosaensis | Dall, 1898 | Extinct | 19 | 3 | <0.001 |
| Lucinidae | Parvilucina | crenella | Dall, 1901 | Extant | 11 | 5 | <0.001 |
| Lucinidae | Pleurolucina | amabilis | Dall, 1898 | Extinct | 7 | 3 | <0.001 |
| Lucinidae | Stewartia | floridana | Conrad, 1833 | Extant | 22 | 5 | <0.001 |
| Ostreidae | Crassostrea | virginica | Gmelin, 1791 | Extant | 21 | 7 | <0.001 |
| Tellinidae | Arcopagia | fausta | Pulteney, 1799 | Extant | 7 | 4 | <0.001 |
| Tellinidae | Eurytellina | alternata | Say, 1822 | Extant | 29 | 7 | <0.001 |
| Tellinidae | Laciolina | magna | Spengler, 1798 | Extant | 8 | 4 | <0.001 |
| Tellinidae | Leporimetis | magnoliana | Dall, 1900 | Extinct | 21 | 8 | <0.001 |
| Tellinidae | Macoma | arctata | Conrad, 1843 | Extinct | 5 | 4 | 0.0082 |
| Tellinidae | Merisca | aequistriata | Say, 1824 | Extant | 16 | 8 | <0.001 |
| Tellinidae | Tellidora | cristata | Récluz, 1842 | Extant | 15 | 4 | <0.001 |
| Tellinidae | Tellinella | listeri | Röding, 1798 | Extant | 4 | 3 | 0.009 |
| Veneridae | Chione | erosa | Dall, 1903 | Extinct | 36 | 7 | <0.001 |
| Veneridae | Chionopsis | cribraria | Conrad, 1843 | Extinct | 11 | 8 | <0.001 |
| Veneridae | Dosinia | discus | Reeve, 1850 | Extant | 8 | 2 | NA |
| Veneridae | Dosinia | elegans | Conrad, 1843 | Extant | 21 | 7 | <0.001 |
| Veneridae | Globivenus | rigida | Dillwyn, 1817 | Extant | 4 | 2 | NA |
| Veneridae | Lirophora | latilirata | Conrad, 1841 | Extant | 41 | 13 | <0.001 |
| Veneridae | Macrocallista | nimbosa | Lightfoot, 1786 | Extant | 32 | 4 | <0.001 |
| Veneridae | Macrocallista | maculata | Linnaeus, 1758 | Extant | 28 | 8 | <0.001 |
| Veneridae | Mercenaria | campechiensis | Gmelin, 1791 | Extant | 48 | 12 | <0.001 |
| Veneridae | Panchione | ulocyma | Dall, 1895 | Extinct | 19 | 6 | <0.001 |
| Veneridae | Petricolaria | pholadiformis | Lamarck, 1818 | Extant | 5 | 4 | <0.001 |
| Veneridae | Timoclea | grus | Holmes, 1858 | Extant | 13 | 6 | <0.001 |

Table 3.1.2 Studied gastropod species, including their extinction status, number of spatially unique occurrence points at 2.5 arc-minutes and $1.25^{\circ}$, and significance level of the niche model under the jackknife test of Pearson et al. (2006). This test was not possible for species with two points, and in theses cases, models were deemed significant when they did not omit either point after thresholding.

| Family | Genus | Species | Author | Extinction status | \# of pts 2.5 <br> arc-minute | \# of pts $1.25^{\circ}$ | P-value |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Bullidae | Bulla | occidentalis | A. Adams, 1850 | Extant | 22 | 5 | <0.001 |
| Calyptraeidae | Crepidula | fornicata | Linnaeus, 1758 | Extant | 56 | 14 | <0.001 |
| Conidae | Conus | delessertii | Récluz, 1843 | Extant | 6 | 3 | 0.025 |
| Conidae | Conus | haytensis | Sowerby II, 1850 | Extinct | 5 | 2 | NA |
| Conidae | Conus | yaquensis | Gabb, 1873 | Extinct | 9 | 2 | NA |
| Conidae | Conus | bassi | Petuch, 1991 | Extinct | 8 | 3 | <0.001 |
| Conidae | Conus | miamiensis | Petuch, 1986 | Extinct | 9 | 3 | 0.026 |
| Conidae | Conus | paranobilis | Petuch, 1991 | Extinct | 4 | 3 | <0.001 |
| Conidae | Conus | daucus | Hwass, 1792 | Extant | 5 | 3 | <0.001 |
| Conidae | Conus | marylandicus | Green, 1830 | Extinct | 15 | 9 | <0.001 |
| Conidae | Conus | oniscus | Woodring, 1928 | Extinct | 22 | 6 | <0.001 |
| Conidae | Conus | adversarius | Conrad, 1840 | Extinct | 56 | 14 | <0.001 |
| Fasciolariidae | Cinctura | rhomboidea | Rogers \& Rogers, 1839 | Extinct | 45 | 11 | <0.001 |
| Fasciolariidae | Fasciolaria | okeechobensis | Tucker \& Wilson, 1932 | Extinct | 6 | 4 | <0.001 |
| Fasciolariidae | Heilprinia | florida | Olsson \& Harbison, 1953 | Extinct | 10 | 4 | <0.001 |
| Fasciolariidae | Heilprinia | carolinensis | Dall, 1892 | Extinct | 5 | 4 | 0.0020 |
| Fasciolariidae | Heilprinia | caloosaensis | Heilprin, 1886 | Extinct | 15 | 5 | <0.001 |
| Fasciolariidae | Pliculofusus | scalarinus | Heilprin, 1886 | Extinct | 24 | 4 | <0.001 |
| Fasciolariidae | Triplofusus | giganteus | Kiener, 1840 | Extant | 31 | 8 | <0.001 |
| Muricidae | Calotrophon | ostrearum | Conrad, 1846 | Extant | 32 | 9 | <0.001 |
| Muricidae | Chicoreus | shirleyae | Vokes, 1966 | Extinct | 6 | 3 | 0.016 |
| Muricidae | Chicoreus | floridanus | Vokes, 1965 | Extinct | 33 | 5 | <0.001 |
| Muricidae | Dermomurex | alabstrum | A. Adams, 1864 | Extant | 7 | 3 | <0.001 |
| Muricidae | Ecphora | bradleyae | Petuch, 1988 | Extinct | 4 | 2 | NA |
| Muricidae | Ecphora | quadricostata | Say, 1824 | Extinct | 28 | 9 | <0.001 |
| Muricidae | Eupleura | metae | Petuch, 1994 | Extinct | 6 | 3 | 0.015 |
| Muricidae | Eupleura | caudata | Say, 1822 | Extant | 9 | 5 | <0.001 |
| Muricidae | Eupleura | leonensis | Mansfield, 1930 | Extinct | 12 | 4 | <0.001 |
| Naticidae | Neverita | duplicata | Say, 1822 | Extant | 51 | 15 | <0.001 |
| Olividae | Oliva | sayana | Ravenel, 1834 | Extant | 16 | 9 | <0.001 |
| Terebridae | Terebra | dislocata | Say, 1822 | Extant | 21 | 9 | <0.001 |

## Environmental data.

Environmental data were derived from the coupled atmosphere-ocean HadCM3
global climate model (GCM) (Gordon et al., 2000; Pope et al., 2000) for the mid-Pliocene Warm Period (mPWP; 3.264-3.025 Ma). Model results were also projected to the Last Glacial Maximum (LGM; ~21 Ka). Boundary conditions for the mPWP GCM used the alternate PRISM3D PlioMIP dataset described in Haywood et al. (2011), and boundary
conditions for the LGM GCM used those in Singarayer \& Valdes (2010) and Singarayer et al. (2011). All experiments were run for 500 model years, and environmental parameters were derived from the final 30 years of each experiment at $1.25 \times 1.25^{\circ}$ resolution $(\sim 140 \times 140 \mathrm{~km}$ at the equator). Where ocean data were unavailable (i.e., sites presenting macrofossil data but where the GCM indicated land), we used an inverse-distance weighted algorithm to extrapolate model data.

We converted the monthly salinity and temperature outputs from the GCMs to maximum, minimum, and average yearly coverages for both surface and bottom conditions using ArcGIS 10.1. We centered and standardized data in each of these 12 coverages, performing a principal components analysis (PCA) on the correlation matrix using the PCARaster function in the ENMGadgets package in R (Barve \& Barve, 2014). Data were transformed in order to create new axes that summarized variation in fewer, independent dimensions, and to reduce co-linearity among variables. We retained the first four principle components, which explained cumulatively $\geq 97 \%$ of the variance in the dataset, for model calibration. The PCA structure for the Pliocene was enforced for the LGM using the PCAProjections function in the ENMGadgets package in R (Barve \& Barve, 2014).

Ideally, we would use an ensemble-modeling approach that considered multiple GCMs (Fordham et al., 2012). However, model output was available to us only from HadCM3, with this GCM having been successfully used within a large range of Quaternary and pre-Quaternary modeling studies.

Table 3.2 Potential mPWP formations ( $\sim 3.1 \mathrm{Ma}$ ) for species' occurrence data used in analyses.
mPWP (~3.1 Ma) Formations

| Duplin | Jackson Bluff |
| :--- | :--- |
| Goose Greek | Mare |
| Guaiguaza | Raysor |
| Hopegate | Tamiami/Pinecrest |
| Intracoastal | Yorktown |

## Ecological niche modeling.

ENMs were generated using a maximum entropy algorithm, Maxent v. 3.3.3 (Phillips et al., 2006). Maxent estimates environmental suitability for a species when the null expectation is equivalent to uniform (Elith et al., 2011), with results often similar to those under general linear models (Fithian \& Hastie, 2012; Renner \& Warton, 2013). We enabled only the linear and quadratic features in Maxent to produce realistic response curves that match those known from physiological experiments of plants and animals (Austin, 1985; Austin et al., 1994; Hooper et al., 2008; Angilletta, 2009). To correct for biases in fossil distributional data, we implemented a 'bias file' within Maxent. The bias file describes the probability that an area was sampled; thus, regions with rock outcrop (i.e., areas where species may actually be detected or sampled) were weighted twice as heavily as regions without rock outcrop. Maxent will then factor out this bias during the modeling process (Dudík et al., 2005). This method essentially accounts for incomplete knowledge of a species distribution (Svenning et al., 2011). Pliocene models were projected to LGM conditions to determine if extinct species retained suitable area during glacial times. To avoid inaccurate projections as a result of novel environmental conditions, we deactivated clamping and allowed for extrapolation following Owens et al. (2013).

## Potential niche characterizations.

The modeling process produces continuous suitability surfaces, which require interpretation to determine limits of suitability for a species. This process is usually done via
thresholding, wherein models are converted to binary output (i.e., $1=$ suitable; $0=$ unsuitable). We used the mean model suitability score as the threshold, given this method provides greater independence from input occurrence data and performs well with low and varying prevalence data (Liu et al., 2005; Freeman \& Moisen, 2008). We recognize that choice of threshold can affect model results (Liu et al., 2005; Jiménez-Valverde \& Lobo, 2007); however, the threshold method we employed does not constrict suitability as severely as traditional methods like least training presence (LTP) or MaxSSS (Pearson et al., 2007; Liu et al., 2013), which often produce approximations closer to the realized niche (RN), rather than the potential niche (PN) or the fundamental niche (FN) (Peterson et al., 2011).

## Niche breadth calculations.

We consider niche breadth in the classic Grinnellian sense (Grinnell, 1917) of abiotic environmental variables, defined by Hutchinson (1957) as a hyper-volume in multidimensional space, within which a species can maintain viable populations. Niche breadths were calculated using NicheA (Qiao et al., 2012). From thresholded niche models, we quantified niche volumes from the first three principle component axes within environmental space, which explained $>89 \%$ of the variance in the dataset (Fig. 3.3). To increase the potential resilience of our results, we used two different methods to calculate niche volumes: minimum volume complex polyhedrons $(\mathrm{CPH})$ around suitable area in three-dimensional environmental space (Cornwell et al., 2006; Monahan \& Tingley, 2012), and minimum volume ellipsoids (MVE) around suitable area in three-dimensional environmental space (Van Aelst \& Rousseeuw, 2009). To our knowledge, this represents one of the first times niches have been quantified in three dimensions, although see Cornwell et al. (2006) and Blonder et al. (2014).

## Geographic area calculations.

Again, to increase the potential resilience of our results, geographic area occupied by a species was calculated in two ways: summing the number of suitable pixels from projected
niche models, and creating minimum convex polygons around the unfiltered (all) occurrence data for each species. To calculate the latter, we used the minimum bounding geometry function in ArcGIS 10.1 and calculated polygon areas using the USA Contiguous Albers Equal Area Conic map projection (Gaston \& Fuller, 2009) (Fig 3.1). We also calculated amount of area projected to remain suitable for these species during the LGM $(\sim 21 \mathrm{Ka})$ by counting suitable pixels in model projections.

## Realized niche characterizations.

To examine whether the breadth of environment occupied by species (a species' RN ) impacts extinction selectivity, we calculated CPH and MVE niche breadth volumes for species' occurrence data in environmental space. Moreover, we tested the sensitivity of these calculations to potential sampling biases by degrading the available fossil record to the same number of occurrence points (lowest number) for all species exceeding this two-point occurrence prevalence. We calculated niche breadth as the environmental distance between the two points on the first principle component layer, which explained $\sim 39 \%$ of the variance in the dataset, following approaches similar to those employed by Colwell \& Futuyma (1971) and Essl et al. (2009). We used the median value from the 100 replicates as the niche breadth for a species. Niche breadths for species with only two occurrence points were calculated in the same fashion, without bootstrap replication. This process is similar to rarefaction, which is commonly utilized for paleontological data, and attempts to correct for differing abundance values (Miller \& Foote, 1996; Barnosky et al., 2005; Kiessling \& Aberhan, 2007). Finally, we thresholded obtained niche models using the LTP method (Pearson et al., 2007), which constricts estimates of suitability to the lowest value associated with an occurrence point. Essentially, the process only predicts suitable environments that a species has occupied (i.e., estimates closer to the RN ). In this study, the mean number of pixels predicted suitable across all species decreased over $200 \%$ using a LTP threshold compared to a mean threshold.

## Niche model significance testing.

For the majority of species, we assessed statistical significance of the niche models using a jackknife procedure of Pearson et al. (2007) (Tables 3.1.1 and 3.1.2). For those species with only two spatially explicit occurrence points, models that correctly predicted both occurrence points were deemed significant (note that both points will always be correctly predicted under a LTP threshold). Species were eliminated if models were not significant using either of these approaches.

## Statistical tests.

We performed binary logistic regressions using both geographic range and niche breadths to determine if variables are correlated with respect to survival or extinction. No significant results were obtained using these multivariate tests. Consequently, we performed univariate analyses. Since area and volume calculations were not normally distributed, we log transformed all variables and used one-way nonparametric Mann-Whitney U tests for analyses (Table 3.3). We tested four hypotheses: (i) whether extant species had greater niche breadths than extinct species, (ii) whether extant species had larger geographic ranges than extinct species, (iii) whether extant species occupied broader realized environmental space than extinct species, and (iv) whether extant species had more suitable area remaining during the LGM than extinct species. We performed ten Mann-Whitney U tests, because we calculated FN breadth in two ways, RN breadth in five ways, and geographic area in two ways, in order to test the resiliency of our results to differing estimation methods (see Table 3.3).

Figure 3.1 Distributional data (blue dots), area polygons (pink), and thresholded niche model projections for FN (light green) and RN (dark green) estimates for two representative bivalve species: Laciolina magna and Merisca aequistriata in the mPWP. Note that because of differences in distributional range for each species, the maps are not shown to the same scale.

## Results

Contrary to our original hypothesis, extant species did not have significantly larger niche breadths than extinct species, although values are close to alpha (a) level of 0.05 ( $P=$ 0.071 and $P=0.088$ for CPH and MVE calculations, respectively) (Table 3.3). Extant species, however, did have significantly larger geographic ranges than extinct species, both when considering suitable area predicted by the model $(P=0.030)$ and area calculated from polygons ( $P=0.002$ ). Consequently, there does not seem to be a one-to-one correspondence between niche breadth predicted by the models and amount of suitable area available geographically (Table 3.3).


Figure 3.2 Histogram of number of occurrences per species at $1.25^{\circ}$ resolution in the mPWP. Note the right-skewed nature of the frequency distribution, which mirrors that for many extant taxa (Gaston, 1998; Gaston \& He, 2002).

The RN, however, does seem to be a significant predictor of extinction (Table 3.3). Extant species occupy significantly larger volumes of environmental space than extinct species, using estimates based on both the occurrence data ( $P=0.006$ and $P=0.009$ for CPH and MVE calculations, respectively) and the LTP niche models ( $P=0.011$ and $P=0.018$ for CPH and MVE calculations, respectively). Moreover, these results are robust to the bootstrap resampling tests ( $P=0.044$ ).

When niche models are projected to glacial conditions (LGM; ~21 Ka), extinct species lose more suitable area than extant species $(P=0.022)$ (Table 3.3). This result holds when change (percent decrease) in suitable area from the Pliocene to the LGM is calculated; in other words, extinct species lose more suitable area, on average, than extant species ( $P<$ $0.01)$.

We tested four hypotheses with respect to the FN, RN, geographic range size, and amount of area lost during the LGM. Given that hypotheses were tested a priori, correction for multiple comparisons is not required. However, conservatively, all previously-significant tests remained significant for the lowest $p$-value for each estimation method applying a Holm-Bonferroni correction (Holm, 1979; Ludbrook, 1998), which performs well while still controlling the family-wise type 1 error rate.. Furthermore, although we were interested in using a one-tailed test to assess whether extant species had greater values for niche breadths and geographic range size, a more stringent two-tailed test still provides significant results for all analyses, with the exception of the rarefaction RN breadth method and geographic area under the mean niche model (see "Two-tailed test" results in Table 3.3). We further stress tested our results by running all analyses using species with $\geq 3$ spatially unique points at $1.25^{\circ}$ resolution. Again, we obtained the same patterns of significance, with the exception of the MVE and rarefaction calculations for RN breadth and geographic area under the mean niche model (see " $\geq 3$ points" results in Table 3.3).

Table 3.3 Results from Mann-Whitney U tests. Tests assessed: (i) whether extant species had greater niche breadths than extinct species, (ii) whether extant species occupied broader realized environmental space than extinct species, (iii) whether extant species had larger geographic ranges than extinct species, and (iv) whether extant species had more suitable area remaining during the LGM than extinct species. Results from both the one-tailed and more conservative two-tailed tests are provided, as well as those from one-tailed tests using only species with $\geq 3$ spatially unique points at $1.25^{\circ}$ resolution.

| Analysis | Calculation method | One-tailed test |  | Two-tailed test |  | $\geq 3$ points |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | W | P-value | W | P-value | W | P-value |
| FN breadth |  |  |  |  |  |  |  |
| Mean niche model | CPH | 1272.5 | 0.071 | 1272.5 | 0.142 | 970.5 | 0.106 |
| Mean niche model | MVE | 1257.5 | 0.088 | 1257.5 | 0.176 | 962.5 | 0.120 |
| RN breadth |  |  |  |  |  |  |  |
| Occurrences | CPH | 1406 | 0.006 | 1406 | 0.012 | 1023 | 0.041 |
| Occurrences | MVE | 1389 | 0.009 | 1389 | 0.018 | 1011 | 0.052 |
| LTP niche model | CPH | 1380 | 0.011 | 1380 | 0.021 | 1035 | 0.032 |
| LTP niche model | MVE | 1354 | 0.018 | 1354 | 0.036 | 1011 | 0.052 |
| Rarefaction | Distance | 1302.5 | 0.044 | 1302.5 | 0.089 | 1006.5 | 0.057 |
| Geographic area |  |  |  |  |  |  |  |
| Polygons analyses | Area (sq km) | 1452 | 0.002 | 1452 | 0.004 | 1052 | 0.022 |
| Mean model projection | Pixel count | 1325 | 0.030 | 1325 | 0.061 | 1011 | 0.052 |
| LGM projection |  |  |  |  |  |  |  |
| Amount of suitable area | Pixel count | 1343.5 | 0.022 | 1343.5 | 0.044 | 1024 | 0.040 |



Figure 3.3 Representations of niche volumes in three-dimensional principle component space for the same two representative species, Laciolina magna and Merisca aequistriata. The left column depicts the minimum volume complex polyhedrons ( CPH ) for both thresholded mean niche models (FN; light pink) and LTP niche models (RN; dark pink). The right column depicts the minimum volume ellipsoids (MVE) for thresholded mean niche models (FN; light pink) and LTP niche models (RN; dark pink).

## Discussion

Our initial hypothesis that extant species have greater FN breadths than extinct species was not supported. Indeed, FN breadth appears to be decoupled from geographic range size, with only the latter a significant predictor of extinction risk. By contrast, along
with geographic range size, the RN emerged as a key predictor of extinction risk, as did the degree of suitable area lost during the LGM. These results suggest that occupied environmental breadth (i.e., RN) provides a greater buffer against extinction than potential tolerance limits (i.e., the FN). In a way, this makes intuitive sense, although the pattern is counter to our original predictions. That is, the degree to which species are able to fill their FNs is what provides a measure of extinction risk.

Our results are congruent with previous studies that find evidence for a positive relationship between niche breadth and species' longevity (Kammer et al., 1997; Keller et al., 1997; Nürnberg \& Aberhan, 2013). Namely, most studies have analyzed RN dynamics using estimates derived from areas occupied by a species or genus. Taken together, these findings necessitate a reformulation of the argument that specialist species are more prone to extinction: being a generalist or specialist sensu stricto appears secondary to the unique historical, dispersal, and biotic constraints that dictate species' occupation of suitable environments at a particular time. Note that this argument, in and of itself, assumes species are often in disequilibrium with the environment (Araújo \& Pearson, 2005; Varela et al., 2009). Species' population dynamics and dispersal ability have been stressed previously as important to estimating extinction risk (Pulliam, 2000; Kotiaho et al., 2005; Anderson et al., 2009; Fordham et al., 2012; Fordham et al., 2013), as has the importance of biotic constraints (Davis et al., 1998; Araújo \& Luoto, 2007; Van der Putten et al., 2010).

Large geographic ranges have long been considered a factor promoting species' longevity, and our results provide additional support for this relationship (Jablonski \& Roy, 2003; Jablonski \& Hunt, 2006; Kiessling \& Aberhan, 2007; Liow, 2007; Payne \& Finnegan, 2007; Foote et al., 2008; Stigall, 2010; Harnik, 2011; Harnik et al., 2012). Geographic range is usually considered a buffer against extinction for three reasons. First, species with large geographic ranges are unlikely to experience environmental perturbations across their entire distributional area, and consequently will survive such disturbances, irrespective of their
tolerances. This argument is primarily geographic in nature. Conversely, a second argument equates large geographic range size with large environmental tolerances. The assumption is that generalist species will have enhanced survival, since environmental changes are unlikely to exceed their broad tolerance limits. This explanation, however, blurs the distinction between geographic area and environmental tolerance as the primary controller of extinction selectivity. Finally, species with larger geographic ranges are frequently assumed to be more abundant (Lawton et al., 1994). Since extinction ultimately occurs when a species’ population size is reduced to zero, abundance is often considered important in gauging extinction risk (Stanley, 1986b; Johnson, 1998; Purvis et al., 2000; Mace et al., 2008). However, geographic range size and abundance are not always positively related: rare species can be widespread and vice versa (Lavergne et al., 2004). Studies attempting to decouple abundance from geographic range size have found that local abundance has little effect on extinction risk, whereas geographic range size does (Kiessling \& Aberhan, 2007; Harnik et al., 2012; although see Stanley [1986b] and Powell [2007] for exceptions).

Certainly, species' geographic ranges are controlled by their RNs and, ultimately, by their FNs. Indeed, disentangling the effect of these variables is challenging (Barve et al., 2011; Harnik, 2011; Peterson et al., 2011; Nürnberg \& Aberhan, 2013). Still, the fact that we recovered a signal for RN breadth and geographic range size, and not for FN breadth, indicates there is some independence in these measures.

## Study considerations.

We focused on the impact of niche breadth and geographic range size on extinction patterns in Pliocene-recent Atlantic Coastal Plain mollusks. Nutrient declines, however, have often been implicated in biotic turnover in the region during this time, with the relative role of temperature and nutrient levels in producing extinction much debated (Stanley, 1986a; Vermeij, 1989; Allmon et al., 1993; Jackson et al., 1999; Roopnarine \& Beussink, 1999;

Allmon, 2001). Many have argued that declining nutrients disrupted species' habitat, which subsequently enhanced speciation and extinction post-mPWP. The formation of the Central American Isthmus around $\sim 3.5 \mathrm{Ma}$ was thought to precipitate these nutrient declines by changing oceanic circulation across the western Atlantic (Allmon, 2001). Although we found that both RN breadth and geographic range size are predictors of extinction risk, our results do not exclude nutrient decline as a significant factor in observed biotic turnover.

Mechanistically, our results warrant consideration in other respects. For instance, as with any paleontological or modern ENM analysis, sampling biases may lead to incorrect geographic range and niche breadth estimates. Our results, however, hold when more stringent rules for species' prevalence are enforced. Sampling biases may also skew the taxa included in our analysis. In other words, species with genuinely small FNs may not be detectable in the fossil record, potentially explaining why the FN was not recovered as a significant predictor of extinction risk. This argument is not particularly compelling here, though, given that we analyzed species with very small to very large geographic range sizes ( 644 to $691,023 \mathrm{~km}^{2}$ ) and niche volumes ( 40.6 to 560 and 14.7 to 192 for MVE and CPH calculations, respectively). Moreover, the frequency distribution for species' prevalence data is similar to those for extant taxa (Gaston, 1998; Gaston \& He, 2002), indicating our data are commensurate with neontological data, which are presumably biologically valid data sources (Fig. 3.2).

Age-area effects may plague analyses that consider geographic range size dynamics through time (Gaston, 1998; Myers et al., 2012; Jablonski et al., 2013), such that newer species have yet to achieve full distributional extent, and older species have artificially shrunken distributions. Neither of these scenarios, however, appears to bias analyses herein. First, origination times did not vary dramatically between species that are still extant and those that are now extinct. In other words, studied species originated anywhere from the Miocene to the Pliocene, irrespective of whether they are now extinct or still extant. Second,
species that went extinct primarily survived past the late Pliocene and early Pleistocene, indicating they were not 'already on their way out' during the mPWP.

In conclusion, our results provide a mechanism for assessing extinction risk, and highlight the importance of both RN breadth and geographic range size as extinction predictors. This information will be vital as we attempt to stem massive biodiversity losses predicted in the coming decades (Thomas et al., 2004; Tewksbury et al., 2008; Barnosky et al., 2011; Barnosky et al., 2012). Macroevolutionarily, the argument that specialist species have higher extinction (and origination) rates still holds (Vrba, 1987; Eldredge, 1989; McKinney, 1997; Nürnberg \& Aberhan, 2013), but must be tempered by additional factors, such as ease of dispersal to suitable environmental areas and biotic factors such as competition. We show that the FN does not impact extinction probabilities, which leads to additional consideration of the arguments presented by Myers and Saupe (2013). Relationships between the FN, RN, and geographic range size are complex, and a variety of data inputs, including ecological parameters pertaining to competition and dispersal abilities, may be required to produce a truly synthetic view of the factors driving macroevolutionary patterns. Of course, the results presented here come from a particular set of taxa and a particular geographic region during a climatically distinctive interval of geologic time, and additional data are required from other taxa and study systems to determine whether our results can be extrapolated more broadly.

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## Appendix S1.1

Appendix S1.1 (a) Maps of distributional data for each of 14 species of marine mollusks in the western Atlantic Ocean (Fig. S1.1.1-S1.1.4). (b) Results from RCP 2.6 (conservative) scenario of future change, including suitability maps (Figs S1.1.5-1.1.8), comparison of models to previously published distributional descriptions (Table S1.1.1), and cumulative potential suitable area lost and gained (Fig. S1.1.9). (c) Results from RCP $4.5 \& 8.5$ scenarios, with figures depicting latitudinal extent changes (Figs S1.1.10 \& S1.1.11), and cumulative potential suitable area lost and gained for these scenarios (Figs S1.1.12 \& S1.1.13). (d) Nomenclatural note on C. anabathrum.

## Appendix S1.1a. Species distributional data

Figure S1.1.1 Distributional data for Anomia simplex, Bulla occidentalis, Conus anabathrum and Conus spurius.


Figure S1.1.2 Distributional data for Crassostrea virginica, Crepidula fornicata, Dinocardium robustum and Lucina pensylvanica.


Figure S1.1.3 Distributional data for Melongena corona, Mercenaria campechiensis, Neverita duplicata and Oliva sayana.


Figure S1.1.4 Distributional data for Strombus alatus and Terebra dislocata.


## Appendix S1.1b. Niche modeling results for RCP 2.6

Figure S1.1.5 Niche modeling results for A. simplex, B. occidentalis, C. anabathrum and C. spurius. Four time slices are shown: present day (1991-2010) and three future projections (2021-2040, 2041-2060 and 2081-2100) from the most conservative scenario of future change (RCP 2.6). A threshold has been applied, allowing for a maximum of $5 \%$ omission error based on presence data.


Figure S1.1.6 Niche modeling results for C. virginica, C. fornicata, D. robustum and $L$. pensylvanica. Four time slices are shown: present day (1991-2010) and three future projections (2021-2040, 2041-2060 and 2081-2100) from the most conservative scenario of future change (RCP 2.6). A threshold has been applied, allowing for a maximum of $5 \%$ omission error based on presence data.


Figure S1.1.7 Niche modeling results for M. corona, M. campechiensis, N. duplicata and $O$. sayana. Four time slices are shown: present day (1991-2010) and three future projections (2021-2040, 2041-2060 and 2081-2100) from the most conservative scenario of future change (RCP 2.6). A threshold has been applied, allowing for a maximum of $5 \%$ omission error based on presence data.


Figure S1.1.8 Niche modeling results for S. alatus and T. dislocata. Four time slices are shown: present day (1991-2010) and three future projections (2021-2040, 2041-2060 and 2081-2100) from the most conservative scenario of future change (RCP 2.6). A threshold has been applied, allowing for a maximum of $5 \%$ omission error based on presence data.


Table S1.1.1 Comparison of models to previously published distributional descriptions. We included multiple descriptions only if they conflicted. Models are congruent if all areas occupied by a species are predicted as suitable. We were less concerned about areas predicted suitable but not thought to be occupied by species, as these regions may be habitable, but the species is prevented from occupying them due to biological or dispersal limitations.
Table S1.1.1: Part 1

\begin{tabular}{|c|c|c|c|c|c|c|}
\hline \& \& \& \& \& \multicolumn{2}{|l|}{Congruence} <br>
\hline Species \& Refs \& Previously published distribution* \& Depth (m) \& Zone \& Maxent \& GARP <br>
\hline \multicolumn{7}{|l|}{Bivalvia} <br>
\hline Anomia simplex \& [1]
[2]

$[3]$ \& $30.3^{\circ} \mathrm{N}$ to $20^{\circ} \mathrm{N} ; 90.5^{\circ} \mathrm{W}$ to $80^{\circ} \mathrm{W}$; USA: Florida: East Florida, West Florida, Florida Keys; Mexico: Campeche State, Yucatán State, Quintana Roo Eastern Canada to Florida, Bermuda, Bahamas, West Indies, Gulf of Mexico, Caribbean Central America, South America (to Argentina) Massachusetts to Florida, Texas; Brazil; Bermuda \& | $0-80 ;$ |
| :--- |
| live 1-11 | \& Temperate to tropical \& Congruent with 2nd \& 3rd references - may be missing suitability in Venezuela and Colombia, but references do not mention such areas \& Congruent with 2nd \& 3rd references - may be missing suitability in Venezuela and Colombia, but references do not mention such areas <br>

\hline Crassostrea virginica \& [1-5] \& $49^{\circ} \mathrm{N}$ to $18^{\circ} \mathrm{N} ; 88.11^{\circ} \mathrm{W}$ to $65^{\circ} \mathrm{W}$; naturally occurs in the Gulf of St Lawrence, Canada, along the Atlantic coast of the United States to the Gulf of Mexico to the Yucatán Peninsula, Mexico, and to the West Indies and the coast of Brazil \& $$
\begin{aligned}
& 0-79 ; \\
& \text { live } 0.3-9
\end{aligned}
$$ \& Temperate to tropical \& Congruent \& Congruent <br>

\hline Dinocardium robustum \& $$
[1,3]
$$

[2] \& | $37^{\circ} \mathrm{N}$ to $20^{\circ} \mathrm{N} ; 94^{\circ} \mathrm{W}$ to $77^{\circ} \mathrm{W}$; Virginia to Florida, Texas; Mexico |
| :--- |
| Maryland to Florida, West Indies, Gulf of Mexico, Caribbean Central America | \& \[

$$
\begin{aligned}
& 0-18 ; \\
& \text { live } 11
\end{aligned}
$$
\] \& Subtropical to tropical \& General congruence - may be missing suitable area in VA and/or MD \& General congruence - potentially missing suitable area in VA and/or MD <br>

\hline Lucina pensylvanica \& [1] \& $35^{\circ} \mathrm{N}$ to $9^{\circ} \mathrm{N} ; 91^{\circ} \mathrm{W}$ to $67^{\circ} \mathrm{W}$; USA: North Carolina, Florida: East Florida, West Florida, Florida Keys; Mexico: Alacran Reef, Quintana Roo; Honduras: Swan Island; Cuba: Holguín \& 0-3 \& Tropical \& Congruent with 1st ref. - may be missing suitable area in Carolinas \& Congruent <br>
\hline
\end{tabular}

Table S1.1.1: Part 2

| Species | Refs | Previously published distribution* | Depth (m) | Zone | Congruence |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | Maxent | GARP |
|  | [2] | Maryland to Florida, Bermuda, Bahamas, West Indies, Gulf of Mexico, Caribbean Central America, South America (Colombia) |  |  |  |  |
| Mercenaria campechiensis | $[1,3]$ $[4]$ $[2,6]$ | $39^{\circ} \mathrm{N}$ to $20^{\circ} \mathrm{N} ; 91^{\circ} \mathrm{W}$ to $76^{\circ} \mathrm{W}$; New Jersey to Florida, Texas; Cuba Chesapeake Bay to Florida, Texas and the Yucatán Peninsula to Cuba New Jersey to Gulf of Mexico, Caribbean Central America and the West Indies | $\begin{aligned} & 0-36 ; \\ & \text { live 3-6 } \end{aligned}$ | Subtropical to tropical | Not congruent model does not predict as far north as actual distribution (FL/ GA vs. NJ/Chesapeake Bay) | Not congruent model does not predict as far north as actual distribution (FL/GA vs. NJ/ Chesapeake Bay) |
| Gastropoda |  |  |  |  |  |  |
| Bulla occidentalis | $[3]$ $[1,7]$ | Texas, Louisiana, Florida, Cuba, Yucatán, Tabasco, Brazil <br> $34.5^{\circ} \mathrm{N}$ to $34^{\circ} \mathrm{S} ; 97.28^{\circ} \mathrm{W}$ to $0^{\circ} \mathrm{W}$; USA: Florida: <br> East Florida, West Florida; USA: Louisiana, Texas; Mexico: Veracruz, Tabasco, Campeche State, Cayos Arcas, Campeche, Yucatán State, Alacran Reef, Quintana Roo; Colombia: offshore islands; Costa Rica, Colombia, Venezuela: Falcón, Isla Margarita; Bermuda, Cuba: North Havana Province, North Matanzas, Camagüey, Holguín; Jamaica, Puerto Rico, Guadeloupe; St Vincent and the Grenadines: Mustique, Grenada; Barbados, Brazil: Maranhão, Ceará, Rio Grande do Norte, Pernambuco, Alagoas, Espírito Santo, Rio de Janeiro, São Paulo, Paraná, Santa Catarina, Rio Grande do Sul | 0-80; <br> live 0-15 | Tropical | Congruent, but predicts suitable area further north than realized distribution | Congruent, but predicts suitable area further north than realized distribution |
| Conus anabathrum | [1] | $35^{\circ} \mathrm{N}$ to $14.5^{\circ} \mathrm{N}$; $91^{\circ} \mathrm{W}$ to $61^{\circ} \mathrm{W}$; USA: Florida: West Florida; Mexico: Campeche State, Yucatán State, Alacran Reef, Quintana Roo | 0-122 | Tropical | Congruent with 1st reference | Congruent with 2nd reference |
|  | [3] | North Carolina, Florida, Texas |  |  |  |  |

Table S1.1.1: Part 3

|  |  |  |  |  | Congruence |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Species | Refs | Previously published distribution* | Depth (m) | Zone | Maxent | GARP |
| Conus spurius | [1] | $28^{\circ} \mathrm{N}$ to $9^{\circ} \mathrm{N} ; 94^{\circ} \mathrm{W}$ to $64.4^{\circ} \mathrm{W}$; USA: Florida: East Florida, West Florida, Florida Keys; Mexico: Campeche State, Yucatán State, Alacran Reef, Quintana Roo; Panama; Venezuela; Cuba: Havana Province <br> Florida, Texas, Gulf of Mexico | $\begin{aligned} & \text { 0-65; } \\ & \text { live 1-8 } \end{aligned}$ | Tropical | Congruent, but predicts suitable area further north than realized distribution | Congruent, but predicts suitable area further north than realized distribution |
| Crepidula fornicata | [1,3] | $48^{\circ} \mathrm{N}$ to $25^{\circ} \mathrm{N} ; 97.2^{\circ} \mathrm{W}$ to $25^{\circ} \mathrm{W}$; Canada to Florida, Texas and Louisiana | $\begin{aligned} & 0-70 ; \\ & \text { live } 0-49 \end{aligned}$ | Temperate to tropical | Congruent, but no mention of a Brazilian distribution | Congruent, but no mention of a Brazilian distribution |
| Melongena corona | [1,4,8] | $30.4^{\circ} \mathrm{N}$ to $24^{\circ} \mathrm{N} ; 87.7^{\circ} \mathrm{W}$ to $80.04^{\circ} \mathrm{W} ; 0-2 \mathrm{~m}$; USA: Florida: East Florida, West Florida, Florida Keys; USA: Louisiana, Texas; Mexico: Tamaulipas | $\begin{aligned} & 0-2 ; \\ & \text { live 0-1.2 } \end{aligned}$ | Tropical | Congruent | Congruent |
| Neverita duplicata | [1,3] | $42.5^{\circ} \mathrm{N}$ to $16^{\circ} \mathrm{N} ; 97.2^{\circ} \mathrm{W}$ to $70^{\circ} \mathrm{W}$; Cape Ann, MA, to Florida to Texas | $\begin{aligned} & 0-58 ; \\ & \text { live } 0-26 \end{aligned}$ | Temperate to tropical | Congruent, but no mention of a Brazilian distribution | Congruent, but no mention of a Brazilian distribution |
| Oliva sayana | [1,3] | $35.34^{\circ} \mathrm{N}$ to $18.7^{\circ} \mathrm{N} ; 97^{\circ} \mathrm{W}$ to $75.33^{\circ} \mathrm{W}$; N . Carolina to Florida to Texas, Gulf of Mexico, Brazil | $\begin{aligned} & 0-130 ; \\ & \text { live } 0-27 \end{aligned}$ | Tropical | Not congruent model does not predict as far north as actual distribution (FL vs. NC) | Congruent |

Table S1.1.1: Part 4

| Species | Refs | Previously published distribution* | Depth (m) | Zone | Congruence |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  |  |  | Maxent | GARP |
| Strombus alatus | [1,3] | $34.42^{\circ} \mathrm{N}$ to $18.7^{\circ} \mathrm{N} ; 97^{\circ} \mathrm{W}$ to $76.68^{\circ} \mathrm{W}$; USA: North Carolina, South Carolina, Florida: East Florida, West Florida; USA: Louisiana, Texas; Mexico: Campeche State, Cayo Arcas, Campeche, Yucatán State, Campeche Bank, Alacran Reef, Quintana Roo | $\begin{aligned} & \hline 0-183 ; \\ & \text { live } 0-46 \end{aligned}$ | Tropical | Not congruent model does not predict as far north as actual distribution (SC vs. NC | Congruent |
| Terebra dislocata | [1,3] | $38^{\circ} \mathrm{N}$ to $6^{\circ} \mathrm{S}$; $97^{\circ} \mathrm{W}$ to $37^{\circ} \mathrm{W}$; USA: Maryland, Virginia, North Carolina, South Carolina, Georgia, Florida: East Florida, West Florida; USA: Louisiana, Texas; Mexico: Campeche State, Yucatán State, Quintana Roo; Costa Rica, Colombia, Venezuela: Sucre, Isla Margarita; Jamaica, Puerto Rico, Brazil: Para, Rio Grande do Norte | $\begin{aligned} & 0-146 ; \\ & \text { live } 0-22 \end{aligned}$ | Subtropical to tropical | Congruent, with exception of potential missing areas in Colombia \& Venezuela | Congruent, with exception of potential missing areas in Colombia \& Venezuela |

[^2]$\begin{array}{ll} \\ 2 & \text { Mikkelsen, P.M. \& Bieler, R. (2008) Seashells of Southern Florida: living marine mollusks of the Florida Keys and adjacent regions: bivalves. Princeton } \\ \text { University Press, Princeton, NJ. } \\ 3 \text { Tunnell, J.W., Andrews, J., Barrera, N.C. \& Moretzsohn, F. (2010) Encyclopedia of Texas seashells: identification, ecology, distribution and history. Texas }\end{array}$
4 Smithsonian Marine Station (2011) Field guide to Indian River Lagoon. Smithsonian Marine Station at Fort Pierce, FA. Available at: http://www.sms.si.edu/IRLFieldGuide/index.htm.
5 Buroker, N.E. (1983) Population genetics of the American oyster Crassostrea virginica along the Atlantic coast and the Gulf of Mexico. Marine Biology,
6 Menzel, R.W. (1989) The biology, fishery and culture of quahog clams, Mercenaria. Clam mariculture in North America (ed. by J.J. Manzi and M. Castagna), pp. 201-242. Elsevier, Amsterdam.

Figure S1.1.9 Cumulative potential suitable area loss and gain over three time slices (20212040, 2041-2060 and 2081-2100) for the lowest-emission scenario of future change (RCP 2.6). Darker reds indicate higher potential suitable area loss or gain. Results are derived from binary model output and have been normalized based on present-day suitability.


## Appendix S1.1c. Results from RCP 4.5 and 8.5 scenarios

## Poleward range shifts.

Even under the higher-emission scenarios (RCP $4.5 \& 8.5$ ), there appear to be few genuine poleward range shifts (Figs S1.1.10 \& S1.1.11). For those species whose centroids are predicted to shift polewards (e.g. Conus anabathrum and Dinocardium robustum for RCP 4.5 or Anomia simplex, C. anabathrum, Crassostrea virginica and D. robustum for RCP 8.5), the shifts primarily occur due to overall reductions in suitable area - the reductions still transpire within the former absolute extent of suitability for the species. The average change in centroid position is 3.46 (MAXENT) and 4.14 (GARP) for RCP 4.5, and 4.37 (MAXENT) and 3.7 (GARP) for RCP 8.5 in an equatorward direction (Table 1.2). As with the RCP 2.6 scenario, predictions for species vary as to how the absolute extent and centroid position change, which emphasizes the idiosyncratic nature of predicted responses.

## Species-specific versus assemblage responses.

Declines in suitable area are predicted to be more severe under the RCP 4.5 and 8.5 scenarios than under RCP 2.6. Thus, even though the particulars of species' responses differ, and some species are predicted to retain or even gain suitable area under RCP 4.5 and 8.5 , the dominant signal is one of declining available suitable environmental conditions for marine mollusks. In RCP 4.5, 11 (MAXENT) or 14 (GARP) of the 14 species are predicted to undergo some degree of range contraction by the end of the century, whereas in RCP 8.5, 12 (MAXENT) and 14 (GARP) of the species are predicted to experience reductions in suitable area by the end of the century (Figs $1.4 \& 1.5$ ). When MAXENT without extrapolation is considered, all species experience declines by 2081-2100 under both RCP 4.5 and 8.5 . Of the species predicted to lose suitable area, average decline in 2081-2100 is $46.4 \%$ (MAXENT) and 64.5\% (GARP) for RCP 4.5, and 61.0\% (MAXENT) and $88.7 \%$ (GARP) for RCP 8.5. GARP predicts $99-100 \%$ declines in suitable area for half of the species considered (A. simplex, Conus anabathrum, Conus spurius, Dinocardium robustum, Lucina pensylvanica,

Mercenaria campechiensis and Strombus alatus) in 2081-2100 for RCP 8.5; MAXENT predicts similarly high losses for these species ( $>45 \%$ ), with the exception of C. spurius. The latter species, however, also loses significant suitable regions under the non-extrapolation iteration of MAXENT. Furthermore, when MAXENT extrapolation is deactivated, suitability in the RCP 8.5 2081-2100 projections resembles that predicted for the GARP models across all species. The two MAXENT iterations differ dramatically because we restricted the ability of MAXENT to extrapolate to conditions outside those in the training region and, potentially, to novel combinations of climate. As indicated by our environmental overlap analyses (see 'Environmental overlap' section of Appendix S1.3), RCP 8.5 2081-2100 projections contain pixels with almost entirely novel environmental combinations.

When patterns across all species are considered, losses of suitable conditions are expected across the entirety of the study region, but are concentrated from $20^{\circ} \mathrm{N}$ to $4^{\circ} \mathrm{S}$ (Figs S1.1.12 \& S1.1.13). The Yucatán Peninsula and the east coast of Florida exhibit the greatest change in suitable conditions through time. Local (to species-wide) extinctions in the RCP 4.5 and 8.5 scenarios are predicted to intensify through time (Figs S1.1.12 \& S1.1.13).

The only species predicted to gain, or at least not lose, suitable conditions through all time slices in RCP 4.5 are Bulla occidentalis, Crassostrea virginica and Conus spurius with Maxent (Figs 1.4 \& 1.5). In RCP 8.5, only B. occidentalis and C. virginica retain suitable area with MAXENT (Figs $1.4 \& 1.5$ ). GARP predicts increases in suitable area in the first time slice for C. virginica under both RCP 4.5 and RCP 8.5 , but suitable area for this species decreases in the remaining time slices. As discussed above, when re-running MAXENT models with extrapolation deactivated, the disparity between the MAXENT and GARP models diminishes, with MAXENT predicting declines in suitable area for all of the above species by the end of this century under both RCP 4.5 and RCP 8.5.

Gains in suitable area remain relatively constant (Figs S1.1.12 \& S1.1.13), regardless of the RCP scenario or time slice. Interestingly, these gains drop off in the 2081-2100 time
slice under GARP because of the dramatic declines in suitable area predicted for all species. Unlike the RCP 2.6 scenario, relatively little area is predicted to remain continuously suitable for the majority of species under RCP 4.5 and 8.5 scenarios. The average geographical area predicted as continuously suitable in all time slices is $52.3 \%$ (MAXENT) and $22.0 \%$ (GARP) for RCP 4.5, and $34.2 \%$ (MAXENT) and $8.0 \%$ (GARP) for RCP 8.5 (Table 1.3). The values are expressed as percentages of present-day suitable area.

Figure S1.1.10 Latitudinal extent (light shading) and change in centroid of suitable conditions (dark line) from the present (P) to each time slice (2021-2040, 2041-2060 and 2081-2100) for the RCP 4.5 scenario. Note that few species are predicted to undergo significant shifts in the centroid of their suitable conditions, with the absolute extent of suitable conditions fairly constant. Those species with centroids that are predicted to shift polewards (e.g. D. robustum) did so because of an overall reduction in suitable area, but the reduction occurs within the former absolute extent of suitability for the species.


Figure S1.1.11 Latitudinal extent (light shading) and change in centroid of suitable conditions (dark line) from the present (P) to each time slice (2021-2040, 2041-2060 and 2081-2100) for the RCP 8.5 scenario. There is more change in centroid position in this scenario, but the change occurs, for the most part, within the absolute bounds of suitability for these species. Note that, for species like $D$. robustum, the absolute range and centroid of suitable conditions are predicted to shift slightly northwards, whereas for species like T. dislocata, the absolute range and centroid of suitable conditions are predicted to shift slightly southwards. This variability highlights the idiosyncratic nature of predicted responses of these species to changing environment.


Figure S1.1.12 Cumulative potential suitable area loss and gain for the moderate-emission scenario of change (RCP 4.5). Darker reds indicate higher potential suitable area loss or gain. Results are derived from binary model output and have been normalized based on presentday suitability.


Figure S1.1.13 Cumulative potential suitable area loss and gain over three time slices (20212040, 2041-2060 and 2081-2100) for the extreme scenario of change (RCP 8.5). Darker reds indicate higher potential suitable area loss or gain. Results are derived from binary model output and have been normalized based on present-day suitability.


## Appendix S1.1d. Nomenclatural note: Conus anabathrum

Conus floridanus Gabb, 1869 is a junior synonym of Conus anabathrum Crosse,
1865. Nevertheless, most museum specimens of this taxon are identified as C. floridanus, and that is the name we used in our online database searches.

## Appendix S1.2

Appendix S1.2 Supporting information on environmental variables and their contributions to model development (Figure S1.2.1, Tables S1.2.1-1.2.3).

## Sensitivity testing of predictor variables

We examined whether the exclusion of bathymetry alters the conclusions of our modeling efforts; in other words, without bathymetry, are dramatic reductions in suitable area still obtained under future climate scenarios. As indicated by the 'no bathy' column in Table S1.2.1, reductions of suitable area are similar to those when bathymetry is included. However, without bathymetry, some species present a reverse trend from that with bathymetry. Notably, reverse patterns are predicted for Conus spurius, Crassostrea virginica and Bulla occidentalis. Conus spurius is projected to gain suitable area rather than lose suitable area under MaXent. The opposite is true for $C$. virginica, which is predicted to lose suitable area when bathymetry is omitted under both modeling algorithms, but gain suitable area when all variables are used. Under GARP, B. occidentalis is predicted to suffer declines in suitable area without bathymetry for RCP 2.6 , whereas this species is predicted to gain suitable area with bathymetry. The same situation is occasioned for the MAXENT RCP 8.5 scenario.

We also assessed whether the number of variables and correlation among them (see Fig. S1.2.1) artificially induced the declines in suitable area observed under future climate change scenarios. To do so, we modeled the species using a less correlated subset of the predictor variables (i.e. bathymetry, diatom phytoplankton concentration, nitrogen concentration, sea surface temperate and sea surface salinity). For most species, significant declines in suitable area are still obtained using the reduced variable set, although the losses are often less dramatic than when all variables are used (as, for example, for Conus anabathrum, Dinocardium robustum, Oliva sayana and Strombus alatus). The patterns diverge more for RCP 2.6 than for RCP 8.5. As with models run without bathymetry, Crassostrea virginica
loses, rather than gains, suitable area under both algorithms. Similarly, Conus spurius gains rather than loses suitable area using GARP (for RCP 2.6) and MAXENT (for RCP 8.6).

These analyses suggest that the results for Conus spurius and Crassostrea virginica may be more dependent on variable selection, and that gain and loss in suitable area, respectively, are likely for these species when a reduced variable set is used and when bathymetry is excluded.

Figure S1.2.1 Pearson correlation of the environmental variables used in this study, performed with the 'cor' function in R.

| Species | RCP | Maxent |  |  |  |  |  |  |  |  | GARP |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 2021-2040 |  |  | 2041-2060 |  |  | 2081-2100 |  |  | 2021-2040 |  |  | 2041-2060 |  |  | 2081-2100 |  |  |
|  |  | All | No bathy | Red. | All | $\begin{aligned} & \text { No } \\ & \text { bathy } \end{aligned}$ | Red. | All | No bathy | Red. | All | No bathy | Red. | All | No <br> bathy | Red. | All | $\begin{aligned} & \text { No } \\ & \text { bathy } \end{aligned}$ | Red. |
| Bivalvia |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Anomia simplex | 2.6 | -40.1 | -35.1 | -30.3 | -44.7 | -37.9 | -35.2 | -32.5 | -34.8 | -29.7 | -30.3 | -43.9 | -14.0 | -29.2 | -48.1 | -14.0 | -24.7 | -44.4 | -11.7 |
|  | 8.5 | -41.8 | -27.3 | -32.4 | -41.4 | -49.4 | -49.4 | -73.8 | -76.0 | -78.2 | -42.1 | -57.0 | -16.1 | -73.0 | -88.9 | -20.7 | -98.9 | -100.0 | -48.5 |
| Crassostrea virginica | 2.6 | 1.6 | -29.2 | -6.5 | 5.3 | -15.6 | -13.9 | 2.0 | -11.9 | -14.7 | 12.4 | -5.2 | -8.2 | 16.3 | -8.1 | -8.2 | 17.9 | -7.1 | -2.7 |
|  | 8.5 | 12.2 | -17.2 | -6.1 | 22.3 | -26.6 | -23.7 | 9.6 | -51.2 | -33.5 | 7.8 | -13.5 | -10.9 | -26.1 | -12.4 | -16.4 | -78.5 | -54.3 | -49.2 |
| Dinocardium | 2.6 | -38.0 | -45.3 | -1.9 | -49.1 | -55.2 | -1.9 | -44.2 | -57.2 | 5.7 | -43.6 | -43.0 | -4.3 | -63.8 | -53.0 | -8.6 | -65.1 | -53.5 | -9.9 |
| robustum | 8.5 | -47.9 | -56.7 | -4.8 | -77.9 | -63.3 | -12.4 | -87.1 | -62.9 | 1.0 | -75.2 | -79.3 | -13.7 | -94.0 | -97.7 | -30.5 | -98.7 | -100.0 | -51.1 |
| Lucina | 2.6 | -5.4 | -0.1 | -6.2 | -0.5 | -11.3 | -1.4 | 0.0 | -15.3 | 2.0 | -21.9 | -25.5 | -30.3 | -27.5 | -32.5 | -34.5 | -29.5 | -32.0 | -34.1 |
| pensylvanica | 8.5 | -5.1 | -14.1 | -7.6 | -11.3 | -23.3 | -16.7 | -57.9 | -46.2 | -69.2 | -59.0 | -58.8 | -39.8 | -86.1 | -86.3 | -59.8 | -100.0 | -99.2 | -83.0 |
| Mercenaria | 2.6 | -35.2 | -23.0 | -26.8 | -42.9 | -37.4 | -29.1 | -44.0 | -32.5 | -25.2 | -66.7 | -66.9 | -23.7 | -66.7 | -73.3 | -26.3 | -58.5 | -63.2 | -27.0 |
| campechiensis | 8.5 | -40.7 | -27.1 | -29.9 | -57.1 | -44.3 | -48.0 | -84.6 | -63.4 | -78.7 | -87.8 | -92.3 | -30.3 | -92.5 | -99.3 | -35.5 | -99.3 | -100.0 | -52.6 |
| Gastropoda |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Bulla | 2.6 | 10.3 | 1.8 | 6.2 | 18.1 | 4.0 | 15.9 | 25.8 | 8.6 | 21.3 | 10.5 | -19.2 | 6.0 | 17.1 | -26.7 | 6.0 | 16.7 | -20.8 | 10.3 |
| occidentalis | 8.5 | 5.9 | -3.8 | 5.3 | 19.3 | -28.8 | 16.8 | 36.8 | -17.7 | 21.8 | -8.9 | -63.0 | -5.4 | -17.3 | -93.9 | -1.0 | -77.8 | -100.0 | -8.5 |
| Conus | 2.6 | -12.7 | -10.6 | -5.0 | -18.8 | -25.9 | -7.6 | -25.4 | -27.3 | -2.5 | -52.6 | -46.5 | -3.5 | -68.4 | -55.5 | -6.0 | -59.1 | -54.5 | -8.5 |
| anabathrum | 8.5 | -13.5 | -13.7 | -9.2 | -28.1 | -29.8 | -6.7 | -45.4 | -26.1 | -38.7 | -73.7 | -72.9 | -8.5 | -97.1 | -92.3 | -16.5 | -100.0 | -97.2 | -61.0 |
| Conus spurius | 2.6 | -1.6 | -7.9 | 2.8 | -1.8 | -14.0 | 4.3 | 4.2 | -10.7 | 13.3 | -8.6 | -18.6 | 7.2 | -17.7 | -29.2 | 12.0 | -12.0 | -26.6 | 15.1 |
|  | 8.5 | -10.8 | -15.0 | -2.5 | -3.8 | -17.5 | 6.8 | -8.2 | -6.7 | 22.3 | -45.0 | -49.0 | -7.2 | -90.2 | -84.0 | -10.8 | -100.0 | -100.0 | -36.1 |
| Crepidula | 2.6 | -14.7 | -7.8 | -11.3 | -25.4 | -12.6 | -16.5 | -22.0 | -9.2 | -15.2 | -2.5 | -24.4 | 0.3 | -10.8 | -33.8 | 0.7 | -11.7 | -32.1 | 0.0 |
| fornicata | 8.5 | -19.9 | -9.4 | -15.9 | -37.9 | -14.9 | -32.9 | -53.5 | -36.6 | -41.8 | -21.1 | -38.7 | -4.7 | -40.0 | -53.7 | -4.4 | -70.3 | -66.8 | -34.9 |
| Melongena | 2.6 | -17.3 | -18.7 | -17.5 | -11.5 | -29.1 | -21.1 | -7.7 | -46.9 | -12.3 | -12.1 | -50.0 | -25.2 | -36.3 | -54.7 | -31.0 | -39.6 | -47.0 | -28.4 |
| corona | 8.5 | -19.2 | -28.8 | -28.1 | -46.2 | -37.1 | -47.4 | -65.4 | -72.7 | -73.7 | -28.6 | -95.7 | -34.2 | -74.7 | -99.1 | -41.9 | -93.4 | -100.0 | -68.4 |
| Neverita | 2.6 | -22.8 | -30.6 | -17.5 | -29.1 | -33.3 | -26.5 | -29.6 | -32.3 | -29.8 | -5.1 | -26.7 | -3.8 | -4.7 | -30.7 | -3.1 | -9.4 | -33.5 | -2.7 |
| duplicata | 8.5 | -22.8 | -30.3 | -19.9 | -35.4 | -37.7 | -44.4 | -55.8 | -51.5 | -76.2 | -4.7 | -38.5 | -4.6 | -15.2 | -57.4 | -22.1 | -54.2 | -83.9 | -69.1 |
| Oliva sayana | 2.6 | -32.4 | -57.9 | -14.5 | -37.2 | -67.7 | -15.6 | -32.4 | -60.2 | -9.7 | -36.2 | -55.9 | -7.0 | -41.8 | -65.0 | -5.6 | -46.3 | -61.7 | -4.8 |
|  | 8.5 | -31.1 | -68.3 | -15.1 | -49.3 | -90.9 | -46.8 | -70.3 | -99.8 | -56.5 | -42.9 | -88.7 | -12.6 | -68.9 | -99.5 | -19.3 | -80.2 | -100.0 | -59.6 |
| Strombus alatus | 2.6 | -20.7 | -16.0 | -11.7 | -32.5 | -28.9 | -13.1 | -31.4 | -29.6 | -1.7 | -23.2 | -54.9 | -24.9 | -45.3 | -65.8 | -29.1 | -48.1 | -61.8 | -25.4 |
|  | 8.5 | -25.5 | -24.0 | -14.4 | -45.8 | -34.1 | -23.7 | -45.0 | -24.6 | -33.7 | -64.1 | -92.8 | -46.6 | -80.7 | -99.6 | -66.7 | -100.0 | -100.0 | -83.6 |
| Terebra | 2.6 | -47.3 | -34.2 | -50.8 | -47.8 | -39.2 | -54.2 | -46.7 | -33.4 | -55.4 | -56.8 | -58.6 | -36.4 | -65.9 | -67.6 | -43.6 | -56.8 | -62.0 | -46.7 |
| dislocata | 8.5 | -49.5 | -39.9 | -52.9 | -60.3 | -48.7 | -63.3 | -85.3 | -58.7 | -82.1 | -65.9 | -85.2 | -41.2 | -75.0 | -99.4 | -64.8 | -90.9 | -100.0 | -91.5 |


| Species/layer | Alkal. |  | DIC |  | D phyt. |  | ND phyt, |  | Nitrogen |  | sss |  | SST |  | Zoopl. |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | $\begin{gathered} \text { Pres. } \\ \Delta \end{gathered}$ | Fut. | Pres. $\Delta$ | $\begin{gathered} \text { Fut. } \\ \Delta \end{gathered}$ | Pres. $\Delta$ | Fut. | Pres. <br> $\Delta$ | $\begin{gathered} \text { Fut. } \\ \Delta \end{gathered}$ | $\begin{gathered} \text { Pres. } \\ \Delta \end{gathered}$ | $\underset{\Delta}{\text { Fut. }}$ | Pres. $\Delta$ | Fut. | Pres. $\Delta$ | Fut. | Pres. $\Delta$ | $\underset{\Delta}{\text { Fut. }}$ |
| Bivalvia |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| A. simplex | -9.0 | 2.3 | 12.1 | -11.6 | 23.0 | -17.9 | -17.2 | 4.1 | 21.1 | -12.1 | -17.2 | 26.6 | -28.5 | 20.8 | -16.0 | 36.4 |
| C. virginica | 0.0 | 0.0 | 29.0 | -25.3 | 12.9 | -10.0 | 12.9 | -5.3 | 18.8 | -19.0 | -20.4 | 27.9 | -24.7 | 40.5 | -19.4 | 23.2 |
| D. robustum | 0.0 | 0.0 | -42.1 | 85.9 | 3.9 | -8.2 | -37.5 | 61.2 | 29.6 | -30.6 | 3.9 | -14.1 | -21.1 | 42.4 | 11.8 | -12.9 |
| L. pensylvanica | 0.0 | 0.0 | 3.4 | -6.0 | 0.0 | 0.0 | -5.7 | 6.0 | 13.9 | -20.3 | -5.7 | 7.7 | -10.8 | 18.1 | 2.6 | -7.5 |
| M. campechiensis | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | -57.1 | 84.8 | 10.7 | -21.7 | -3.6 | 2.2 | -29.8 | 34.8 | 15.5 | -19.6 |
| Gastropoda |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| B. occidentalis | 7.8 | -5.2 | 0.0 | 0.0 | 2.1 | -1.9 | -12.6 | 13.9 | 28.1 | -22.7 | 0.3 | 1.0 | -1.3 | 2.8 | 4.6 | -3.8 |
| C. anabathrum | 0.0 | 0.0 | 0.0 | 0.0 | 2.9 | -19.1 | -74.7 | 94.9 | 10.2 | -26.4 | -0.8 | -0.6 | -5.3 | 7.3 | 17.1 | -57.3 |
| C. spurius | -5.1 | 7.6 | 0.0 | 0.0 | 0.2 | 1.0 | -12.6 | 12.5 | 26.9 | -29.2 | 6.2 | -5.1 | -6.0 | 6.3 | 0.0 | 0.0 |
| C. fornicata | -7.0 | 10.2 | 0.0 | 0.0 | 5.5 | -14.7 | -21.8 | 24.5 | 23.3 | -38.9 | -1.5 | 1.9 | -22.1 | 31.3 | 0.0 | 0.0 |
| M. corona | -6.3 | 15.6 | 0.0 | 0.0 | 0.0 | 0.0 | -52.1 | 77.8 | 97.9 | -64.4 | 4.2 | -11.1 | -18.8 | 37.8 | 0.0 | 0.0 |
| N. duplicata | 0.0 | 0.5 | 0.0 | 0.5 | 1.7 | -4.7 | -10.6 | 13.1 | 3.4 | 0.5 | -13.0 | 17.8 | -7.5 | 8.4 | 2.4 | -7.5 |
| O. sayana | -38.0 | 59.8 | 0.0 | 0.0 | 0.0 | 0.0 | -8.8 | 14.1 | 9.5 | -13.0 | 0.0 | 2.2 | -29.2 | 50.0 | 38.7 | -31.5 |
| S. alatus | 0.0 | 0.0 | 2.4 | -4.1 | 0.0 | 0.0 | -17.8 | 30.6 | 11.5 | -27.2 | -7.9 | 14.5 | -26.1 | 39.3 | 2.8 | -10.4 |
| T. dislocata | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | -12.1 | 3.2 | 4.6 | -5.3 | -26.0 | 9.6 | -46.2 | 47.9 | 12.7 | -100 |

[^3]Table S1.2.3 Percentage contribution of each environmental variable to the MAXENT model. Alkal., total alkalinity; bathy., bathymetry; DIC, dissolved inorganic carbon; D phyt., diatom phytoplankton concentration; ND phyt., non-diatom phytoplankton concentration; SSS, sea surface salinity; SST, sea surface temperature; zoopl., zooplankton concentration.

| Species/variable | Bathy. | Alkal. | DIC | D phyt. | ND phyt. | Nitrogen | SSS | SST | Zoopl. |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Bivalvia |  |  |  |  |  |  |  |  |  |
| A. simplex | 56.9 | 0.2 | 7.5 | 3.0 | 2.7 | 6.6 | 4.7 | 9.3 | 9.0 |
| C. virginica | 72.1 | 0.0 | 0.4 | 0.2 | 0.2 | 10.7 | 2.6 | 12.4 | 1.5 |
| D. robustum | 66.2 | 0.4 | 0.5 | 1.4 | 2.9 | 10.8 | 9.3 | 4.1 | 4.4 |
| L. pensylvanica | 64.2 | 0.0 | 0.0 | 0.0 | 0.6 | 6.7 | 8.8 | 3.5 | 16.1 |
| M. campechiensis | 70.6 | 0.0 | 0.0 | 0.0 | 2.0 | 10.1 | 3.8 | 6.5 | 7.1 |
| Gastropoda |  |  |  |  |  |  |  |  |  |
| B. occidentalis | 60.9 | 0.6 | 14.7 | 1.7 | 2.4 | 15.1 | 0.5 | 0.2 | 3.8 |
| C. anabathrum | 54.8 | 5.4 | 0.0 | 0.5 | 7.9 | 15.3 | 0.6 | 1.1 | 14.4 |
| C. spurius | 68.6 | 0.9 | 11.5 | 0.1 | 2.7 | 8.8 | 4.8 | 2.6 | 0.0 |
| C. fornicata | 65.6 | 0.5 | 0.0 | 0.2 | 4.3 | 8.4 | 4.9 | 16.2 | 0.0 |
| M. corona | 66.3 | 0.3 | 0.0 | 0.0 | 5.6 | 13.9 | 11.1 | 2.8 | 0.2 |
| N. duplicata | 75.7 | 0.0 | 0.0 | 0.3 | 6.0 | 2.0 | 11.4 | 4.5 | 0.0 |
| O. sayana | 75.5 | 1.5 | 3.7 | 0.0 | 0.1 | 6.6 | 5.5 | 4.0 | 3.1 |
| S. alatus | 57.5 | 0.0 | 1.0 | 0.0 | 2.4 | 9.8 | 19.3 | 7.2 | 2.7 |
| T. dislocata | 58.9 | 0.0 | 0.0 | 2.5 | 3.6 | 5.7 | 12.1 | 15.3 | 1.9 |

## Appendix S1.3

Appendix S1.3 Supporting information for model extrapolation analyses: (a) mobility-oriented parity surfaces (Fig S1.3.1, Table S1.3.1); and (b) environmental overlap analyses (Fig S1.3.2).

## Appendix S1.3a. Mobility-oriented parity surfaces (MOP)

MOP consistently identifies the mid-Atlantic and the south-west corner of the projection region (Pacific Ocean) as containing values outside those in the calibration region. Interestingly, these areas are also predicted to be suitable in many of our models (Table S1.3.1), a case of algorithm extrapolation, and this suitability is likely an artefact of unrealistic model response curves. Out-of-range environments also occur off the coast of Brazil, near Rio de Janeiro, for both the present-day and future projections - a region deemed suitable for many of our species such that predictions in these areas should be treated with appropriate caution. The northern reaches of our study region contain values for environmental variables outside those of the calibration region for most species analyzed. Suitable area for these species, however, do not overlap with the masked regions, with the exception of a few pixels for Anomia simplex d'Orbigny, 1853, Conus spurius Gmelin, 1791 and Dinocardium robustum Lightfoot, 1786 (Table S1.3.1) - too few to affect our conclusions. These out-of-range values do not limit suitability in a northward direction, however, because a buffer (area of non-suitability) exists between predicted suitable area and the out-of-range environmental space for most species.

Figure S1.3.1 MOP values for all species comparing the training-region environment with the present-day projection (top) and the RCP 8.5 emission scenario 2081-2100 time slice (bottom). Comparisons are made using the environmentally-closest $5 \%$ of pixels in the training region to a given pixel in the projection region. Values close to one (greens to blues) indicate high environmental dissimilarity, whereas values close to zero (orange to brown) indicate high environmental similarity. Note that the present-day and future projections are scaled independently of each other. See Table S1.3.1 for species names.


Table S1.3.1 Indication of model extrapolation in specified regions. Crosses indicate cases where the model predicts suitable area in that region, but the area also contains values for environmental variables that are outside those found in the training region. For most species, only a few suitable pixels are implicated in the respective regions.

| Species | Present |  |  | (RCP 8.5) 2081-2100 |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | SW <br> Pacific | mid- <br> Atlantic | Brazilian coast | SW <br> Pacific | mid- <br> Atlantic | Brazilian coast |
| Bivalvia |  |  |  |  |  |  |
| Anomia simplex | $\times$ |  | $\times$ |  |  |  |
| Crassostrea virginica |  |  | $\times$ |  |  | $\times$ |
| Dinocardium robustum |  | $\times$ | $\times$ |  | $\times$ | $\times$ |
| Lucina pensylvanica | $\times$ |  | $\times$ | $\times$ | $\times$ | $\times$ |
| Mercenaria campechiensis |  |  |  |  |  |  |
| Gastropoda |  |  |  |  |  |  |
| Bulla occidentalis | $\times$ |  | $\times$ | $\times$ | $\times$ | $\times$ |
| Conus anabathrum |  |  |  |  |  |  |
| Conus spurius | $\times$ |  | $\times$ | $\times$ | $\times$ | $\times$ |
| Crepidula fornicata |  | $\times$ | $\times$ |  | $\times$ | $\times$ |
| Melongena corona |  |  | $\times$ |  |  |  |
| Neverita duplicata |  |  | $\times$ |  |  |  |
| Oliva sayana |  | $\times$ | $\times$ |  |  | $\times$ |
| Strombus alatus | $\times$ | $\times$ | $\times$ | $\times$ | $\times$ |  |
| Terebra dislocata |  |  | $\times$ |  |  |  |

## Appendix S1.3b. Environmental overlap masks

Results from these analyses indicate present-day projections are largely unaffected by novel combinations of environmental parameters, with the exception of the areas outside the ranges of values altogether (MOP) (e.g., the region off the coast of Brazil). Conversely, future time slices possess a large number of pixels with novel environmental combinations (Figs S1.3.2). As expected, the RCP 8.5 2081-2100 time slice contains the greatest number of novel climatic combinations, with virtually no expected analogue pixels. The absence of analogue pixels compared to the present-day calibration region is somewhat surprising; however, the
extreme nature of this climate change scenario should also be considered. GARP predicts virtually no suitable area for the majority of species under the RCP 8.5 2081-2100 time slice, whereas MAXENT typically predicts at least some suitable areas. The two algorithms diverge most dramatically in this scenario and time slice, which can be explained in part by the nonanalogue climatic conditions. This discrepancy diminishes under MAXENT without extrapolation, as the model truncates suitability at the edge of known environmental values (or, potentially, combinations of pixels) like GARP.

Figure S1.3.2 Environmental overlap masks for all species for present-day and RCP 2.6 and RCP 8.5 2081-2100 time slices. Blue indicates analogous environmental combinations, whereas purple indicates novel environmental combinations. Note that the RCP 8.5 2081-2100 time slice contains virtually no analogous environment, meaning that future combinations of variables all differ from those in the present-day training region (although the values are not necessarily outside the range of values within the training region). See Table S1.3.1 for species names.


## Appendix S2.1

Appendix S2.1 Supporting information on model results and distributional data (Figures S2.1.1S2.1.5, Tables S2.1.1-2.1.2).

Figure S2.1.1 Ecological niche models for the present, LIG, and mPWP time slices for Bulla occidentalis, Crassostrea virginica, Crepidula fornicata, and Dinocardium robustum. Binary and continuous predictions are presented, with binary predictions thresholded using the mean suitability value from the continuous output. For the binary predictions, yellow=suitable and dark blue=unsuitable, whereas for the continuous predictions, darker grays indicate higher suitability.


Figure S2.1.2 Ecological niche models for the present, LIG, and mPWP time slices for Lucina pensylvanica, Mercenaria campechiensis, Neverita duplicata, and Terebra dislocata. Binary and continuous predictions are presented, with binary predictions thresholded using the mean suitability value from the continuous output. For the binary predictions, yellow=suitable and dark blue=unsuitable, whereas for the continuous predictions, darker grays indicate higher suitability.


Figure S2.1.3 Distributional data for Anomia simplex, Bulla occidentalis, Crassostrea virginica and Crepidula fornicata for the three time slices: mid-Pliocene Warm Period (mPWP; ~3.1 Ma), Last Interglacial (LIG; $\sim 130 \mathrm{Ka}$ ), and present-day (PI).


Figure S2.1.4 Distributional data for Dinocardium robustum, Lucina pensylvanica, Mercenaria campechiensis and Neverita duplicata the three time slices: mid-Pliocene Warm Period (mPWP; $\sim 3.1 \mathrm{Ma}$ ), Last Interglacial (LIG; ~130 Ka), and present-day (PI).


Figure S2.1.5 Distributional data for Oliva sayana and Terebra dislocata for the three time slices: mid-Pliocene Warm Period (mPWP; $\sim 3.1 \mathrm{Ma}$ ), Last Interglacial (LIG; $\sim 130 \mathrm{Ka}$ ), and present-day (PI).


Table S2.1.1 Data on climatic preference and larval strategy for the species analyzed.
Distributional data are shown for each time slice: mid-Pliocene Warm Period (mPWP; ~3.1 Ma), Last Interglacial (LIG; ~130 Ka), and present-day (PI). The "all" column indicates the total number of distributional records for each time slice/species, and the "unique" column specifies the spatially explicit distributional records used for modeling.

| Species |  | Climatic Zone | Larval Strategy | Distributional Data |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | mPWP |  | LIG |  |  | PI <br> Unique |
|  |  | All |  | Unique | All | Unique |  | All |
|  |  |  | Temperate-Tropical | Planktonic | 219 | 13 | 85 | 15 | 96 | 31 |
|  |  | Temperate-Tropical | Planktonic | 42 | 7 | 24 | 10 | 62 | 37 |
|  |  | Subtropical-Tropical | Planktonic | 59 | 7 | 46 | 11 | 74 | 22 |
|  |  | Tropical | Benthic | 127 | 7 | 29 | 8 | 79 | 37 |
|  |  | Subtropical-Tropical | Planktonic | 198 | 14 | 94 | 12 | 70 | 24 |
|  |  | Tropical | Planktonic | 82 | 6 | 60 | 9 | 191 | 58 |
|  |  | Temperate-Tropical | Planktonic | 157 | 16 | 31 | 10 | 103 | 42 |
|  |  | Temperate-Tropical | Planktonic | 134 | 16 | 54 | 14 | 88 | 28 |
|  |  | Tropical | Planktonic | 76 | 9 | 28 | 8 | 81 | 25 |
|  |  | Subtropical-Tropical | Benthic | 58 | 9 | 37 | 13 | 89 | 20 |

Table S2.1.2 Model evaluation results. P-values were obtained with the jackknife procedure of (Pearson et al., 2007) for time slices/species that had $<25$ occurrence points (single rows), and with the partial Receiver Operating Characteristic Analysis (Peterson et al., 2008) for time slices/species that had $>25$ occurrence points. All models were statistically significant.


## Appendix S2.2

Appendix S2.2 Supporting information on Neogene stratigraphy of the Atlantic Coastal Plain, with correlational chart (Figure S2.2.1) and table on Pliocene to recent geological units (Tables S2.2.1-2.2.2).

The Neogene stratigraphy of the Atlantic Coastal Plain is complex. Although numerous papers have been published on the subject, different stratigraphers have proposed quite different stratigraphic relationships. Part of the confusion stems from how these stratigraphers have diagnosed and applied terminology to the stratigraphic units (e.g., whether they did so based on morphology/elevation, lithology or biostratigraphy). Additional confusion can arise because geologic names have been applied to stratigraphic units and later expanded to terraces and vice versa (Colquhoun et al., 1968). Moreover, in many instances, we simply lack reliable age constraints and knowledge of the geological relationships of the region, and many more years of detailed study are needed to elucidate the stratigraphic framework of the Neogene Atlantic Coastal Plain.

Here, we attempt to provide an up-to-date compilation on Pliocene-recent stratigraphy of the Atlantic Coastal Plain. These data have been compiled from extensive literature review and detailed discussions with stratigraphers. We stress that they in no way represent a consensus opinion on the Pliocene-recent stratigraphy of the Atlantic Coastal Plain. The chart is provided as a schematic only, and is not intended to relate information regarding unconformities, hiatuses, or facies. Note that, when possible, we used the updated Berggren zonations from Wade et al. (2011). The " $\sim$ " indicates that the age range is approximate and was determined from stratigraphic position or from the ages of associated units. I hope that this stratigraphic chart and
table provide a useful reference for those working on Pliocene-recent material from the Atlantic Coastal Plain.

Table 2.2.1 Table of viable formations used for the mPWP and LIG time slices in this study.

| mPWP (~3.1 Ma) Formations | LIG (~130 Ka) Formations |  |
| :--- | :--- | :--- |
|  |  |  |
| Duplin | Anastasia | Norfolk |
| Goose Greek | Canepatch | Pamlico |
| Guaiguaza | Coffee Mill Hammock | Satilla |
| Hopegate | Croatan | Socastee |
| Intracoastal | Falmouth | Tabb |
| Jackson Bluff | Flanner Beach | Wando |
| Mare | Fort Thompson |  |
| Raysor | Ironshore |  |
| Tamiami/Pinecrest | Jaimanitas |  |
| Yorktown | Neuse |  |
|  |  |  |

Table of viable formations used for the mPWP and LIG time
slices in this study.


Figure 2.2.1 Correlational chart of Pliocene to recent geological units of the Atlantic Coastal Plain.
Table S2.2.2: Part 1. Northwest Florida

| Region | Formation | Member | Unit | $\begin{array}{\|l} \hline \begin{array}{l} \text { Age } \\ \text { (Ma) } \end{array} \\ \hline \end{array}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Qu |  |  | <0.135 | The Prairie Frm (135-60 Ka) (Mateo 2005; Otvos 2005, 2009; Shen et al 2008); Biloxi Frm ( $132-116 \mathrm{Ka}$ ) (Otvos 2005, 2009, 2013); and Gulfport Frm (132-118 Ka) (Otvos 2013) are not valid formations according to the Florida Geological Survey (Means, pers comm 2013). These formations were based on elevation and not named following stratigraphic guidelines. According to Otvos (1992), the Prairie Frm deposits interfinger with transgressive Biloxi units; they cover Biloxi deposits and the landward flank of the Gulfport Belt. According to Otvos (2009, 2013), the Biloxi is partially correlated with the above-lying Gulfport Frm. Kolbe et al (2011) cite these as present in NW Florida. Huddlestun (pers comm 2013) also indicated the Biloxi Frm of Otvos is present in the coastal area as far east as St. George Island and is in the same stratigraphic position as the Satilla Frm of GA. |  |  |  |  |  |
|  | Miccosukee |  |  | -3.3-2.6 | Cooke and Mossom (1929); Otvos (1998) | Found in E and Citronelle to W; Miccosukee Frm is more clayey; the transition between these two units occurs around central Gladson County (Means, pers comm 2013); unit could be a member or facies of the Citronelle Frm. Huddlestun (pers comm 2013) indicated he has no reasonable evidence that the Citronelle, Miccosukee, and Jackson Bluff Frms are anything but lithofacies of one depositional event: the Citronelle/Miccosukee Frms are a shore/shoreface deposit or lithofacies, whereas the Jackson Bluff Frm is an offshore, shelf bottom deposit or lithofacies. The Intracoastal Frm represents a farther offshore deposit or lithofacies, where only minor siliciclastics are present but may dominate in some beds (the siliciclastics having been deposited closer to shore). | Age is uncertain, as deposit is fairly unfossiliferous; age range is thus an estimate and inferred from stratigraphic position; Kolbe et al (2011) indicated a slightly younger age for both the Citronelle and Miccosukee Frms (2.4-1.7 Ma). | Considered time-equivalent of Cypresshead Frm (GA) and correlated in part with Nashua Frm in NE Florida (Huddlestun 1988); time equivalent with Citronelle Frm (Rupert 1990; Otvos 1988, 1998); Huddlestun (pers comm 2013) indicated Miccosukee, Citronelle, Jackson Bluff, Cypresshead and Intracoastal Frms are time equivalents. | Note that in this compilation, the Miccosukee Frm is only partially correlated with the Cypresshead Frm. |  |
|  | Citronelle |  |  | *3.3-2.6* | Stringfield and LaMoreaux (1957); Huddlestun (1988); Otvos (1988); Means (2009) | Citronelle found only in the uplands from S GA to TX (Otvos 1995, 2004). There is a questionable, thin bed that may be younger and perhaps eolian atop the Citronelle Frm. Huddlestun (pers comm 2013) indicated he has no reasonable evidence that the Citronelle, Miccosukee, and Jackson Bluff Frms are anything but lithofacies of one depositional event: the Citronelle/Miccosukee Frms are a shore/shoreface deposit or lithofacies, whereas the Jackson Bluff Frm is an offshore, shelf bottom deposit or lithofacies. The Intracoastal Frm represents a farther offshore deposit or lithofacies, where only minor siliciclastics are present but may dominate in some beds (the siliciclastics having been deposited closer to shore). Otvos (1992) indicated that in the western panhandle of FL and southern AL, the unit unconformably overlies the Perdido Key Frm, but this formation is not recognized by the Florida Geological Survey (Means, pers comm 2013). Means (pers comm 2013) indicated that in the central FL panhandle, the unit unconformably overlies the Jackson Bluff Frm; however, Huddlestun (pers comm 2013) indicated the Citronelle and Jackson Bluff Frms are timeequivalent. | *Age range is an estimate. Age of the Citronelle Frm has been debated for years because of the lack of index fossils and has been variously assigned to the Miocene, Pliocene or Pleistocene (Rupert 1990): see Means (2009) for a review. Authors cited within the "supporting references" section all indicate a Pliocene age. Means (2009) indicated the age is no later than Late Pliocene, but this was before the PlioPleistocene boundary change. Markewich et al (1992) and Kolbe et al (2011) cited a slightly younger age ( 2.4 and $2.5-1.7 \mathrm{Ma}$, respectively). | Frm grades into Miccosukee Frm (Cooke and Mossom 1929); correlated with Cypresshead Frm (Huddlestun 1988; Otvos 1988, 1998; Means 2009); Huddlestun (pers comm 2013) indicated the Miccosukee, Citronelle, Jackson Bluff, Cypresshead and Intracoastal Frms are time equivalents. | Note that in this compilation, the Citronelle Frm is only partially correlated with the Cypresshead Frm. |  |

Table S2．2．2：Part 2．Northwest Florida

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Table S2.2.2: Part 3. Southwest Florida

| Region | Formation | Member | Unit | $\begin{aligned} & \hline \begin{array}{l} \text { Age } \\ (\mathrm{Ma}) \end{array} \end{aligned}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Lake Flirt Formation \& |  |  | <0.1 |  |  |  |  |  |  |
|  | H\| | Coffee Mill Hammock |  | 0.14-0.11 | Puri and Vanstrum (1969); Lyons (1991) | Considered a unit of the Ft. Thompson Frm, although others have argued for formational status (e.g., Brooks 1968, 1974; Lyons 1991; the validity of the Ft . Thompson Frm as a lithological unit has been debated by the Florida Geological Survey in their most recent map of Florida (2001). | Petuch and Roberts (2007) indicated the Coffee Mill Hammock Member and the Ft. Thompson Frm are younger (from $0.6-0.01 \mathrm{Ma}$ ). | Correlated with the Princes Anne Frm (Lyons 1991) [this rm is included within the Satilla Frm by Huddlestun . Lyons (1991) indicated the Socastee, Pamlico (in part), Norfolk [now Shirley, Tabb or Acredale Frms], ge, Princess Anne, Silver Bluff, and Anastasia Frms have been cited within M1, which Lyons (1991) does not agree with. Lyons (1991) argued only the Princess Anne Frm and Member of the Ft . Thompson Frm are in interval M1. |  |  |
|  |  | Undifferentiat ed |  | 0.6-0.12 | Wehmiller and Belknap (1978); Karrowet al (1996); Missimer (2001a); Hickey tal (2010); Missimer and Wise (2012) | The Ft. Thompson Frm has also been said to include an Okaloacoochee Member, but the Florida Geological Survey is skeptical about using the Ft . Thompson as a lithological unit in general, and thus this member is not presented here. | Hickey et al (2010) indicated that reliable dates for the Ft . Thompson Frm are difficult to obtain, but placed the interval around $0.6-0.4 \mathrm{Ma}$; Brooks (1974) cited an age of $0.22+\mathrm{Ma}$; others cited slightly older ages: 0.95 0.55 Ma (Webb et al 1989) and 0.9-0.1 Ma (Kolbe et al 2011). Petuch and Roberts (2007) cited a younger top age for the Frm ( 0.01 Ma ). |  |  |  |

Table S2.2.2: Part 4. Southwest Florida

| Region | Formation | Member | Unit | $\begin{aligned} & \text { Age } \\ & \text { (Ma) } \end{aligned}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Bermont |  |  | 1.6-1.1 | Hulbert and Morgan (1989); Webb et al (1989); Campbell and Campbell (1995); Knorr and Harries (2007): Kolbe et a (2011) | The unit i s only found in southern florid. | Younger ages have been cited previously for the Bermont Frm, including: 1-0.5 Ma (DuBar 1974; Willard et al 1993; Blackwelder 1981a); and 0.5-0.4 Ma (Mitterer 1974, 1975); however, these younger ages may be suspect for a number of reasons, see Lyons (1991). Petuch and Roberts (2007) also indicated a younger top age for Frm (of 0.6 Ma ). | Partially correlated with the James city and Waccamaw Frms (NC and SC) (Ward e) al 1991). | DuBar (1991) indicated that the unit correlates with the Canepatch Frm (SC), but this is not supported in this compilation, with the Canepatch Frm younger than the Bermont Frm here. |  |
|  | Calosahatchee |  |  | 2-1.7 | Cunningham et al (2001); Missimer (2001a,b); Kolbe et al (2011); Missimer and Wise (2012) | A "lower" and "upper" Caloosahatchee have been referred to in publications, but the Frm in places (e.g. the Sarasota mine) can have 2 to 3 discontinuities/unconformities. | Missimer (2001b) cited an age of 2.1 or 1.77 Ma to 0.6 Ma , but the latter age does not accord with other dates for the Caloosahatchee Frm or with other formations in the sequence. Furthermore, a more up-to-date GSA abstract (Missimer and Wise 2012) indicated the Frm straddles the Gelasian-Calabrian boundary. Older ages cited for the Frm include: 2.35-1.71 and 2.5-2 Ma in the same publication (Missimer 1993); 2.4-2 Ma (Willard et al 1993); $2.5-1.8 \mathrm{Ma}$, but there was no provenance data for the sample (Bender 1972, 1973 Lyons 1991); 2.55-2.35 Ma for the lower Caloosahatchee and 1.9-1.7 (Campbell and Campbell 1995). | Correlated with the Waccamaw and Nashua Frms (DuBar 1991) (only partially correlated with the Nashua Frm in this compilation: here, the Nashua Frm is primarily older]; correlated with the James City and Waccamaw Allmon et al 1996a). | DuBar (1991) indicated the Frm is correlated with the Nashua Frm, but the Nashua Frm is primarily older in this report; Lyons (1991) indicated the Frm is correlated with the Chowan River Frm (NC and VA), but the unit is younger here; Missime (1993) indicated the lower Caloosahatchee is correlated with the is not supported in this compilation; the Anastasia Frm is younger here. |  |

Table S2.2.2: Part 5. Southwest Florida

Table S2.2.2: Part 6. Southwest Florida

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Table S2.2.2: Part 7. Southwest Florida

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Undifferentiated |  | 4.3-2.1 | Missimer (1984); Meeder (1987); Missimer (1990); Scott (1992); Missimer (1993); Missimer (1997); Missimer (1999); Guertin et al (2000); Missimer (2001b); Cunningham et al (2003); Knowles et al (2009); Williams et al (2009); Kolbe et al (2011) | According to Missimer (1990, 1993), the definition of the Hawthorn is used to establish the base of the Tamiami Frm. He suggested that the Tamiami Frm may underlie the Caloosahatchee or the Ft . Thompson Frms. Missimer (1993) defined 9 or more members of the Tamiami Frm; however, correlation among them is problematic. These 9 units can be mapped on the basis of dominant lithology in southwest FL, including: the Pinecrest Sand Member, the unnamed limestone facies, the Golden Gate Reef Member (of Meeder 1987), the Bonita Springs Marl Member (of Missimer 1984), the HYOTISSA facies, the Ochopee Limestone Member, the sand facies, the Buckingham Limestone Member, and the tan clay and sand facies. Only 1 to 4 of these occur in a vertical stratigraphic section at any given locality. In contrast to Missimer (1990, 1993), Hunter (1968) indicated the Pinecrest Sand, Ochopee Limestone and Buckingham Limestone were lateral equivalents. Missimer (1990), on the other hand, indicated the Buckingham Limestone is the lowermost facies and is probably equivalent in age to the clay and sand facies. The Tamiami Frm additionally has been broken into at least three other members (Fruitville, Golden Gate Reef, and Bonita Springs Marl, cited youngest to oldest) by Meeder (1987) and Petuch and Roberts (2007), but these remain controversial. Meeder (1987) did not formally define the Golden Gate Reef Member in terms of the stratigraphy and relationships with other major lithological units, and Missimer (1984) only informally suggested the Bonita Springs Marl Member. Much controversy and confusion surrounds the surface and near-surface deposits of southern Florida, especially the Tamiami Frm. This is for a variety of reasons, see Jones et al (1991) and Scott (1992) for details. Based on the sequence stratigraphic framework of Zullo and Harris (1992) at the APAC and SMR Pits, the authors concluded that Petuch's Units 0-1 belong to the Caloosahatchee Frm and Units 2-11 were within the Tamiami Frm. Units 2-9 were divided into the upper Tamiami Frm, and Units 10-11 were within the lower Tamiami Frm. Further subdivision placed Units 2-3 into the upper Pinecrest Beds and Units $4-9$ into the lower Pinecrest Beds. Petuch and Drolshagen (2011), however, now consider Units 2-4 to belong to the Fruitville Member (Tamiami Frm), Units 5-9 to belong to the Pinecrest Member (Tamiami Frm), Unit 10 to belong to the Buckingham Member (Tamiami Frm) and Unit 11 to be the Sarasota Member (Murdock Station Frm). | Missimer (1993) cited the Frm as $4.2-2.8 \mathrm{Ma}$, while Campbell and Campbell (1995) indicated the Tamiami Limestone is $4-3.8 \mathrm{Ma}$; Petuch and Roberts (2007) placed the Tamiami Frm older than 2.1 Ma; Williams et al (2000) and Knowles et al (2009) also cited the Tamiami Formation as older, from 5.3-4.3 Ma; Kolbe et al (2011) indicated an age of 4.3-2.5 Ma in parts of both NE and S Florida; Scott (2011) placed an older bottom age for the Tamiami at 5.3 Ma . | The lower Tamiami and lower Pinecrest Beds are correlated with the Jackson Bluff Frm (Zullo and Harris 1992; Zullo and Portell 1993) (note that the lower Tamiami Frm, depending on the definition, does not correlate with the Jackson Bluff Frm in this compilation]. |  |  |
|  | Peace River Formation |  |  | 11-4.5 | Emslie and Morgan (1994); McCartan et al (1995); Missimer (1999); Guertin et al (2000); Kolbe et al (2011) | The unconformity between the Peace River Frm and the overlying Tamiami Frm is likely only 0.2 Ma (Missimer 1999), and deposition may have stopped as late as 4.3 Ma (not 4.5 Ma ), an age which Guertin et al (2000) also cited. |  |  |  |  |

Table S2.2.2: Part 8. Southern Florida

| Region | Formation | Member | Unit | $\begin{aligned} & \text { Age } \\ & \text { (Ma) } \end{aligned}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Qu |  |  | <0.090 |  |  |  |  |  |  |
|  | Miami Limestone |  |  | 0.13-0.09 | Broecker and Thurber (1965); Osmond et al (1965); Guertin et al (2000); Neal et al (2008); Hickey et al (2010) | The Miami Limestone sits above the Ft. Thompson Frm, previously considered part of the Key Largo Frm (Hickey et al 2010). | Kolbe et al (2011) cited an older age of 0.9-0.1 Ma, while Scott (2011) indicated a younger top age of 0.01 Ma . | DuBar (1991) indicated the Miami Limestone interfingers with the Anastasia Frm in the N , the Key Largo Frm in the S, and the Ft. Thompson Frm in the NW, but according to Neal et al (2008) and Hickey et al (2010), the unit sits above the Ft . Thompson Frm; here the Ft. Thompson is above and partially interfingers/correlative. Hickey et al (2010) indicated the unit is a lateral equivalent to the upper part of the Key Largo Limestone. |  |  |
|  | Anastasia |  |  | 0.132-0.0 | Osmond et al (1970); Murphy (1973); Mitterer (1974); McNeil (1985); Portell et al (2003); Banks et al (2007); Burdette et al (2009); Burdette (2010) | Portell (pers comm 2013) indicated the unit is present from St. Augustine to southern Palm Beach County. | Kolbe et al (2011) cited an older age for this Frm ( $0.9-0.1 \mathrm{Ma}$ ); publications such as Osmond et al (1970), Murphey (1973), and Mitterer (1974) cited slightly younger top ages (around 90 to 100 Ka ) compared to the others of around 115 to 116 Ka (e.g., Banks et al 2007; Finkle et al 2008; Burdette 2010); Petuch and Roberts (2007) indicated an age of 0.1-0.01 Ma. | The Miami Oolite of the Miami Limestone is considered contemporaneous with the Anastasia Frm (Cooke and Mossom 1929); the Anastasia Frm interfingers with the Miami Limestone at the top of the section and probably correlates with the Caloosahatchee and Ft. Thomson Frms (Missimer et al 2000) [however, the Caloosahatchee Frm is too old in this compilation to correlate]; if congruent with OIS Se , the unit correlates with the Biloxi and Gulfport Frms (ME). | Missimer et al (2000) indicated the unit probably correlates with the Caloosahatchee and Ft . Thomson Frms, but the Caloosahatchee Frm is too old in this report. |  |

Table S2.2.2: Part 9. Southern Florida

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Table S2.2.2: Part 10. Southern Florida

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Table S2.2.2: Part 11. Northeast Florida

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Table S2.2.2: Part 12. Northeast Florida

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Table S2.2.2: Part 13. Northeast Florida

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Tamiami equivalent |  |  | $\sim 4.3 .8$ | Portell (pers comm 2013) | Quarries in Palatka are known to contain Tamiami-aged fossils (mostly Encope tamiamiensis); whether the unit below the Nashua Frm at this site is lithologically the Tamiami Frm has not yet been confirmed (Portell, pers comm 2013); Kolbe et al (2011) included the Tamiami Frm as a unit below the Cypresshead/Nashua Frms in NE Florida, but this has not been confirmed by the Florida Geological Survey. |  |  |  |  |
|  | Wabasso Beds |  |  | $\sim 5.5-4.3$ | Huddlestun (1988); Markewich et al (1992) | The Wabasso Beds is an informal name applied to lower Pliocene, phosphatic, calcareous, and microfossiliferous, variably argillaceous, silty, fine-grained to very fine grained sand in the subsurface of the coastal area of GA, southern SC, and eastern FL (Huddlestun 1988); Scott (2001) indicated the Wabasso Beds are also within the Peace River Frm in S Florida, but that they do not outcrop at the surface. The Wabasso Beds were treated as formational rank by Krantz (1991), but there seems to be no evidence for this, although Huddlestun (pers comm 2013) would like to see them formalized. | The unit belongs within zone PL1 or $\mathrm{N}-18$ (Huddlestun 1988); the unit is no older than 5.7 Ma and no younger than 4.2-4.0 Ma (Markewich et al 1992). | The unit is probably time equivalent to the Sunken Meadow Member of the Yorktown Frm in SE VA and NE NC. | Krantz (1991) indicated the lower Duplin Frm is time equivalent with the Sunken Meadow Member of the Yorktown Frm and the Wabasso Beds, but this is not supported in this compilation; here, the Duplin Frm is younger than the Wabasso Beds and the Sunken Meadow Member. |  |

Table S2．2．2：Part 14．Georgia

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Table S2.2.2: Part 15. Georgia

| Region | Formation | Member | Unit | Age (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Cypresshead |  |  | ~3.4-2.6* | Huddlestun (1988); Fountain (2010) | Markewich (pers comm 2013) indicated the "Cypresshead" of Huddlestun (1988) sits directly on Miocene sediments in many parts of GA. Huddlestun (pers comm 2013) indicated the terraces on top of the Cypresshead Frm [like the Wicomico, Penholoway, and Talbot] are merely overprinted on the older Cypresshead Frm and not genetically related to the Frm. Markewich et al (2013) also discussed terrace deposits within GA. | *No age data are available for Cypresshead sediments in Georgia outcrops (Markewich et al 1992); Markewich (pers comm 2013) indicated the Cypresshead Frm is at least middle Pleistocene in age. She suggested the upper part of what Huddlestun (1988) mapped as the Cypresshead Frm is called the Wicomico barrier (dated around 300 Ka , see Markewich et al 2013), but Huddlestun (pers comm 2013) indicated the Cypresshead Frm is within zone PL3 and slightly younger than PL4 and has no genetic relationship to overlying terraces/barrier complexes. The age also differs from that cited by Krantz (1991) (2.5-1.9 Ma), Alber et al (2003) (3.6-1.0 Ma) and Scott (2011) (5.3-1.8 Ma). Dating on the Frm is difficult due to lack of fossil material (Means pers comm 2013). | Equivalent with the Citronelle and Miccosukee Frms, overlies the Raysor Frm, and correlates with the Talbot Frm of the Carolinas (Otvos 1998); Campbell and Campbell (1995) think the unit is coincident with the Waccamaw Frm, but Ward and Gilinsky (1993) disagreed [the unit is not correlated in this report]; considered a Nashua equivalent (Huddlestun 1988; Markewich et al 1992); the unit underlies the Satilla Frm (Alber et al 2003); Huddlestun (pers comm 2013) indicated the Miccosukee, Citronelle, Jackson Bluff, Cypresshead and Intracoastal Frms are time equivalents. | Krantz (1991) indicated that the unit is correlated with the Chowan River and Bear Bleff frms, but this relationship is not supported in this compilation: these formations are younger than the Cypresshead Frm here; Markewich et al (1992) also indicated the erm is coinident with the Bear Bluff Frm in the Carolinas, but this is not supported in this compiliation, with the Cypresthead Frm older here. Otvos (1998) indicated the unit is correlated with the Talbot Frm of the Carolinas, otherwise referred to as the Canepatcth ${ }^{\text {rim lor the }}$ Tabb Frm in SE VA), but the Frm is not correlated in this report. |  |

Table S2．2．2：Part 16．Georgia

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Table S2.2.2: Part 17. Southeast and central South Carolina

| Region | Formation | Member | Unit | $\begin{aligned} & \text { Age } \\ & \text { (Ma) } \end{aligned}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Qu [eolian] |  |  | <0.070 |  |  |  |  |  |  |
|  |  | upper |  | -0.087* | McCartan et al (1980); Mccatran et al (1982); S Szabo (1985) | Youngest of SC coastal region (Soller and Mills 1991). McCartan et al (1980) indicated the Wando Frm includes deposits formerly within the Pamlico, Princess Anne andSilver Bluff Frms the authors argued that these names should not be used in 5 Carolina. The Wando Frm is divided into an upper and lower unit by Wehmiller et al (1988) equivalent to (respectively) the Princess Anne and Pamlico Terraces of Colquhoun. | *Age of unit is unclear: if younge ages for the Socastee and Canepatch Frms are assumed (see discussion below), then the dates indicated for the Wando Frm do not match this compilation. Szabo(1985) found ages of $129,000+/-$ 10,000 for the lower Wando Frm and $87,000+/-4000$ for the upper Wando Frm. The unit has generally been identified as latest Pleistocene in age (McCartan et a (McCartan et al 1982), isotope stage 5a ( $\sim 80 \mathrm{Ka}$ ) (McCartan et al 1984), 100 Ka based on isotopic data (Soller and Mills 1991), and an older age of 250 Ka (Wehmiller and Belknap 1982), but these athors correlated the Wand Flanner Beach Frms, so their definition of formations may have differed. All of MIS 5 may be recorded in the Wando Frm (Muhs et al 2003), and there is evidence for multiple amino zones present, but these cannot be directly associated with Useries ages (Corrado et al 1986; Marris 2000; York et al 2001; see 130 Ka (Andrus et al 2009). | The unit may correlate with the Core Creek Sand of Mixon and Pilkey (1976) in northeastern NC (Soller and Mills 1991), but Corrado et interpretation; the unit is also tentatively correlated with the Lynnhaven Member of the Tabb Frm of Johnson and Peebles (1986) (Soller and Mills 1991). |  |  |
|  | Wando | lower |  | -0.129* | McCartan et al (1980); Mcartan et al (1982); S Sabo (1985); Soller and Mills (1991) |  |  | Unconformably overlies the Cooper Frm or the Santee Limestone and underlies (McCartan et al 1980); the unit may correlate with the Core Creek Sand (Mixon and Pilkey 1976) in NE NC and tentatively correlated with the Lynnhaven Member of the Tabb Frm (Johnson and Peebles 1986; Soller and Mills 1991). | Wehmiller and Belknap 1982) correlated the Wando Frm with the Socastee and Flanner Beach Frms, which supposedly underlie the Wando Frm in this report; the definitions of these formations may have changed or may differ from those to this discrepancy. |  |
|  | Ten Mile Hill beds |  |  | -0.25-0.20 | McCartan et al (1990); Weems et al (1994); Andrus et al (2009) | Deposited in a marsh environment near Charleston (Weems et al 1994); equivalent to unit Q3 of McCartan et al (1984) (McCartan et al 1990; Weems et al 1994). |  | The unit may correlate with the Socastee Frm (Szabo Weems et al 1994). 1985; McCartan et al 1990; Weems et al 1994). |  |  |

Table S2.2.2: Part 18. Southeast and central South Carolina

| Region | Formation | Member | Unit | $\begin{array}{\|l} \hline \begin{array}{l} \text { Age } \\ (\mathrm{Ma}) \end{array} \\ \hline \end{array}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Socastee |  |  | ${ }^{0.24-0.1 *}$ | McCartan et al (1982); Wehmiller and Mills (1991) et al (1988); Soller | Dockal (1996) indicated the Neuse Frm has priority over the Socastee Frm and the two units are synonymous, but the "Socastee" name is still in use for sediments of this age in SC. | *Age is still fairly unclear in spite of years of study, with part of the problem stemming from different definitions of various units within the region: the Frm is typically assigned an age of ${ }^{\sim} 240-180 \mathrm{Ka}$ (McCartan et al 1982; Wehmiller et al 1988; Soller and Mills 1991). but Hollin and Hearty (1990) indicated the age is younger, dating to late isotope stage 5 (~90 70 Ka ), which conforms with what Dockal (1996) found for the age of the Neuse Frm (Cape Fear Coquina) in southern NC, which is thought to be synonymous with the Socastee Frm ( $\sim 75-55 \mathrm{Ka}$ ); Muhs et al (2003) indicated the dates of Hollin and Hearty (1990) would be consistent with aminostratigraphic comparison with the Sea Islands VLPG data. | Correlated with the Flanner Beach (NC), Norfolk (VA) Inow Shirley, Tabb or Acredale Frms and Omar (DE) Frms (McCartan et al 1922); correlated with the Flanner Beach Frm ard with the Shirley Frm and Sedgefield Member of the Tabe Frm (Soller and Mills 1991); correlated with the Flanner Beach Frm Harris 1996; Dockal 199; Soller and Mills 1991). |  |  |
|  | Ladson |  |  | -0.45-0.40 | $\begin{array}{\|l} \hline \begin{array}{l} \text { McCartan et al } \\ (1990) \end{array} \\ \hline \end{array}$ | Named by Malde (1959) in the Charleston area; may be equivalent to the Canepatch Frm of the Myrtle Beach area of DuBar (1971), but the "Ladson" name is older and thus retained (Weems et al 1994). The unit is interpreted as a fluvial/deltaic deposit (Wehmiller et al 1988). Like the Canepatch Frm, the unit is also referred to as unit Q4 (Weems et al 1994; Bowen 2009) |  | Equivalent to the upper (1974) (Wehmiller et al 1988); considered a Charleston-area equivalent of the Canepatch Frm of Myrtle Beach (Corrado et al Bowen 2009). |  |  |
|  | Waccamaw equivalent |  |  | 2.1-1.7 | See references for Waccamaw Frm | The Waccamaw Frm or an equivalent unit is noted here by McCartan et al (1982), Weems and Lemon (1984, 1989), and Corrado et al (1986) |  | Correlative to the Waccamaw Frm. |  |  |

Table S2．2．2：Part 19．Southeast and central South Carolina

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Table S2.2.2: Part 20. Southeast and central South Carolina

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting <br> References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Goose Creek Limestone | upper |  | 3.75-3.55 | Campbell and Campbell (1995); Ward and Huddlestun (1988) | The unit was originally mapped from Charleston, SC (Toumey 1848; Weems et al 1982); Campbell and Campbell (1995) indicated the unit is found in NE GA, eastern SC and SE NC. Campbell and Campbell (1995) suggested the Raysor Marl unconformably overlies the Goose Creek Limestone, which is a reversed relationship from previous publications. According to Campbell and Campbell (1995), the Raysor Frm and upper Goose Creek Limestone Frm appear to be coeval lithofacies distinct from and older than the Duplin Frm at the Natural Well stratotype. L. Campbell (pers comm 2013) indicated the lower Goose Creek limestone as found at the type section lies stratigraphically under the Raysor sands, and Raysor-equivalent strata to the east are referred to as "upper Goose Creek Limestone" and include the "Bear Bluff" deposits. Ward (pers comm 2012) does not support the name Goose Creek. | The unit is considered as 3.9-3.2 Ma or within zone NN 15 to midNN 14 (Bybell 1990). | According to Campbell and Campbell (1995), the upper Goose Creek Limestone Frm and the Raysor Frm appear to be laterally equivalent, coeval lithofacies, and both are older than the Duplin Frm. Here, the Duplin Frm is wholly equivalent to the Raysor Frm. Ward and Huddlestun (1988) placed the Goose Creek Frm above the Raysor Frm in their stratigraphic chart, which Huddlestun (pers comm 2013) indicated was incorrect and was reversed in a later publications by these authors. | The Bear Bluff is congruent with the upper Goose Creek Limestone Frm (Campbell and Campbell 1995); this relationship is not supported in this compilation, with the Bear Bluff Frm younger than the Goose Creek Frm here. | Plio-Pleistocene stratigraphy in S Carolina is complicated by a lack of fossils within the deposits and by differing definitions of stratigraphic units (e.g., should they be defined based on morphology/elevation vs. lithology vs. biostratigraphy); work has just begun to address these |
|  |  | lower |  | 4.0-3.8 | Ward and Huddlestun (1988); Campbell and Campbell (1995) |  |  | According to Campbell and Campbell (1995), the Raysor Marl unconformably overlies the lower Goose Creek Limestone, a reversal of the inferred stratigraphic sequence presented in other reports. |  | questions. As a result, <br> although numerous <br> papers have been <br> published on the <br> Pleistocene <br> stratigraphy of the <br> South Carolina Coastal <br> Plain, different groups |
|  | Wabasso Beds |  |  | ~5.5-4.3 | Huddlestun (1988): Markewich et al (1992); Campbell and Campbell (1995) | The Wabasso Beds is an informal name applied to lower Pliocene, phosphatic, calcareous, and microfossiliferous, variably argillaceous, silty, fine-grained to very fine grained sand in the subsurface of the coastal area of GA, southern SC, and eastern FL (Huddlestun 1988); Scott (2001) indicated the Wabasso Beds are also in the Peace River Frm in S Florida, but that they do not outcrop at the surface. The Wabasso Beds were treated as formational rank by Krantz (1991), but there seems to be no evidence for this, although Huddlestun (pers comm 2013) would like to see them formalized. | The unit is included within zone PL1 or N-18 (Huddlestun 1988); the unit is considered no older than 5.7 Ma and no younger than 4.2-4.0 Ma (Markewich et al 1992). | The unit is probably time equivalent to the Sunken Meadow Member of the Yorktown Frm in SE VA and NE NC. | Krantz (1991) indicated the lower Duplin Frm is time equivalent to the Sunken Meadow Member of the Yorktown Frm and Wabasso Beds, but this relationship was not supported in this compilation; here, the Duplin Frm is younger than the Wabasso Beds and the Sunken Meadow Member. | of stratigraphers have proposed quite different stratigraphic correlations using different mixes of data. For example, Doar (2009) indicated the following formations for the Plio Pleistocene of SC and SE VA: Wicomico, Penholoway, Ladson, Ten Mile Hill Beds, Pamlico, Princess Anne and Silver Bluff. |

Table S2.2.2: Part 21. Central/northeast SC \& southeast North Carolina

Table S2.2.2: Part 22. Central/northeast SC \& southeast North Carolina

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Waccamaw | upper |  | 1.7-1.5 | Graybill et al (2009); Badyrka et al (2010) | The youngest change in polarity (Matuyama Reverse Chron to Brunhes Normal Chron at about 0.78 Ma ) occurs between the Waccamaw (Reverse) and Canepatch (Normal) formations near Myrtle Beach, SC (Liddicoat 2012). | Bybell (1990) indicated an age range of $1.8-1.0 \mathrm{Ma}$, which is close to that cited here; same for Akers (1972) of $1.6-0.7 \mathrm{Ma}$, which is younger, and Blackwelder (1981a,b, and unpub data cited within Lyons 1991) of 1.6-1.1 Ma; Campbell (1993) and Campbell and Campbell (1995) indicated an older age for both the lower and upper Waccamaw Frm (2.2-1.9 Ma or 2.4-1.5 Ma for the upper), but this is contrary to the recent dating work done (Graybill et al 2009 and Badryka et al (2010) and not used here. Mabry and Thayer (2001) indicated a late Pleistocene age of $\sim 130-10 \mathrm{Ka}$. | The unit underlies the Canepatch Frm, overlies the Bear Bluff Frm, and correlates with the James City Frm (Ward et al 1991; Blackwelder and Ward 1979); correlative with the Caloosahatchee Frm based on faunal similarity (Lyons 1991), Campbell and Campbell (1995) agreed that the upper Waccamaw Frm correlates with the Caloosahatchee Frm; the Waccamaw Frm is correlated with the James City and Caloosahatchee Frms (Allmon et al 1996a); the James City Frm is a correlate (Harris 1996). | Campbell (1992) indicated the unit is laterally equivalent with the Cypresshead Frm, which is not supported in this report, as the Cypresshead is older here. |  |
|  |  | lower |  | 2.1-1.7 | $\begin{array}{\|l\|} \hline \text { Graybill et al (2009); } \\ \text { Badyrka et al } \\ \text { (2010); McGregor } \\ \text { et al (2011) } \end{array}$ | The Waccamaw is divided into a lower and upper unit by an unconformity (Krantz 1991; Akers 1972; Ward et al 1991; Campbell and Campbell 1995). | Graybill et al (2009) is listed in support, but these authors found a slightly younger age for the lower Waccamaw Frm of 1.55 Ma , in addition to an age of 2 Ma and 1.8 Ma ; Campbell (1993) and Campbell and Campbell (1995) indicated an older age for both the lower and upper Waccamaw Frm ( 2.5 or 2.4 Ma for the lower), but this is contrary to the recent dating work done and is not used here. Akers (1972) and Krantz (1991) indicated an age of 1.9-1.7 Ma , which is similar to the age cited here. | The lower Waccamaw Frm is correlated with the Bacons Castle Frm (Krantz 1991). |  |  |

Table S2.2.2: Part 23. Central/northeast SC \& southeast North Carolina

| Region | Formation | Member | Unit | Age <br> (Ma) | $\begin{array}{\|l\|} \hline \text { Supporting } \\ \text { References } \end{array}$ | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Bear Bluff |  |  | 2.6-2.1 | McCartan et al <br> (1982); Krantz <br> (1991); Markewich <br> et al (1992); <br> Campbell (1993) | The Bear Bluff Frm of southeastern NC and northeastern SC lies above the Duplin Frm (Markewich et al 1992). Campbell (1992) concluded that the upper Goose Creek Limestone and the type Bear Bluff are the same unit based on faunal and lithological similarity and recommended that the Bear Bluff Frm be abandoned (the authors argued that the unit is actually part of the upper Goose Creek Limestone at the stratotype of the Bear Bluff Frm), but the Bear Bluff Frm is still in use by the USGS. Campbell and Campbell (1995) similarly argued that the Bear Bluff stratotype is pre-Natural Well Duplin Frm in age, which is contrary to other stratigraphic opinions, and is similar to the upper Goose Creek Limestone. Campbell (pers comm 2013) indicated that the name "Bear Bluff" has generally been misapplied to faunally and lithologically dissimilar beds that in fact are much younger, after the 2.5 Ma boundary, equivalent to the Chowan River Frm [old Croatan Frm]. L. Campbell (pers comm 2013) indicated that the placement of the Bear Bluff Frm as younger than the Raysor Frm is based on Dubar including the lower Waccamaw Frm aragonitic beds as the datable material in his composite "Bear Bluff", and that the unit is actually similar to the upper Goose Creek Limestone and/or Raysor Frm. | All ages roughly point to about 2.5 Ma , with some minor differences: McCartan et al (1982) cited an age of 2.4-1.8 Ma; Krantz (1991) cited an age of $2.5-$ 1.9 Ma ; Campbell (1993) cited an age of 2.5 Ma , and suggested older ages obtained (e.g., 3.7 Ma ) were from older sediments like the Goose Creek Limestone; Markewich et al (1992) cited an age of PL.5 (roughly equivalent to somewhere within 3.1-2.3 Ma); L. Campbell (pers comm 2013) indicated the Bear Bluff Frm is as old as 3.8 Ma or older and equivalent to the Raysor Frm. | Correlated with the Chowan River Frm (Ward et al 1991); correlated with the Chowan River Frm and Cypresshead Frm (Krantz 1991) [note that the Cypresshead Frm is older in this compilation, and thus not correlated with the Bear Bluff Frm here); the Bear Bluff Frm is correlated with the Chowan River Frm and also potentially with the upper Pinecrest Beds of Florida (Allmon et al 1996a); Huddlestun (pers comm 2013) indicated the Bear Bluff Frm is younger than the Citronelle or Cypresshead Frms and not correlated with the Citronelle Frm. | Campbell (1993) indicated the molluscan fauna are younger than that of the Pinecrest Beds but older than that in the Caloosahatchee Frm, however, here the Pinecrest Beds are partially equivalent to the Bear Bluff Frm; Markewich et al (1992) indicated the unit lies above the Duplin Frm and is equivalent to the Cypresshead Frm (GA) and Nashua Frm of NE FL, but while partially time equivalent with the Nashua Frm, the unit is younger than the Cypresshead Frm in this compilation. |  |

Table S2.2.2: Part 24. Central/northeast SC \& southeast North Carolina

| Region | Formation | Member | Unit | $\begin{array}{\|l\|l\|} \hline \text { Age } \\ \text { (Ma) } \end{array}$ | $\begin{array}{\|l\|} \hline \text { Supporting } \\ \text { References } \\ \hline \end{array}$ | Notes | Other age details or opinions | Correlation | Other opinions on correlations | $\begin{array}{\|l\|} \hline \begin{array}{l} \text { General } \\ \text { regional notes } \end{array} \\ \hline \end{array}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Duplin |  |  | 3.3.3.31 |  | Members of the Yorktown Frm are mapped as far south <br> as the Neuse River in NC, but south of the river they cannot be differentiated and are placed in the Duplin Frm (Ward 2001); Campbell and Campbell (1995) indicated that much confusion exists towards the Duplin Frm; for example, whether the unit should be interpreted narrowly and restricted to the stratotype section, or should be interpreted more broadly and include several transgressive-regressive sequences. | Krantz (1991) cited the lower Duplin Frm as 4.8-3.5 Ma Campbell and Campbell (1995) indicated Dowsett and Cronin (1990) were dating the Duplin Frm from sites that yielded Raysor Frm index fossils. |  | Krantz (1991) indicated the lower Duplin Frm is time equivalent with the Sunken Meadow Member of the Yorktown Frm and the Wabasso Beds, but this is not supported in this compilation; here, the Duplin Frm is younger than the Wabasso Beds and the Sunken Meadow Member of the Yorktown Frm Ward (2008) placed the Duplin and Raysor Frms as correlative with the the Yorktown Frm as younger than the Duplin and Raysor Frms; however, in this compilation, the Duplin and Raysor Frms correlate with the upper part of the Yorktown Frm. | The Penholoway Frm (Owens 1989), early Pleistocene in age (Soller and Mills 199 was abandoned by Huddlestun (1988) bu reinstated by Weems and Lemon (1989) an used by Soller and Mills (1991). The unit is not included in this column because the North Carolina Geological Survey doe not subscribe to using terrace formation names when naming units; however, changing stratigraphi understanding and nomenclature could Dating on the Penholoway Frm indicates the unit is not older than the |

Table S2.2.2: Part 25. Central/northeast SC \& southeast North Carolina

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Goose CreekLimestone | upper |  | 3.75-3.55 | Ward and <br> Huddlestun (1988): <br> Campbell and <br> Campbell (1995) | The unit was originally mapped from Charleston, SC (Toumey 1848; Weems et al 1982). Campbell and Campbell (1995) indicated the unit is found in NE GA, eastern SC and SE NC. Campbell and Campbell (1995) suggested the Raysor Marl unconformably overlies the Goose Creek Limestone, which is a reversed relationship from previous publications. According to Campbell and Campbell (1995), the Raysor Frm and upper Goose Creek Limestone appear to be coeval lithofacies distinct from and older than the Duplin Frm at the Natural Well stratotype. L. Campbell (pers comm 2013) indicated the lower Goose Creek Limestone as found at the type section lies stratigraphically under the Raysor sands, and to the east, Raysor-equivalent strata are referred to as "upper Goose Creek Limestone" and include the "Bear Bluff" deposits. | Age cited at 3.9-3.2 Ma or zone NN 15 to mid-NN 14 (Bybell 1990). | According to Campbell and Campbell (1995), the upper Goose Creek Limestone and the Raysor Frm appear to be laterally equivalent, coeval lithofacies, and both are older than the Duplin Frm. The current compilation has the Duplin Frm wholly equivalent to the Raysor Frm. Ward and Huddlestun (1988) placed the Goose Creek above the Raysor Frm in their stratigraphic chart, which Huddlestun (pers comm 2013) indicated is incorrect and was reversed in later publications by these authors. | The Bear Bluff Frm is congruent with the upper Goose Creek Limestone (Campbell and Campbell 1995); however, this relationship is not supported in this compilation, as the Bear Bluff Frm is younger than the Goose Creek Limestone here. | lupper part of Quaternary zone NN19 of Martini (1971) around 970 Ka (Weems et al 1994); equivalent beds in the Stallvill Quadrangle yielded U-Th dis- equilibria ages of 700 Ka (Szabo 1985). The Penholoway is said to overlie the (lower) Waccamaw Frm and outcrops from Cape Fear River southward to Charleston, SC, and potentially correlates with the younger Waccamaw Frm and with unit Q5 of McCartan et al (1984) I |
|  |  | lower |  | 4.0-3.8 | Ward and Huddlestun (1988); Campbell and Campbell (1995) |  |  | According to Campbell and Campbell (1995), the Raysor Marl unconformably overlies the lower Goose Creek Limestone, a reversal of the inferred stratigraphic sequence presented in other reports. |  | and Colquhoun (1986) (from Soller and Mills 1991). See overview of stratigraphic naming issues and associated problems of dating formations in Corrado et al (1986). |

Table S2.2.2: Part 26. Central and northeast North Carolina

Table S2.2.2: Part 27. Central and northeast North Carolina

Table S2.2.2: Part 28. Central and northeast North Carolina

| Region | Formation | Member | Unit | $\begin{array}{\|l\|} \hline \text { Age } \\ (\mathrm{Ma}) \end{array}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Yorktown | Morgarts Beach <br>  <br>  <br>  <br> Rushmere |  | 4.6-3.1 | Hazel (1983); Snyder et al (1983); Dowsett and Cronin (1990); Cronin (1991); Krantz (1991); Dowsett and Wiggs (1992) | Campbell (1993) indicated the members proposed by Ward and Blackwelder (1980) are not lithostratigraphic units and should not be in use; however, the units are still widely cited in the literature. The members of the Yorktown Frm are mapped as far south as the Neuse River in NC (Ward 2001, 2008). The Yorktown Frm is usually used for lower and lower upper Pliocene sediments that occur north of the Neuse Hing on the Albemarle Block, whereas the Duplin Frm is used for age equivalent sediments that occur south of Neuse Hing on the Onslow Block (Ward et al 1991). The uppermost Moore House Member is restricted to southeastern Virginia (Ward et al 1991). | ~ 4.8-2.8 Ma, with the upper limit near the middle of zone N21 (Cronin et al 1984; Lyons 1991); however, Ramsey (1992) indicated the dates may be closer to 4.5-3 Ma (following Krantz 1991); late zone N18 and zone N19 or PL1-PL3 (Akers 1972); upper zone N19 (Blackelder 1981); ; 5.-3 Ma (Hazel 1983, Snyder et al 1983, Cronin 1991, Ramsey 1992); PL.1b-PL3, authors favor younger dates in this range (Dowsett and Cronin 1990; Dowsett and Wiggs 1992); 3.2 Ma (Campbell 1993); 5.3-3.4 Ma (Pazzaglia 1993); 3.5-2.9 Ma (Willard 1994); 3.8 Ma (Campbell pers comm 2013); Denison et al (1993) suggested younger dates (age N21 or N22, $2.1-1.4$ Ma), but these may have resulted from differing definitions of stratigraphy: the authors placed the Yorktown Frm as immediately succeeded by the Croatan Frm, which is now the Flanner Beach, and thus they could have been sampling what is now the Chowan River Frm (in NC). | The Moore House Member is the youngest unit and does not seem to be correlated with any unit in SC or GA (Krantz 1991); the Yorktown Frm is the same age as the Duplin and Raysor Frms (Cronin et al 1984; Ward and Huddlestun 1988; Dowsett and Wiggs 1992) and the Jackson Bluff Frm (Huddlestun 1988; Allmon et al 1996a); Akers (1972) correlated the unit with the Jackson Bluff and Agurgurxquite Frms of Mexico; Cronin (1991) correlated the unit with the lower Pinecrest Beds and the Duplin and Raysor Frms of NC, SC and GA; Cronin and Dowsett (1996) indicated units $10-5$ of the Pinecrest Beds are equivalent to these members of the Yorktown [only partially in this report]. | Campbell (1993) correlated the Moore House Member of Ward et al (1991) and Krantz (1991) with the Chowan River Frm, which is restricted to 3.5 Ma , but the Yorktown Frm (Moore House Member) is below the Chowan River Frm in this compilation. Ward and Gilinsky (1993) did not agree with Campbell (1993) in equating the Moore House Member of the Yorktown Frm with the Chowan River beds (Campbell and Campbell 1995). Evidence suggests that the Chowan River Frm is younger than 3.5 Ma . Harris (1996) indicated the Rushmere and Morgarts Beach Members of the Yorktown Frm = Duplin Frm, but in this report, the Duplin Frm is only partially correlated with the upper part of the Yorktown Frm. Campbell et al (2011) indicated the lower Goose Creek Limestone of SC, Unit 3 of the Yorktown Frm, the Tamiami Limestone and lower Jackson Bluff Frm correlida are all Leptopecten unit (Early Pliocene), but while the Yorktown Frm seems to span all these units, the Jackson Bluff in this report overlies the Tamiami Limestone and is age-equivalent to the the lower. upper Goose Creek, not |  |

Table S2.2.2: Part 29. Central and northeast North Carolina

| Region | Formation | Member | Unit | $\begin{array}{\|l\|} \hline \begin{array}{l} \text { Age } \\ (\mathrm{Ma}) \end{array} \\ \hline \end{array}$ | Supporting <br> References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Sunken Meadow |  | 4.8-4.6 | Cronin et al (1984); <br> Ward and <br> Huddeletun (1988); <br> Krantz (1991) <br> althouh he cited a <br> athege from 4.8-3.5 <br> Ma for this member |  |  |  | Jones et al (1991), Willard et al (1993) and Williams et al (2009) indicated the Sunken Meadow Member is equivalent to Unit 11 of the lower Pinecrest, but this is not supporte in this compilation; in others (e.g. Scott 1995) indicated the Sunken Meadow Member is not correlated with any Thamiami sediments, at Temast not in 5 Florida. |  |

Table S2.2.2: Part 30. Southeastern Virginia

| Region | Formation | Member | Unit | $\begin{array}{\|l\|l} \hline \text { Age } \\ \text { (Ma) } \end{array}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Powells Crossroads |  |  | $<0.04$ | Oaks and Coch (1963) | Little information could be found on this Frm, which is not used extensively in the literature. The unit outcrops at Virginia Beach and was named by Spencer and Campbell (1987); it now includes the Sand Bridge (at top) and London Bridge Frms, which were reduced to member rank. | The Sand Bridge Frm, now part of Powells Crossroads, had a radiocarbon age of 40 Ka (Oaks and Coch 1963); the Sand Bridge is Wisconsin in age ( $\sim 85-10 \mathrm{Ka}$ ) (Coch 1965). |  |  |  |
|  | Acredale |  |  | <0.04 | Oaks and Coch (1963); Spencer and Campbell (1987) | Little information could be found on this Frm, which is not used extensively in the literature; the Kempsville, Norfolk and Great Bridge Frms were reduced to member ranks and assigned to the Acredale Frm in the Virginia Beach area (Spencer and Campbell 1987). | Very few papers are available on this Frm; Oaks and Coch (1963) indicated a middle or late Pleistocene age for the Frm; Spencer and Campbell (1987) indicated a late Pleistocene age. | The unit overlies the Pliocene Croatan Frm [now either the James City or Chowan River Frms] (Spencer and Campbell 1987). |  |  |
|  | Tabb |  |  | 0.12-0.039 | Szabo (1985) ohnson and Berquist (1989); Johnson and Hobbs (1990) Mirecki et al (1995) Scott et al (2010) | The Talbot Frm, as mapped by Wentworth (1930) in southeastern VA, is now called the Tabb Frm (Johnson and Berquest 1989); the unit is also mapped as the Norfolk Frm by Bick and Coch (1969) and others (see Hobbs 2004). | Szabo (1985) found an age for the Norfolk Frm of $71+/-5 \mathrm{Ka}$ [The Norfolk was divided into the Shirley and Tabb Frms]. Mixon et al (1982) thought the 72 Ka average for the Norfolk Frm was too young and resulted from loss of thorium due to burial in permeable, water-saturated these dates may be appropriate for younger units (Tabb Frm), rather than the Shirley Frm; Mixon et al (1989), Pazzaglia (1993), and Rader and Evans age; Johnson and Berquist (1989) indicted Mixon (1982) dated sediments correlative with the Sedgefield Member at $75-120 \mathrm{Ka}$; correlative sediments at the Gomez Pit in Norfolk, VA, were dated to 125-80 Ka (Mirecki et al 1995); the majority of ages average around 76 Ka for the Frm (Scott et al 2010); Johnson and Hobbs (1990) suggested a 65 Ka for the Poquoson Member of the Tabb Frm; Scott et al (2010) found OSL dates of $39.6+/-6.6 \mathrm{Ka}$ and $44.4+/-5.2 \mathrm{Ka}$ for the Poquoson Member; overall, the Frm appears to have been deposited during MIS-3 or $\sim 125$ 40 Ka (Swift et al 2003, Scott et al 2010 ). | The unit unconformably overlies the Norfolk Frm [now the Shirley, Tabb or Acredale Frms] or the Yorktown Frm and sediments (Johnson 1976); the Tabb Frm is correlated with the Wachapreague and Nassawadox Frms (Toscano and York 1992). |  |  |

Table S2.2.2: Part 31. Southeastern Virginia

| Region | Formation | Member | Unit | $\begin{array}{\|l\|} \hline \text { Age } \\ \text { (Ma) } \end{array}$ | $\begin{array}{\|l\|} \hline \text { Supporting } \\ \text { References } \\ \hline \end{array}$ | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Shirley |  |  | $0.240-0.164$ | Johnson and Berquist (1989), which was supported by Mixon et al (1989); Toscano (1992); Rader and Evans (1993); Hobbs (2004) | This formation was previously mapped as a facies of the Norfolk Frm (Johnson and Berquist 1989); Peebles et al (1984) divided the Norfolk Frm, as redefined by Oaks and Coch (1973), into an older unit-the Shirley Frm, as named by Johnson and Berquist (1989)-and the Tabb Frm. | Johnson and Berquist (1989) found U -series dates from corals of ~204-164 Ka (late middle Pleistocene), and these dates were supported by Mixon et al (1989), Rader and Evans (1993) and Hobbs (2004); Toscano (1992) cited an age of 250-200 Ka; Mirecki et al (1995) found older ages for correlative sediments at Gomez Pit in Norfolk, VA, of $400-258$ Ka, with correlative sediments at the Rappahannock River even older at around 915-585 Ka; Pazzaglia (1993) cited a middle Pleistocene age, and Swift et al (2003) indicated an age of around 150 125 Ka in their chart, but these dates seem young. |  | Correlated with the Great Bridge Frm [now Acredale Frm] (Mirecki et al 1995), but this relationship is not supported in this compilation; the Acredale Frm is younger than the Shirley Frm here. |  |
|  | Chuckatuck |  |  | $\sim 0.8<0.2^{*}$ | Johnson and Berquist (1989); Mixon et al (1989); Radar and Evans (1993) | The unit was previously mapped in the area of the type section as the Wicomico Frm and the Windsor Frm, named by Johnson and Berquist (1989). | *The age is uncertain, but confined by the late middle Pleistocene age of the Shirley Frm, and the probable early Pleistocene age of the Charles City Frm (Johnson and Berquist 1989); the Frm is potentially middle Pleistocene (Mixon et al 1989; Radar and Evans 1993); the chart in Swift et al (2003) placed the unit around 200 Ka , which seems on the younger side. | The unit unconformably underlies the Shirley Frm and overlies the Charles City Frm or the Windsor Frm (Johnson and Berquist 1989). |  |  |
|  | Charles City |  |  | ~1.6-1.0* | Johnson and Berquist (1989); Mixon et al (1989) | The upper portion of the Windsor Frm as mapped by Bick and Coch (1969) is called the Charles City Frm (Johnson and Berquist 1989); the unit was mapped into the Carolinas, but has spotty outcrops according to Soller and Mills (1991). | *The age is uncertain, as the unit contains no distinctive fossils for dating (Hobbs 2004), but is considered early Pleistocene based on stratigraphic position (Johnson and Berquist 1989; Mixon et al 1989); as such, the unit was given dates for the upper James City Frm deposits. Swift et al (2003) placed the Frm around 300 Ka in their chart, but this seems too young an age for the unit. | The unit disconformably overlies the early Pleistocene Windsor Frm (Johnson and Berquist (1989); the unit overlies the Windsor Frm and underlies the Chuckatuck Frm (Mixon et al 1989). |  |  |

Table S2.2.2: Part 32. Southeastern Virginia

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Table S2.2.2: Part 33. Southeastern Virginia

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Chowan River | Colerain |  | 2.6-2.1 | Ages have been obtained anywhere from 3 to 1.9 Ma ; see discussion in "Other age details or opinions" section. | The Chowan River Frm was named by Blackwelder (1981b) for sediments previously mapped as the Yorktown Frm and the Croatan Frm. The unit unconformably overlies the Yorktown Frm and unconformable underlies the James City Frm (Ward et al 1991; Snyder and Riges 1993). | Ages have been obtained anywhere from 3 to 1.9 Ma . Ages have centered around 2.5 or 2.1 Ma , but have been found as old as 2.8 or $3 \mathrm{Ma:} \mathrm{2.4-1.9} \mathrm{Ma}$ (Bender unpublished data, from Blackwelder 1981a,b); N21 (~2.41.9 Ma (Cronin et al 1984); 2.8 Ma (Groot 1991); 2.9-2.6 or 2.22.1 Ma (Krantz 1991); 2.5 Ma (Ramsey 1988, 1992); 2.5 Ma (Campbell 1993); 3.4-2 Ma from their stratigraphic chart (Pazzaglia 1993); 3-2.8 Ma (Campbell and Campbell 1995); 2.40-1.9 Ma (Hobbs 2004). | Correlated with the Bear Bluff and Cypresshead Frms (Krantz 1991) [note that in this report, the <br> Cypresshead and Bear Bluff Frms are not time equivalent); correlated with deposits in SC known as the Bear Bluff Frm (Ward et al 1991); correlated with Pinecrest Beds 2 and 3 of the APAC Pit (Campbell 1993); the Chowan River fauna is older than the lower Waccamaw Frm, but younger than the Duplin Frm (Campbell and Campbell 1995); the upper Pinecrest Beds (units 4-2 sensu Allmon et al 1996a,b) are separated by a hiatus and may be equivalents of the Chowan River Frm of SE VA and NE Carolinas (Dowsett and Cronin 1996; Jones et al 1991); the Bear Bluff (SC), Caloosahatchee (FL) and Chowan River Frms are equivalent (Blackwelder 1981a; Ward and Blackwelder 1987) [note that the Caloosahatchee Frm is younger than the Chowan River Frm in this report]; equivalent to the Bear Bluff Frm (Harris 1996). | Campbell (1993) correlated the unit in part with the Moore House Member of the Yorktown Frm of Krantz (1991) and Ward et al (1991), which is restricted to 3.5 Ma , but the Yorktown Frm (Moore House Member) is below the Chowan River Frm in this compilation. Ward and Gilinsky (1993) did not agree with Campbell (1993) in equating the Moore House Member of the Yorktown Frm with the Chowan River beds (Campbell and Campbell 1995). Evidence suggests that the Chowan River Frm is younger than 3.5 Ma . |  |

Table S2.2.2: Part 34. Southeastern Virginia

| Region | Formation | Member | Unit | $\begin{array}{\|l} \hline \begin{array}{l} \text { Age } \\ (\mathrm{Ma}) \end{array} \\ \hline \end{array}$ | $\begin{array}{\|l\|} \hline \text { Supporting } \\ \text { References } \\ \hline \end{array}$ | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Yorktown | Moore House <br> Morgarts Beach <br> Rushmere |  | 4.6-3.1 | $\begin{aligned} & \text { Hazel (1983); Snyder } \\ & \text { et al (1983); Cronin } \\ & \text { (1991); Dowsett and } \\ & \text { Cronin (1990); Krantz } \\ & \text { (1991); Dowsett and } \\ & \text { Wiggs (1992) } \end{aligned}$ | Campbell (1993) indicated the members proposed by Ward and Blackwelder (1980) are not lithostratigraphic units and should not be in use; however, the units are still widely cited in the literature. The members of the Yorktown Frm are mapped as far south as the Neuse River in NC (Ward 2001, 2008). The Yorktown Frm is usually used for lower and lower upper Pliocene sediments that occur north of the Neuse Hing on the Albemarle Block, whereas the Duplin Frm is used for age equivalent sediments that occur south of Neuse Hing on the Onslow Block (Ward et al 1991). The uppermost Moore House Member is restricted to southeastern Virginia (Ward et al 1991). | ${ }^{\sim} 4.8-2.8 \mathrm{Ma}$, with the upper limit near the middle of zone N21 (Cronin et al 1984; Lyons 1991); however, Ramsey (1992) indicated the dates may be closer to $4.5-3 \mathrm{Ma}$ (following Krantz 1991); late zone N18 and zone N19 or PL1-PL3 (Akers 1972); upper zone N19 (Blackwelder 1981b); 4.5-3 Ma (Hazel 1983; Snyder et al 1983; Cronin 1991; Ramsey 1992); PL1b-PL3, authors favor younger dates in this range (Dowsett and Cronin 1990; Dowsett and Wiggs 1992); 3.2 Ma (Campbell 1993); 5.3-3.4 Ma (Pazzaglia 1993); 3.5-2.9 Ma (Willard 1994); 3.8 Ma (Campbell pers comm 2013); Denison et al (1993) suggested younger dates (age N21 or N22, $\sim 2.1-1.4 \mathrm{Ma}$ ), but these may have resulted from differing definitions of stratigraphy: the authors placed the Yorktown Frm as immediately succeeded by the Croatan Frm, which is now the Flanner Beach, and thus they could have been sampling what is now the Chowan River Frm (in NC). | The Moore House Member is the youngest unit and does not seem to be correlated with anything in SC or GA (Krantz 1991); the Yorktown Frm is the same age as the Duplin and Raysor Frms (Cronin et al 1984; Ward and Huddlestun 1988; Dowsett and Wiggs 1992) and the Jackson Bluff Frm (Huddlestun 1988; Allmon et al 1996a); Akers (1972) correlated the unit with the Jackson Bluff and Agurgurxquite Frms of Mexico; Cronin (1991) correlated the unit with the lower Pinecrest Beds and the Duplin and Raysor Frms of NC, SC and GA; Cronin and Dowsett (1996) indicated units 10-5 of the Pinecrest Beds are equivalent to these members of the Yorktown [only partially in this report). | Campbell (1993) correlated the Moore House Member of Ward et al (1991) and Krantz (1991) with the Chowan River Frm, which is restricted to 3.5 Ma , but the Yorktown Frm (Moore House Member) is below the Chowan River Frm in this compilation. Ward and Gilinsky (1993) did not agree with Campbell (1993) in equating the Moore House Member of the Yorktown Frm with the Chowan River beds (Campbell and Campbell 1995). Evidence suggests that the Chowan River Frm is younger than 3.5 Ma . Harris (1996) indicated the Rushmere and Morgarts Beach Members of the Yorktown Frm = Duplin Frm, but in this report, the Duplin Frm is only partially correlated with the upper part of the Yorktown Frm. Campbell et al (2011) indicated the lower Goose Creek Limestone of SC, Unit 3 of the Yorktown Frm, the Tamiami Limestone and lower Jackson Bluff Frm correlated by a Leptopecten unit (Early Pliocene), but while the Yorktown Frm seems to span all these units, the Jackson Bluff in this report overlies the Tamiami Limestone and is age-equivalent to the upper Goose Creek, not the lower |  |

Table S2.2.2: Part 35. Southeastern Virginia

| Region | Formation | Member | Unit | $\begin{array}{\|l\|} \hline \begin{array}{l} \text { Age } \\ \text { (Ma) } \end{array} \end{array}$ | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Sunken Meadow |  | 4.8-4.6 | Cronin et al (1984); Ward and Huddlestun (1988); Krantz (1991), although he cited a range from 4.8-3.5 Ma for this member | The lowest initial transgressive deposit, the Sunken Meadow Member of the Yorktown Frm, contains a somewhat different molluscan assemblage from the rest of the Yorktown Frm and is separated from the other units by a depositional hiatus (Blackwelder 1981a). |  | Krantz (1991) indicated the Sunken Meadow Member is time equivalent with the Wabasso Beds and the lower Duplin rern; the latter relationship is not suppoted here, but the Sunken Meadow Member is correlated with the Wabasso Beds. |  |  |

Table S2.2.2: Part 36. Lower Delmarva Peninsula, Chesapeake Bay Coast

Table S2.2.2: Part 37. Lower Delmarva Peninsula, Chesapeake Bay Coast

| Region | Formation | Member | Unit | Age <br> (Ma) | Supporting References | Notes | Other age details or opinions | Correlation | Other opinions on correlations | General regional notes |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $\begin{aligned} & \overline{0} \\ & 0 \\ & 2 \\ & 3 \\ & 3 \\ & 0 \end{aligned}$ | Omar |  |  | 0.5-0.2 | Mixon (1985); Groot <br> et al (1990); Toscano <br> and York (1992) | The unit is composed of multiple depositional packages with disconformities in between (Toscano and York 1992). | Mixon (1985) indicated the oldest Pleistocene unit, the Accomack Member of the Omar Frm, is ~ 200 Ka ; Owens and Denny (1979) indicated an age of $126-90 \mathrm{Ka}$; Groot et al (1990) found amino acid dates of 100,200 and 500 Ka; Toscano and York (1993) indicated the unit placed within MIS $7 / 9$ thru 13 , which is $\sim 528$ 200 Ka ; Swift et al (2003) cited ages of $400-200 \mathrm{Ka}$; and Ramsey (2010) cited ages of 400-325 Ka. | Correlated with the Shirley Frm (Toscano and York 1992) (note that it is only partly correlated here]. |  |  |
|  | Yorktown |  |  | $\sim 4.8-3.1$ | Hazel (1983); Snyder et al (1983); Cronin et al (1984); Ward and Huddlestun (1988); Dowsett and Cronin (1990); Cronin (1991); Krantz (1991); Dowsett and Wiggs (1992) | See notes and references for individual members in the "SE Virginia" and "C \& NE North Carolina" sections; this is a composite age for all of the Yorktown Frm. |  |  |  |  |

Table S2.2.2: Part 38. Lower Delmarva Peninsula, Atlantic Coast

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## Appendix S2.3


#### Abstract

Appendix S2.3 Supplemental data files for niche comparison tests for: (a) environmental comparisons using a PCA applied to all six variables, (b) environmental comparisons using a PCA applied to the three most important variables, (c) environmental comparisons using raw temperature variables, (d) geographic comparisons using projections from ecological niche models (ENMs), (e) maximum temperature comparisons, and (f) minimum temperature comparisons.


## Appendix S2.3a. Environmental comparisons using a PCA applied to all six variables

Results from niche comparison tests for a principle component analysis (PCA) applied to three most important environmental variables (maximum and minimum surface temperature and maximum surface salinity) using script of Broennimann et al. (2012). The first two panels represent the niche of the species along the first two axes of the PCA in the respective time periods. The solid and dashed lines represent $100 \%$ and $50 \%$ of the available (background) environment, respectively. The bottom left panel represents the contribution of the climatic variables to the two axes of the PCA and the percentage of inertia explained by the two axes. The top histogram is the simulated similarity values (D) and observed similarity value (red bar) for the niche equivalency test. The bottom two histograms are the simulated and observed (red bar) similarity values for the niche similarity tests. Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.

Anomia simplex: LIG-mPWP

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency


## Similarity mPWP->LIG Similarity LIG->mPWP




Anomia simplex: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.004$

## Similarity PI->LIG



Similarity LIG->PI


Anomia simplex: PI—mPWP

correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency


## Similarity mPWP->PI



Similarity PI->mPWP


Bulla occidentalis: LIG-mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->LIG


D
p.value $=0.10589$

Bulla occidentalis: LIG—PI


axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency


## Similarity PI->LIG



Similarity LIG $\rightarrow$ PI

p.value $=0.002$


axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$

Crassostrea virginica: LIG—mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency

## niche overlap: $D=0.355$

## Similarity mPWP->LIG



Similarity LIG->mPWP


Crassostrea virginica: LIG—PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.002$

Similarity PI->LIG


Similarity LIG->PI


axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency
niche overlap:
$D=0.427$

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$

correation circie

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->LIG



Similarity LIG->mPWP


Crepidula fornicata: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG $\rightarrow$ PI

correation circie

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency
niche overlap:

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


Dinocardium robustum: LIG-mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency


Similarity mPWP->LIG
Similarity LIG->mPWP



Dinocardium robustum: LIG-PI


axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG->PI


Dinocardium robustum: PI—mPWP

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency


## Similarity mPWP->PI

p.value $=0.01399$

Similarity PI->mPWP


Lucina pensylvanica: LIG-mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency


## Similarity mPWP->LIG



Similarity LIG->mPWP


Lucina pensylvanica: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency


Similarity LIG $->$ PI


## Lucina pensylvanica: PI—mPWP


correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency


## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$

Mercenaria campechiensis: LIG-mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency


## Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP




Mercenaria campechiensis: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency


D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG->PI


Mercenaria campechiensis: PI—mPWP

correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency


## Similarity mPWP->PI



Similarity PI->mPWP


correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->LIG Similarity mPWP->LIG



Neverita duplicata: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency


D
p.value $=0.002$

## Similarity PI->LIG

p.value $=0.002$

Similarity LIG->PI


Neverita duplicata: PI—mPWP

correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


## Similarity mPWP->PI



Equivalency


## Similarity PI->MPWP



## Oliva sayana: LIG-mPWP



axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency

p.value $=0.002$

## Similarity mPWP->LIG



Similarity LIG->mPWP


Oliva sayana: LIG—PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG $->$ PI


## Oliva sayana: PI—mPWP


correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency
niche overlap:
$D=0.445$

Similarity mPWP->PI


Similarity PI->mPWP


Terebra dislocata: LIG-mPWP

correlation circle

axis1 $=45.78 \%$ axis2 $=27.97 \%$


Equivalency


Similarity mPWP->LIG
Similarity LIG->mPWP


Terebra dislocata: LIG-PI

correlation circle

axis1 $=44.18 \%$ axis2 $=28.88 \%$


Equivalency

D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG->PI


correlation circle

axis1 $=46.5 \%$ axis2 $=27.75 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->MPWP


D
p.value $=0.002$

## Appendix S2.3b. Environmental comparisons using a PCA applied to the three most important variables

Results from niche comparison tests for a principle component analysis (PCA) applied to the three most important environmental variables (maximum and minimum surface temperature and maximum surface salinity) using the script of Broennimann et al. (2012). The first two panels represent the niche of the species along the first two axes of the PCA in the respective time periods. The solid and dashed lines represent $100 \%$ and $50 \%$ of the available (background) environment, respectively. The bottom left panel represents the contribution of the climatic variables to the two axes of the PCA and the percentage of inertia explained by the two axes. The top histogram is the simulated similarity values (D) and observed similarity value (red bar) for the niche equivalency test. The bottom two histograms are the simulated and observed (red bar) similarity values for the niche similarity tests. Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.

Anomia simplex: LIG-mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:


## Similarity mPWP->LIG


D
p.value $=0.00999$

Similarity LIG->mPWP

correlation circle

axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency


Similarity PI->LIG


Similarity LIG->PI


Anomia simplex: PI—mPWP


axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.426$

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP



axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency


## Similarity mPWP->LIG



Similarity LIG->mPWP


Bulla occidentalis: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency
niche overlap:

D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG->PI


D
p.value $=0.28971$

Bulla occidentalis: PI—mPWP


axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


Crassostrea virginica: LIG-mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency


## Similarity mPWP->LIG



Similarity LIG->mPWP


D
p.value $=0.002$

Crassostrea virginica: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency

D
p.value $=0.002$

Similarity PI->LIG


Similarity LIG->PI


D
p.value $=0.002$

## Crassostrea virginica: PI—mPWP



axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.314$


## Similarity mPWP->PI



Similarity PI->mPWP


Crepidula fornicata: LIG—mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->LIG Similarity LIG->mPWP


D
p.value $=0.02997$


D
p.value $=0.002$

Crepidula fornicata: LIG—PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$

niche overlap: $D=0.455$

Similarity PI->LIG


Equivalency


Crepidula fornicata: PI-mPWP


axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.158$


## Similarity mPWP->PI



Similarity PI->mPWP


Dinocardium robustum: LIG-mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:
$D=0.519$

D
p.value $=0.002$

## Similarity mPWP->LIG

Similarity LIG $\rightarrow$ mPWP


D
p.value $=0.002$

Dinocardium robustum: LIG-PI

axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency


D
p.value $=0.002$

## Similarity PI->LIG



Similarity LIG->PI


## Dinocardium robustum: PI-mPWP



axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.466$

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->MPWP


D
p.value $=0.002$

Lucina pensylvanica: LIG-mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:
$D=0.302$

Similarity mPWP->LIG Similarity LIG->mPWP


D
p.value $=0.02198$

Lucina pensylvanica: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$

Similarity PI->LIG

D
p.value $=0.002$

Equivalency
niche overlap: $D=0.422$

D
p.value $=0.002$


## Lucina pensylvanica: PI—mPWP



axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.311$

D
p.value $=0.002$

## Similarity mPWP->PI


p.value $=0.02997$

Similarity PI->mPWP


Mercenaria campechiensis: LIG—mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency


D
p.value $=0.002$

## Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP




Mercenaria campechiensis: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency


Similarity LIG->PI


D
p.value $=0.02398$

## Mercenaria campechiensis: PI—mPWP



axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency
niche overlap:
$D=0.5$

p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


## Neverita duplicata: LIG-mPWP



axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:
$D=0.407$

D
p.value $=0.002$

## Similarity mPWP->LIG

Similarity LIG->mPWP

D
p.value $=0.07792$

D
p.value $=0.002$

Neverita duplicata: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency


D
p.value $=0.002$

Similarity PI->LIG


Neverita duplicata: PI-mPWP


axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency


## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$

Oliva sayana: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency
niche overlap: $D=0.43$


D
p.value $=0.002$


Oliva sayana: LIG-mPWP


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:
$D=0.446$

## Similarity mPWP->LIG



Similarity LIG->mPWP


Oliva sayana: PI—mPWP


axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency

D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$


axis1 $=81.77 \%$ axis2 $=13.74 \%$


Equivalency
niche overlap:
$D=0.286$


D
p.value $=0.002$

## Similarity mPWP->LIG


p.value $=0.01798$

Similarity LIG $\rightarrow$ mPWP


Terebra dislocata: LIG-PI


axis1 $=80.81 \%$ axis2 $=15.07 \%$


Equivalency

D
p.value $=0.002$

Similarity PI->LIG


Similarity LIG->PI


## Terebra dislocata: PI—mPWP



axis1 $=82.63 \%$ axis2 $=13.89 \%$


Equivalency


D
p.value $=0.002$

## Similarity mPWP->PI



Similarity PI->mPWP


D
p.value $=0.002$

## Appendix S2.3c. Environmental comparisons using raw temperature variables

Results from niche comparison tests using raw average bottom temperature and maximum surface temperature conducted with a modified script of Broennimann et al. (2012). The histograms are the simulated and observed (red bar) similarity values (D). Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.











## Appendix S2.3d. Geographic comparisons using projections from ecological niche models

Results from niche comparison tests using ENMTools (Warren et al., 2008, 2010) on projections of ecological niche models. The histograms are the simulated and observed (red bar) similarity values (D). Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.











## Appendix S2.3e. Maximum temperature comparisons

Results from comparison of maximum temperature tolerances using script of Broennimann et al. (2012). The right histogram is the simulated similarity values (D) and observed similarity value (red bar) for the niche equivalency test. The left two histograms are the simulated and observed (red bar) similarity values for niche similarity tests. Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.



Similarity mPWP->LIG
Similarity LIG->mPWP
Equivalency



D
p.value $=0.004$
niche overlap: $D=0.598$

D
p.value $=0.002$

## Anomia simplex: LIG-PI




## Similarity PI->LIG

Similarity LIG->PI

Equivalency


Anomia simplex: PI—mPWP


Max temp - mPWP


Similarity mPWP->PI
Similarity PI->mPWP


Equivalency


Bulla occidentalis: LIG-mPWP

Temp max - LIG


Similarity mPWP->LIG

Similarity LIG->mPWP
D
p.value $=0.004$
ornell

Temp max - mPWP

niche overlap: $\mathrm{D}=0.63$

Max temp- LIG


Max temp - PI


Equivalency


Bulla occidentalis: PI—mPWP



Similarity mPWP->PI
Similarity PI->mPWP
Equivalency

p.value $=0.95504$

p.value $=0.01798$

D
p.value $=0.002$

Crassostrea virginica: LIG-mPWP


Crassostrea virginica: LIG-PI

Temp max - LIG


Temp max - PI


Equivalency

D
p.value $=0.002$



## Similarity mPWP->LIG

Similarity LIG->mPWP

p.value $=0.002$

D
p.value $=0.002$

Equivalency


## Crassostrea virginica: PI—mPWP

Temp max - PI


Temp max - mPWP


## Similarity mPWP->PI

## Similarity PI->mPWP


D
p.value $=0.00599$

p.value $=0.002$
niche overlap: $D=0.55$
Equivalency

D
p.value $=0.002$

## Crepidula fornicata: LIG-PI




Similarity PI->LIG



Equivalency
niche overlap: $\mathrm{D}=0.655$


D
p.value $=0.002$

## Crepidula fornicata: PI—mPWP




Similarity mPWP->PI
Similarity PI->mPWP


p.value $=0.002$

Equivalency
D
p.value $=0.002$

## Dinocardium robustum: LIG-mPWP

Temp max - LIG


Temp max - mPWP


Equivalency




Similarity PI->LIG
Similarity LIG->PI


Equivalency


## Dinocardium robustum: PI-mPWP



Temp max - mPWP


Equivalency

D
p.value $=0.002$

Lucina pensy/vanica: LIG-mPWP



## Similarity mPWP->LIG


D
p.value $=0.002$
离
p.value $=0.004$

## Equivalency


D
p.value $=0.002$

Temp max - LIG


Temp max - PI


Equivalency


## Lucina pensylvanica: PI—mPWP



## Similarity mPWP->PI


D
p.value $=0.80919$

Similarity PI->mPWP


Equivalency

D
p.value $=0.002$

Mercenaria campechiensis: LIG-mPWP

Temp max - LIG


Temp max - mPWP


## Similarity mPWP->LIG

Similarity LIG->mPWP

D
p.value $=0.01199$

p.value $=0.002$

Equivalency

iche overlap
$D=0.726$
p.value $=0.00599$

Mercenaria campechiensis: LIG-PI



Similarity PI->LIG
Similarity LIG->PI

p.value $=0.02597$
p.value $=0.02597$
niche overlap: $\mathrm{D}=0.527$

Equivalency

D
p.value $=0.002$

Mercenaria campechiensis: PI-mPWP



## Similarity mPWP->PI

Similarity PI->mPWP

D
p.value $=0.004$

p.value $=0.002$

Equivalency

Neverita duplicata: LIG-mPWP

Temp max - LIG


Temp max - mPWP


Equivalency
容

Neverita duplicata: LIG-PI

Temp max - LIG


Temp max - PI


Equivalency
niche overlap:
$D=0.472$

Neverita duplicata: PI—mPWP



Similarity mPWP->PI
Similarity PI->mPWP

D
p.value $=0.002$

p.value $=0.002$

Equivalency
niche overlap:
$D=0.765$

Oliva sayana: LIG-mPWP


Temp max - mPWP


Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP



Equivalency
p.value $=0.01399$

Oliva sayana: LIG—PI



## Similarity PI->LIG

Similarity LIG->PI

p.value $=0.00799$

D
p.value $=0.15185$

Equivalency
niche overlap: $\mathrm{D}=0.4$




Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP
Equivalency

p.value $=0.002$

D
p.value $=0.002$
niche overlap: $D=0.739$

D
p.value $=0.02797$


Temp max - PI


Equivalency
niche overlap:
$D=0.526$


D
p.value $=0.002$



Similarity mPWP->PI


D
p.value $=0.01598$
p.value $=0.42757$

Equivalency
niche overlap: $\mathrm{D}=0.344$

## Appendix S2.3f. Minimum temperature comparisons

Results from comparison of minimum temperature tolerances using script of Broennimann et al. (2012). The right histogram is the simulated similarity values (D) and observed similarity value (red bar) for the niche equivalency test. The left two histograms are the simulated and observed (red bar) similarity values for niche similarity tests. Observed values falling within the null distribution do not allow for discrimination of similarity or differences based on the environment available to the entities in question. If the observed value falls to the right of the histogram, niches are statistically more similar than expected given the environmental background, whereas if the observed value falls to the left of the histogram, niches are statistically more different than expected given the environmental background.

Anomia simplex: LIG-mPWP



## Similarity mPWP->LIG Similarity LIG->mPWP


D
p.value $=0.20579$

D
p.value $=0.002$

Equivalency
niche overlap:
$\mathrm{D}=0.507$


D
p.value $=0.002$

## Anomia simplex: LIG-PI




Similarity PI->LIG
Similarity LIG $\rightarrow$ PI



Equivalency
niche overlap:
$D=0.808$





Similarity PI->mPWP


niche overlap:
$\mathrm{D}=0.669$

D
p.value $=0.00799$


Temp min- mPWP


## Similarity mPWP->LIG Similarity LIG $->$ mPWP



D
p.value $=0.004$

Equivalency


D
p.value $=0.002$

Bulla occidentalis: LIG-PI

Temp min - LIG


Temp min - PI


Similarity PI->LIG
Similarity LIG->PI

D
p.value $=0.09191$

p.value $=0.0999$
niche overlap: $D=0.759$

D
p.value $=0.002$

Bulla occidentalis: PI—mPWP


Temp min - mPWP


Similarity mPWP->PI Similarity PI $\rightarrow$ mPWP

䓂
p.value $=0.1039$

Equivalency
p.value $=0.002$

## Crassostrea virginica: LIG-mPWP



## Crassostrea virginica: LIG-PI



Temp min - PI


Similarity PI->LIG

Similarity LIG->PI


Equivalency

niche overlap: $\mathrm{D}=0.596$

## Crassostrea virginica: PI—mPWP




Similarity mPWP->PI
Similarity PI->mPWP


p.value $=0.002$
niche overlap $\mathrm{D}=0.66$

Equivalency
D
p.value $=0.00799$

## Crepidula fornicata: LIG-mPWP




## Similarity mPWP->LIG




p.value $=0.002$

Equivalency
niche overlap:
$\mathrm{D}=0.454$

D
p.value $=0.002$

## Crepidula fornicata: LIG-PI




## Similarity PI->LIG

Similarity LIG->PI

D
p.value $=0.00599$

D
p.value $=0.002$

Equivalency
niche overlap: $\mathrm{D}=0.602$



Similarity mPWP->PI Similarity PI->mPWP



D
p.value $=0.004$

Equivalency

D
p.value $=0.002$

Dinocardium robustum: LIG-mPWP



Similarity mPWP->LIG
Similarity LIG->mPWP
Equivalency

D
p.value $=0.10789$

D
p.value $=0.004$

D
p.value $=0.002$

## Dinocardium robustum: LIG-PI




Similarity PI->LIG


Similarity LIG->PI


Equivalency
m.

Dinocardium robustum: PI-mPWP



Similarity mPWP->PI

Similarity PI->mPWP
D
p.value $=0.002$

Equivalency

D
$p$. value $=0.002$

Lucina pensy/vanica: LIG-mPWP



## Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP


p.value $=0.67732$

D
p.value $=0.004$

Equivalency
niche overlap:
$D=0.512$


D
p.value $=0.002$

Lucina pensy/vanica: LIG-PI

Temp min - LIG


Temp min - PI


Equivalency
niche overlap:
$D=0.8$




## Similarity mPWP->PI Similarity PI->mPWP



Equivalency
D
p.value $=0.002$

Mercenaria campechiensis: LIG-mPWP


Temp min - mPWP


Similarity mPWP->LIG
Similarity LIG->mPWP

D
p.value $=0.81918$

D
p.value $=0.002$

## Equivalency

niche overlap: $\mathrm{D}=0.65$

D
p.value $=0.002$

Mercenaria campechiensis: LIG-PI



Similarity PI->LIG
Similarity LIG->PI

D
p.value $=0.002$

D
p.value $=0.002$
Equivalency
niche overlap:
$\mathrm{D}=0.707$


Mercenaria campechiensis: PI—mPWP

Temp min - PI


Temp min - mPWP


## Equivalency

D
p.value $=0.002$

## Neverita duplicata: LIG-mPWP



Temp min - mPWP


Equivalency
niche overlap:
$D=0.507$


D
p.value $=0.002$
Neverita duplicata: LIG-PI

Temp min - LIG


Similarity LIG->PI
D
p.value $=0.002$

Temp min - PI


Equivalency
niche overlap:
$D=0.653$

Neverita duplicata: PI—mPWP



Similarity mPWP->PI


Similarity PI->mPWP

niche overlap: $\mathrm{D}=0.663$

D
p.value $=0.002$

## Oliva sayana: LIG-mPWP



## Oliva sayana: LIG-P|




Similarity PI->LIG
Similarity LIG->PI
Equivalency



D
p.value $=0.002$
niche overlap:
$D=0.546$

D
p.value $=0.002$

## Oliva sayana: PI-mPWP

Temp min - PI


Temp min - mPWP


## Similarity mPWP->PI



Equivalency


D
p.value $=0.002$

## Terebra dislocata: LIG-mPWP




## Similarity mPWP->LIG Similarity LIG $\rightarrow$ mPWP


p.value $=0.17782$

p.value $=0.002$

## Equivalency

niche overlap: $\mathrm{D}=0.419$

D
p.value $=0.002$



Similarity PI->LIG
Similarity LIG->PI

D
p.value $=0.002$

D
p.value $=0.002$

Equivalency
niche overlap: $\mathrm{D}=0.67$

Temp min - PI


Temp min - mPWP


Similarity mPWP->PI


Similarity PI->mPWP

Equivalency
D
p.value $=0.002$


[^0]:    Figure 1.5 Percentage change in suitable area in the western North Atlantic for each of the 14 marine mollusk species from the present day to three future time slices (2021-2040, 2041-2060 and 2081-2100) for all (RCP) emission scenarios. See Table 1.1 for full species names.

[^1]:    Figure 2.2 Representative results from the analyses using a PCA on the three most important environmental variables (maximum and minimum surface temperature, and maximum surface salinity) for Anomia simplex and Oliva sayana. Comparisons are shown for the Last Interglacial (LIG, $\sim 130 \mathrm{Ka}$ ), mid-Pliocene Warm Period (mPWP, $\sim 3.1 \mathrm{Ma}$ ), and present-day (PI). The histograms show the null distribution of similarity values (D), with the observed value in red. All comparisons indicate that niches are statistically more similar than expected given the environmental backgrounds. For other comparisons, see Appendix S2.3 and Table 2.1.

[^2]:    *Note that small islands cited as within a species' dis`tribution may not be accounted for in our models because of the large pixel size $\left(1^{\circ} \times 1^{\circ}\right)$.

[^3]:    Table S1.2.2 Changes in suitable area for 14 mollusk species in the western Atlantic Ocean under different models. Data are for
    MAXENT models. Species names are as in Table S 1.2 .1 . Present $\Delta$, percent change in suitable area from the present-day model when the designated variable is set to future conditions and all others kept at present-day conditions; future $\Delta$, percent change in suitable area from the RCP 2.6 2081-2100 projection when designated variable is held constant at present-day conditions (with all other variables set at future conditions); alkal., total alkalinity; bathy., bathymetry; DIC, dissolved inorganic carbon; D phyt., diatom
    phytoplankton concentration; ND phyt., non-diatom phytoplankton concentration; SSS, sea surface salinity; SST, sea surface temperature; zoopl., zooplankton concentration.

