An Inquiry Concerning the Nature of Racial Discourse

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Abstract

In this dissertation, I assess the nature of racial discourse from an interdisciplinary perspective. I argue against the new biological racial realism, according to which races are genetic natural kinds or distinct parts of the human phylogenetic tree. I show—on both empirical and theoretical grounds—that the reality of race cannot be supported in this way. Then, I turn to evolutionary biology and psychology for a proper account of race that *can* underwrite racial discourse. According to this account, there is no specific psychological mechanism that has evolved to track races in humans: racial cognition in early infancy is the result of a psychological mechanism that humans have evolved to assess similarities/differences in human faces, and racial cognition later in life is the result of various mechanisms that evolved to track social groups of one kind or another.

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Finally, I cannot thank enough to my parents and, my brother, Sinan. Their love and support were my best friends during this journey that I embarked alone in 2012.

In writing this dissertation, I used a previously published work for Chapter 3.

Chapter 3 is a reprinted version of the article: "Osmanoglu, K., & Schulz, A.W. (2019). It Just Looks the Same: An Evolutionary Psychological Account of Differences in Racial Cognition Among Infants and Older Humans. *Review of Philosophy and Psychology, 10*, 631-647.

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Introduction

The question “Do races exist?” has come to be a topic of much discussion in philosophy and related disciplines. Answers to this question can be gathered under two camps: while (i) naturalists argue for the biological reality of races—i.e. the idea races can be distinguished by biological features—(ii) social constructivists argue that races are socially constructed groups. However, there is a gap between these two camps: the answer to the race question does not have to be monistic— race does not have to be either biologically or socially real. On the contrary, a plausible account of racial cognition and discourse might need to be pluralistic, as it might need to be faithful to the biological, psychological, *and* sociological realities of this thought and discourse.

In this dissertation, I lay out and defend such a pluralistic approach. First, I show that race does not have biological reality in the way that biological racial realists argue for: the common, socially recognized races do not correspond to biologically meaningful categories. However, second, I then show how evolutionary biology *can* shed light on why human beings do racially categorize: namely, by pointing to the fact that humans have evolved minds that, for a variety of contingent reasons, tend towards the construction of social categories. In this way, this dissertation is, ultimately, an attempt to bridge the gap between social sciences and evolutionary biology.

Before talking about the structure of the dissertation, it would be useful to explain what this dissertation does not aim at. This dissertation is not a project in “conceptual engineering” (Chalmers, 2018; Machery, 2017) in that it does not suggest what “race” *should* mean (as e.g. (Haslanger (2012) does). Rather, it is an *explanatory* project: the first two chapters of the dissertation *explain* why “race” cannot be seen as a biological category per se, and the last chapter *explains* why people nonetheless engage in racial classification. That said, it is a natural implication of my discussion that we should move away from seeing these classifications as deep features of human society, and that we therefore should build the kinds of social structures that minimize the problems that come from racialization.

The dissertation has the following structure.

In Chapter 1, the focus will be on the phylogenetic conceptions of race, which is one of the most promising views of biological racial realism (BRR). According to this view, races are lineages of reproductively isolated breeding populations. However, I will argue that phylogenetic conceptions of race fail to prove that races are biologically real. I will develop and defend my argument against the phylogenetic views of race by relying on current research in population genetics, human evolution, and social sciences. Ultimately, I will argue that (i) race, so understood, is not a biologically legitimate category and (ii) philosophers should direct their resources to understand problems that arise due to racialization, and thereby they should find solutions to those problems.

Chapter 2 criticizes Quayshawn Spencer's (2014) radical solution to the race problem. Spencer argues that race as used in the current US racial discourse picks out a biologically real entity. First, Spencer states that the current US census classification yields five different races. Second, he argues that recent human population genetic research also yields an interesting level of genetic clustering at the K=5 level. Thus, he contends that the current US racial discourse matches nicely with the recent genetic population clustering results. Therefore, he argues that race, in its US meaning, picks out a biologically real entity. However, I argue that Spencer's argument fails to prove that race is a biologically real entity in a broader sense. Moreover, this broader sense of race is much more interesting than the US sense and does much better justice to the social reality of universal race discourse. Furthermore, there are internal worries with Spencer's argument.

In Chapter 3 (co-written with Armin Schulz), I will present and defend a novel account of racial cognition. Forms of racial cognition begin early: from about 3 months onwards, many human infants prefer to look at own-race faces over other-race faces. What is not yet fully clear is what the psychological mechanisms are that underlie racial thoughts at this early age, and why these mechanisms evolved. In this chapter, I propose answers to these questions. Specifically, I use recent experimental data to argue that early racial cognition is simply the result of a "facial familiarity mechanism": a mental structure that leads infants to attend to faces that look similar to familiar faces, and which probably has evolved to track potential caregivers. I further argue that this account can be combined with the major existing treatments of the evolution of racial cognition, which apply to (near-) adult humans. The result is a heterogeneous picture of racial thought, according to which early and later racial cognition result from very different psychological mechanisms.

Finally, I'll conclude the dissertation with future looking thoughts about philosophy of race.

Chapter 1:

Against Phylogenetic Conceptions of Race

1. Introduction

Biological racial realism continues to be a much-discussed topic, with several recent papers presenting arguments for the plausibility of some type of “biological race.” For instance, Spencer (2014), by relying on current research in population genetics, argues that races are human population clusters; Pigliucci and Kaplan (2003) argue that human races are ecotypes; and Philip Kitcher (1999, 2007) and Robin Andreasen (1998, 2004, 2007) argue for phylogenetic conceptions of race. In this chapter, the focus will be on the latter two—i.e. on phylogenetic conceptions of race (for more on Pigliucci & Kaplan’s argument for races as ecotypes, see Andreasen (2007) and Spencer (2017)). In general, phylogenetic conceptions define races as lineages of reproductively isolated breeding populations (Andreasen, 2007). However, while different phylogenetic conceptions agree that there should be reasonable breeding isolation among human populations for races to evolve, they differ on the current existence of human races: while Andreasen (1998, 2000, 2004, 2005, 2007) argues that races once existed as separate lineages in the human population tree, they are on their way out now; Kitcher (2002, 2007) argues that races still exist in the United States today.

Note that the discussion of races as phylogenetic lineages is independent from the question of whether races are genetic natural kinds, according to which genetic information can be used to assign individuals to population clusters corresponding to major geographic areas, i.e. Africa, Eurasia (Europe, the Middle East, and Central and South Asia), East Asia, Oceania, and America.[1] Although genetic variation among populations is important for phylogenetic conceptions of race, the core idea of these latter conceptions is just this: human evolution can be represented as a branching process. It does not matter if races are genetic natural kinds or not, or if there is enough genetic differentiation among populations to classify them as races. What matters is if human races are monophyletic groups on a phylogenetic tree, i.e. isolated breeding populations.[2] So, even if it were shown that racial terms do not pick out genetic natural kinds, this does not prove that racial terms do not pick out any other biological kinds. Hence, the latter question, i.e. can races be biologically real as phylogenies, still needs to be discussed—and will be the topic of this chapter.

In this chapter, I proceed as follows. In Section 2, I discuss three systematic approaches and three species concepts. In Section 3, I lay out and discuss Kitcher's and Andreasen's arguments for the phylogenetic conceptions of race. In Section 4, I raise biological objections against phylogenetic conceptions of race. In Section 5, I present sociological objections to phylogenetic views of race. Then, in section 6, I conclude.

2. Systematics and the Problem of Species

Kitcher (1999) and Andreasen (1998), independently, advanced and defended very similar accounts of phylogenetic conceptions of race. Both accounts argue that races should be defined phylogenetically: races should be characterized in terms of ancestor-descendent relations.

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[1] See Chapter 2 for discussion and criticism of races as genetic natural kinds.

[2] I should note that Kitcher's phylogenetic concept of race gives more importance to genetic variation than Andreasen does with her cladistics race concept. I will lay out the differences between them below. Note also that, sooner or later, reproductive isolation is likely to lead to significant genetic differentiation. The point is just that we *can* have the former without the latter.

However, before continuing with the arguments in favor of phylogenetic conceptions of race, a brief discussion of defining *species* in biology is apt.

Biologists have given various definitions for "species."[3] Most of these species concepts can be gathered under three general approaches: interbreeding, ecological, and phylogenetic. Each of these approaches has been spelled out in many ways, and each of these continues to be taken seriously in the literature (see e.g. Ereshefsky, 1992). For present purposes, it is mostly the latter that is important, but a few words about the other two are useful as well.

The phylogenetic approach aims to define species by relying on genealogical history.[4] According to this species concept, "an organism [is] a member of a given species if and only if it is historically related to other organisms in the species" (Baum & Donoghue 1995, p. 560). At the core of this approach is monophyly: a taxonomic group should constitute of an ancestor and all its descendants, so that "species must compromise all the descendants of a particular ancestor" (Baum 1992, p. 1). To understand this better, let us look at the figure below.

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[3] For instance, Mayden (1997) counts 22 species concepts, and Zachos (2016) counts 32 species concepts. This shows that the biological literature faces the existence of myriad species concepts, which makes it hard for biologists to delimit the boundaries of species taxa.

[4] For a great discussion on different versions of the phylogenetic species concept, see Velasco (2009)

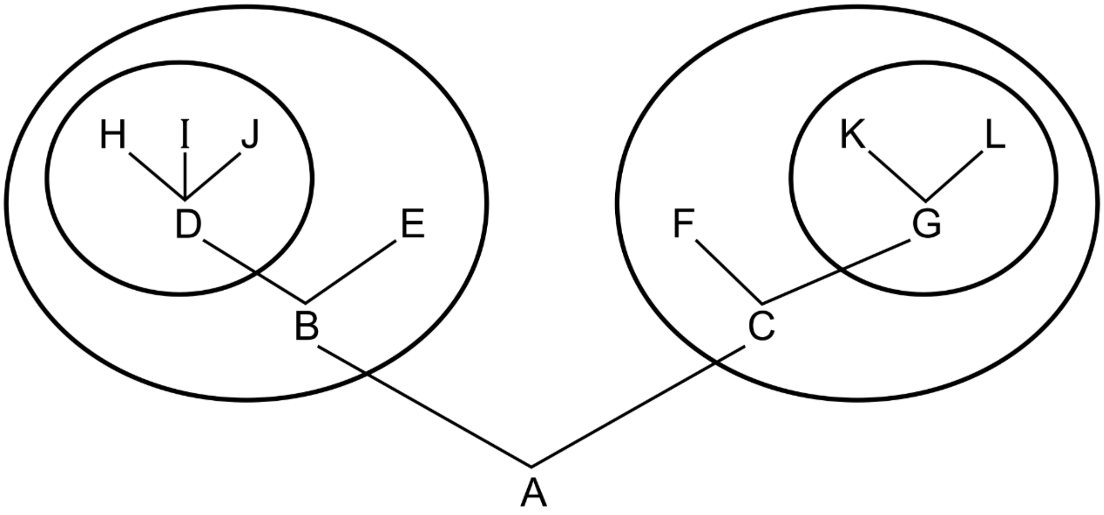

Figure 1: Monophyly figure

There is a simple method to determine the monophyletic groups in a branching structure: the cut method (Sober, 2000). If you cut any branch on this structure, the nodes immediately above the cut will represent a monophyletic group: (B, D, E, H, I, J) is a monophyletic group, and so is (D, H, I, J), and so is (C, F, G, K, L) etc. It is crucial to note that, again, a monophyletic group should be composed of an ancestor and all of its descendants: if we subtract, for instance, L and K from the taxon (C, G, K, L), the remaining species do not constitute a monophyletic group as it does not consist of an ancestor and *all* of its descendants (Sober, 2000). Cladistics demands taxa to be monophyletic.

However, it is also important to note that monophyly can only be a necessary and not a sufficient criterion to delimit species. Monophyletic groups occur at all levels in the genealogical hierarchy—i.e. monophyletic groups can be found at many levels within a clade (Baum, 1992; Baum & Donoghue, 1995b; Mishler & Brandon, 1987; Mishler & Donoghue, 1982). Therefore, a different criterion, in addition to monophyly, is needed to determine which monophyletic groups should constitute phylogenetic species (as opposed to, say, genera or families) on the genealogical hierarchy. Mishler and Donoghue (1982) assert that "species ranking criteria could include group size, gap size, geological age, ecological and geographical criteria, degree of intersterility, tradition and possibly others" (p. 499). Indeed, a key ranking criterion that has been defended here is "exclusivity": it sees species as the smallest monophyletic group (Baum, 1992; Baum & Shaw, 1995). A group of organisms is "exclusive" when all of the members of the group are more closely related to each other than they are to any organisms outside the group (Baum, 1992; Baum & Shaw, 1995). In a purely divergent phylogeny, monophyletic groups tend to be exclusive. On the other hand, in a reticulated genealogy, the monophyletic groups tend to be non-exclusive (Baum, 1992). For instance, although the group that is based on an individual's maternal grandparents is a monophyletic group, it is not exclusive: that individual is more closely related to its father, who is not a member of that monophyletic group, than to its maternal first cousins, who are members of that monophyletic group (Baum, 1992).

All in all, although some philosophers, such as Velasco (2009), and scientists, such as Baum (1992), Baum and Shaw (1995), and Baum and Donoghue (1995a), agree that the phylogenetic species concept should use the concept of exclusivity as a criterion to define species taxa, it is still open to discussion which exclusive groups should be species.[5] This will become important again below.

The second approach towards defining species is called the interbreeding approach. The most well-known version of the interbreeding approach is Mayr's biological species concept (BSC). Mayr (1982) presents two formulations of his biological species concepts. First, Mayr (1982) writes, "Species are groups of actually or potentially *interbreeding natural populations* which are reproductively isolated from other such groups" (p. 273). Second, a "species is a

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[5] For instance, while Mishler and Brandon (1987) present a pluralistic and a pragmatist view, arguing that different taxa are ranked as species for different reasons, Mishler (1999) argues that we should eliminate the rank of species.

reproductive community of populations (reproductively isolated from others) that occupies a specific niche" (Mayr 1982, p. 273).[6] He also notes that "[i]solating mechanisms are biological properties of individuals which prevent the interbreeding of populations that are actually or potentially sympatric" (Mayr 1982, p. 274).[7] These two formulations present three properties of biological species concept: species should be actual or potential interbreeding populations, species are reproductive communities, and species are separated from other organisms by isolating mechanisms, which "prevent interbreeding among interspecific organisms or prevent the production of fertile offspring if such interbreeding does occur" (Ereshefsky 1992, p. 672).

The third and final approach towards defining speciation is the ecological approach to species. The defenders of the ecological approach argue that "[a] species is a lineage (or a closely related set of lineages) which occupies an adaptive zone minimally different form that of any other lineage in its range and which evolves separately from all lineages outside its range" (Van Valen 1976, p. 233). According to this view, species are ecological units, what counts as species depends on the adaptive zone. The core idea of this concept is that of niche occupation: species should occupy minimally different niches to be accepted as distinct species. There is much controversy surrounding this species concept (see Ghiselin (1987, 1997); Mayr (2000); Meyer (1990); Ridley (1989)), however, I will not evaluate this controversy here.

I will not discuss the details of the interbreeding and the ecological species concepts. What matters here is just that the phylogenetic species concept (a) struggles with distinguishing species

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[6] Reproductive isolation is at the core of the BSC. For the latter, niche occupation and reproductive isolation are really just two sides of the same coin. By contrast, *only* niche occupation—independently of its relation to reproductive isolation—is at the core of the ecological species concepts. See below for more on the importance of "niches" in species concepts.

[7] Mayr (1982) restricts isolating mechanisms *only* to biological properties of species, unlike Dobzhansky (1937), who argues that isolating mechanisms can be divided into the biological and the geographical categories.

from other taxonomic groups, and (b) is not the only species concept in existence. Put differently, the key point here is that there is still much controversy surrounding species concepts even in the core areas of biology. Indeed, some authors have gone so far as to suggest that we have reasons to doubt the existence of the species category *in toto* (Ereshefsky, 1998). With these points in mind, it is now possible to discuss phylogenetic conceptions of race.

3. Phylogenetic Conceptions of Race

Andreasen (1998, 2000, 2004, 2005, 2007) adapts the cladistic classification of species to show that a biologically objective definition of races is possible: she argues that cladistic races are groupings of organisms produced by nature.[8] Specifically, Andreasen (1998) says: "Races are monophyletic groups: they are ancestor-descendant sequences of breeding populations, or groups of such sequences, that share a common origin" (p. 214). Put differently, Andreasen (1998) argues that cladistic classification can be applied to taxonomic levels below the species level, and that these cladistic subspecies (within the species of *homo sapiens*) are (the) human races.

In the background of this view is the fact that she thinks that it is possible to represent human evolution, until recently at least—a critical point to which I return momentarily—as a branching process. She notes that several research groups provide evidence for the view that, for much of its time, human evolution followed a branching pattern (L. Luca Cavalli-Sforza, 1997; Luigi Luca Cavalli-Sforza, Paolo Menozzi, & Alberto Piazza, 1994; Mountain & Cavalli-Sforza, 1997; Nei & Roychoudhury, 1993; Vigilant, Stoneking, Harpending, Hawkes, & Wilson, 1991; A. C. Wilson & Cann, 1992). She cites the following population tree:

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[8] See Spencer (2017).

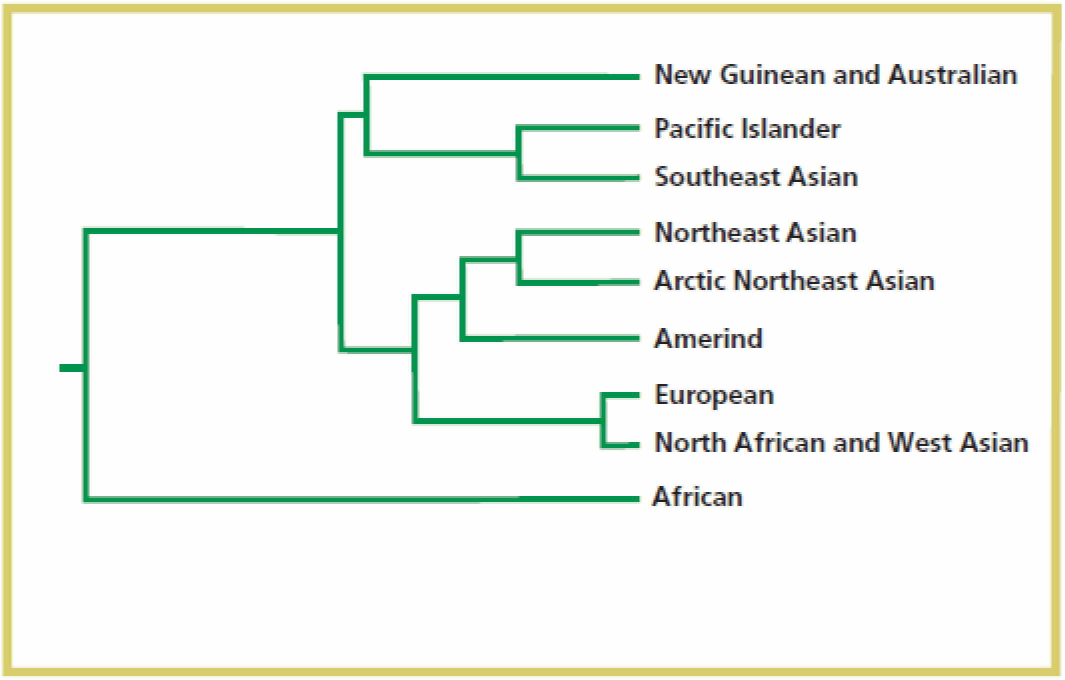

Figure 2: The figure of the population tree. (Reprinted by permission from Springer Customer Service Center GmbH: Springer Nature, NATURE GENETICS, The application of molecular genetic approaches to the study of human evolution, Cavalli-Sforza, L. L., & Feldman, M. W. [COPYRIGHT] (2003).)

For what follows in section 5 below, it is useful to note immediately that, according to this tree, Pacific Islander and Southeast Asian is a cladistic race, but "Asian" is not.[9]

It is furthermore important to note that it does not matter for Andreasen if the tree above—derived from Cavalli-Sforza's work—is the correct one. The crucial point is whether patterns and processes of human evolution can be represented in *a* tree—the exact details of that tree can be left open here.

There is one further key point that should be flagged about Andreasen's cladistic race concept: she thinks that biological races once existed but that they faded away due to recent

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[9] It is critical to note that L. L. Cavalli-Sforza, P. Menozzi, and A. Piazza (1994) and L. Luca Cavalli-Sforza (1997), unlike Andreasen, interpreted the results of their studies as evidence to undermine the existence of biological human races.

historical events, such as discovery of new lands, immigration, and colonization. These events lead to the reproductive isolation among population groups that has occurred in the distant past to be breaking down today. She contends that the phylogenetic tree reconstructed by L. L. Cavalli-Sforza et al. (1994) demonstrates that Old World human populations were reproductively isolated from each other for a substantial amount of time. The reconstructed phylogenetic trees do not imply the existence of races today, they only describe racial ancestry (Andreasen, 1998). Therefore, she concludes that races once existed in the past.

In short, according to Andreasen, if they are anything, "races are ancestor-descendant sequences of breeding populations that share a common origin" (Andreasen 2004, p.425). In this way, Andreasen contends that race is biologically real (in a historical sense)—but probably soon will cease to be.

Kitcher's phylogenetic conception, unlike Andreasen's cladistic race concept, has two components: genetic and phylogenetic. Kitcher (1999), like Andreasen, asserts that races should, in the first instance, be defined phylogenetically. On his view, races are founding populations: populations that do not interbreed and have been phenotypically and genetically differentiated because of this lack of interbreeding. These populations stay separated from each other because of migration and geographic barriers. This isolation causes very low to none genetic flow to occur among founding populations over the time. Therefore—and this is the second aspect of Kitcher's account—genetic and phenotypic differentiation occurs among these populations. The genetic or phenotypic differentiation among populations is thus a good guide to demarcate races. For instance, when previously separated populations are brought back together, the gene exchange is still very low among them. In other words, there is still significant amount of reproductive isolation among once separated populations to sustain distinctive phenotypic and genetic properties that identify races (Andreasen, 2007; Kitcher, 1999). Although there is no substantive data, Kitcher relies on interracial relationships and reproduction in the US to argue that historically separated and reproductively isolated groups do not interbreed as much even though they are brought back together. Therefore, he concludes that biologically meaningful races still exist in the US today.

In this way, it becomes clear that both accounts define races phylogenetically. The difference is that, first, although genealogy is sufficient to define races in Andreasen's cladistic account, in Kitcher's account, it is a necessary and not a sufficient condition. On Kitcher's account, in addition to genealogy, there needs to be genetic or phenotypic differentiation among distinct races. Second, Andreasen requires monophyly for populations to be races, i.e. populations should be reproductively isolated for a considerable time for cladistic races to evolve. However, Kitcher does not require monophyly. On Kitcher's view races can either be historical lineages (founder populations), or non-dimensional lineages, i.e. populations that are reproductively isolated at a specific space and time.[10] Lastly, Andreasen argues that races once existed but they are on their way out today, but Kitcher argues that races still exist in the U.S. today. However, for present purposes, the focus will be on the communalities of the two views: namely, that they define races at least partly phylogenetically. For this feature of these accounts alone encounters two serious sets of objections: biological and sociological. The next section will focus on the biological objections; the one after that will focus on the sociological objections.

4. Biological Objections to the Cladistic View of Races

The first objection against the phylogenetic race concepts concerns the existence of an evolutionary tree of human populations to begin with. Recall that the phylogenetic race conception—like the phylogenetic concept of species—*requires* that the human tree of life

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[10] Races in the U.S. today are an example of non-dimensional races.

contains distinct breeding populations. While this objection also applies to Kitcher's phylogenetic conception of race, it is particularly problematic for Andreasen's cladistic race concept (as noted in section 3, Kitcher's conception does not require human populations to be reproductively isolated for a significant amount of time). Recall also that Andreasen, in her defense of cladistic races, relies heavily on Cavalli-Sforza's work on population genetics. However, as I argue in what follows, current research in population genetics and human evolution show that these assumptions are problematic: it is not clear that human populations can be represented as branches on an evolutionary tree, i.e. that humans ever had cladistic races in the past. This is for two reasons: i) there are alternative explanations of human genetic patterning and ii) the existence of genetic patterning is dubious to begin with.

First, if the defenders of the phylogenetic conceptions of race are right, and human populations stayed reproductively isolated for a significant period, significant genetic differentiation should have occurred among these populations due to their historical splits (as also noted by Kitcher). Hence, evidence of such genetic variation might be thought to be the evidence for a branching pattern of human evolution. However, the situation is more complex than that.

Particularly, genetic differentiation can occur due to restricted gene flow and to genetic interchange without a historical split (Templeton, 2006). For instance, there could be limited gene flow among distant populations because most dispersal of genes happen in local populations (Templeton, 2006). However, this does not necessarily mean that distant populations are reproductively isolated. So, according to the stepping-stone models, genes are passed from one generation to another and they spread through distant geographic locations.[11] According to these models, there are no sharp genetic differentiations among populations that separate them into distinct lineages on a tree. Genetic differentiation, according to the stepping-stone models, increases as geographical distance increases among populations, i.e. genetic distance is proportional to geographic distance: this is called isolation-by-distance. Isolation-by-distance causes genetic differentiation to occur among human populations as human groups interchange genes with nearby populations more than they do with geographically distant populations.[12] Therefore, genetic differentiation caused by isolation by distance accumulates gradually with distance; however, it does not cause sharp genetic breaks between human populations.[13]

In short: it may be true that there are genetic differences among different human populations; however, this may not be due to branching pattern of human evolution but to geographical distance: human populations interchange genes more with closer neighbors than with further neighbors. So, there are no biological "fault lines" that can be used to divide human populations into "races." [14] Put differently: while it is true that there is genetic differentiation among populations, the patterns of genetic differentiation in current human populations is better explained by isolation-by-distance model than a tree model (Eller, 1999; Templeton, 1998, 2006, 2013). Therefore, genetic differentiation alone does not guarantee a branching pattern of evolution

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[11] The stepping stone model of population structure is a type of isolation by distance model (see Kimura and Weiss (1964)).

[12] It is possible to see the isolation-by-distance pattern in many different geographical scales. For instance, Lasker and Crews (1996) and Santos, Epplen, and Epplen (1997) show that there was high gene flow between geographically close populations.

[13] For classical discussions of isolation by distance, see Wright (1943) and Kimura and Weiss (1964).

[14] Genetic distance among populations data presented by, e.g., L. L. Cavalli-Sforza et al. (1994) and Bowcock et al. (1991) also fit isolation-by-distance pattern rather than a tree model of human population evolution. Moreover, whenever a set of human genetic distance is tested for treeness, it turns out that the data is consistent with isolation by distance (L. L. Cavalli-Sforza et al., 1994) but not with treeness (Templeton, 1998).

of human populations—and it should not be taken as a straightforward evidence for the cladistic view of races.

At any rate, if the existence of genetic differentiation among local populations were considered evidence for the existence of races, then many species would have thousands of "races," and that would trivialize the concept of race. In such a case, races would be nothing more than a placeholder for local populations. Therefore, this would make race a trivial biological concept that is not a taxonomic unit and that does not have a specific place in phylogenetic taxonomy.[15]

The second biological worry for the cladistics concept of race is that the existence of genetic patterning is dubious to begin with (Templeton, 2013, 2017). One way to see this is by noting that there are various methods to test genetic data for treeness, but that these methods do not provide support for the existence of an intra-human evolutionary tree.[16]

One of the standard measures to check if population genetic distance data fit treeness is the cophenetic correlation.[17] The cophenetic correlation measures the correlation between the observed population genetic distances to the expected values generated by the estimated tree (Rohlf, 1988; Templeton, 1998, 2006). According to this measure, to justify the treeness of a generated tree, there needs to be a cophenetic correlation of genetic differentiation greater than 0.9—and any value below 0.8 is considered as poor fit—between the estimated tree and the observed population genetic distances. That is because since the trees are estimated from the given

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[15] To elevate the local populations to the level of race, or subspecies, a certain amount of genetic differentiation should exist among local populations. For instance, according to one measure, F_{st} static, there should be 25% or more genetic differentiation among local populations for them to be considered as different races, or subspecies. (H. M. Smith, Chiszar, & Montanucci, 1997; Templeton, 2013; Wright, 1978).

[16] For a great discussion of major methods of inferring phylogenetic trees, such as distance methods, parsimony methods, and likelihood methods, see Felsenstein (2004).

[17] See Templeton (1998, 2006, 2013) for more on this.

genetic distance data, a large and positive value of cophenetic correlation is expected from the get-go. The estimated trees should not be accepted as an actual evolutionary tree. Therefore, researchers should go one step further and test how well the population genetic distances in fact fit treeness: they should test the correlation between the population genetic distances and the expected values generated by the estimated tree (Templeton, 2006).

However, in fact, we do not find a high cophenetic correlation. For instance, data sets used by researchers such as Bowcock et al. (1994), Mountain and Cavalli-Sforza (1997), and Nei and Takezaki (1996) show that the cophenetic correlation value ranges from 0.45 to 0.79 when they are tested for treeness (Templeton, 1998, 2006); for the data set used by Mountain and Cavalli-Sforza (1997), the cophenetic correlation is 0.79.[18] This shows that the very same data sets that are used by researchers to show that there is an evolutionary tree of human populations *reject* treeness for human populations. Indeed, the small cophenetic correlation seems to fit better to the isolation-by-distance model of human divergence, rather than a tree-based view.[19] Therefore, the cladistic race concept faces the problem that it lacks compelling empirical support for the hypothesis that "reasonable" genetic differentiation (Andreasen, 2005, 2007) arises among human populations due to branching structure of human populations.

Andreasen (2007) responds to this objection by arguing that it "applies only to phylogenetic trees constructed using genetic distance based methods. [Therefore this] argument is somewhat limited in scope" (p. 496). However, this response will not in fact salvage Andreasen's cladistic

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[18] The low cophenetic correlation of Cavalli-Sforza et al.'s tree is important here, because Andreasen relies heavily on their work. However, as noted in the text, even if she supports the existence of evolutionary tree of human populations with other research, she would fail again: there are no datasets that provide compelling evidence for a tree structure of human populations.

[19] That is because small cophenetic correlation is expected for isolation-by-distance model: human populations were not genetic isolates and they frequently interchanged genes with nearby populations.

races. Andreasen supports her response by appealing to the clustering methods used by Rosenberg et al. (2002). Rosenberg et al. (2002), by running the program STRUCTURE on genetic survey of 52 populations, were able to sort individuals into five biologically meaningful groups, when the K value is set to 5. Rosenberg et al. (2002) found out that "genetic clusters often correspond closely to predefined regional or population groups or collections of geographically and linguistically similar populations" (p, 2384). Andreasen probably equates clusters with reproductively isolated breeding populations, which, as such, is closer to Kitcher's approach than her own. Therefore, she thinks that the results of Rosenberg et al.'s (2002) provide evidence for the existence of isolated lineages in human populations in the past.

However, clustering programs like STRUCTURE can overestimate genetic structure when analyzing a data set characterized by isolation-by-distance (Frantz, Cellina, Krier, Schley, & Burke, 2009; Safner, Miller, McRae, Fortin, & Manel, 2011). Bayesian clustering methods like STRUCTURE generate clusters when a population is characterized by isolation by distance: they incorrectly detect boundaries when they are presented with strong patterns of isolation by distance (Safner et al., 2011). However, the apparent "races," or isolated populations, or discrete clusters of Rosenberg et al. (2002), disappear with better sampling.

For instance, Serre and Paabo (2004) present an analysis to demonstrate the importance of fine-scale geographical sampling and how study design can affect conclusions about population structure. Many global studies on populations find that individuals can fit into discrete clusters depending on their geographic origin (Bamshad et al., 2003; Bowcock et al., 1991; Bowcock et al., 1994; L. Luca Cavalli-Sforza, 1997; L. L. Cavalli-Sforza, Piazza, Menozzi, & Mountain, 1988; Jorde et al., 1997; Mountain & Cavalli-Sforza, 1997; Serre & Paabo, 2004). In particular, Serre and Paabo (2004) found that if sampling is based on individuals and geography rather than on "populations," discrete genetic clusters of humans fade away: "gradual variation and isolation-by-distance are better representations of human genetic diversity than are discontinuities among continents or "races"" (p. 1679). Similarly, Behar et al. (2010) sampled Old World populations more finely and used STRUCTURE: they found that most individuals have mixed ancestries and they do not belong to a "pure" population.[20]

All of this shows that Andreasen is wrong to argue that programs like STRUCTURE provide evidence for the hypothesis that cladistic races existed in the past. Therefore, relying on clustering analysis will not save Andreasen's cladistic race concept.

It is important to flag that both objections are epistemic objections: they note that the data do not clearly favor a tree-based view of human evolution. There is no clear data that favor the hypothesis that human population evolution had a branching pattern and there is data that support that a non-branching pattern represents human population evolution better than branching patterns (Templeton, 1998, 2002, 2013; Wolpoff, Hawks, & Caspari, 2000; Wolpoff, Thorne, Smith, Frayer, & Pope, 1994). Given this, a defender of the phylogenetic concept of race, such as Andreasen, might argue that the above does not show that the cladistic race concept is untenable. This is because human populations *were* isolated breeding populations in the past, but, as time passed, the contact between isolated groups has increased (outbreeding), thereby genetic differences among populations have decreased, or faded away. Hence, we do not now find evidence of the branching pattern of human evolution—though such a pattern did arise. This point

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[20] Kopec (2014) also, similarly, criticizes Andreasen for her use of population clusters as evidence for the existence of biological races. However, while we both argue that the existence of population clusters does not support biological races in humans, our motivation of doing so and our conclusions are different from each other. Moreover, Kopec (2014) and I provide different kinds of support for the views that we put forward. While Kopec (2014) argues that there is still work to be done to determine whether population clusters pick out biologically meaningful human races, my conclusion is more radical than that. As I make clearer below, I argue that we should stop searching whether there are biologically meaningful human races as the concept of "race" is inherently a social one. Therefore, research in biology will not settle the debate in philosophy of race.

is especially compelling for Andreasen's cladistic race concept, since she argues for the unique position that cladistic races existed in the past, but they may be on their way out today.

However, this response, too, only goes so far. First, as noted above, the issue is not just that the data do not underwrite the fact that human populations are currently divided into distinct genetic groupings, but also that these data do not favor a *tree-based view of human evolution*. Put differently, current research shows that there always was gene-flow among populations, i.e. that human populations were never pure isolates (Hunley, Healy, & Long, 2009; Templeton, 2006, 2013; Wolpoff et al., 1994).[21]

Second, recall (as noted in section 2) that the monophyletic approach of the phylogenetic species concept defines species as the smallest exclusive monophyletic taxa. Andreasen modifies this according to her cladistic race concept, and she argues that *subspecies* are the smallest exclusive monophyletic taxa. However, this inherits all the problems that the phylogenetic species concept encounters with—and more. For instance, there are monophyletic groups at each level in the hierarchy of biological classification, e.g. there are monophyletic groups in species, genus, family and so on. Also, it is possible to find smaller exclusive monophyletic taxa below the subspecies level. Given all of this, it is not clear why we need to draw the line at the subspecies level and not below the subspecies level, e.g. at the family level to define races in humans.[22] Put

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[21] It is worthwhile emphasizing again that this does not mean that all humans are genetically same. There is genetic differentiation among humans that has occurred due to isolation-by-distance, i.e. as geographic distance increased so did the genetic differentiation, and other restrictions on gene flow, but these genetic differences are not in favor of the existence of discrete human populations. Therefore, there are/were not cladistic races in human species.

[22] For other reasons why there are no subspecies in humans, see Templeton (2013).

it differently, Andreasen does not give us any principled reason why we should not apply cladistic classification to levels below the subspecies, and call those exclusive monophyletic taxa races.

All in all, therefore, phylogenetic conceptions of race fail to prove that race is biologically a legitimate category. However, there are yet further difficulties with the cladistic concept of race.

5. Sociological problems with the phylogenetic conceptions of race

One of the main reasons of why philosophers have tried to answer the question, “What is race?” is understanding the nature of race, and thereby shedding light on social, political, and economic problems related to racial categorization. Philosophers aim to amend injustices arising due to racialization. If we accept the cladistic race concept, can it give an account of the roles that racialization plays? Put differently: why should we think that cladism has anything to do with races at all?

It is widely accepted that racialization causes disparities in health, education, and housing (Sundstrom, 2002), and inequalities in economic, political, and legal domains (Haslanger, 2012). For instance, (Sundstrom, 2002) writes,

> Differences in the health status of individuals in the USA correlate to racial differences. Infant mortality rates, rates of disease and death from disease, running the gamut from serious illnesses, such as certain forms of cancer or HIV, to such conditions as diabetes, as well as hypertension, high cholesterol, and obesity, which lead to cardiovascular disease: these are higher for African Americans, and people of color in general, than they are for whites. The range of this phenomenon is staggering, and the severity of this situation is increasing (p. 97).

On top of this, several scholars argue that being a member of race *X* in a society in which race plays a critical role correlates with—or even *means*—being subjugated in a general sense. For example, Haslanger (2012) defines racialized groups as follows: “A group is racialized iff$_{\text{df}}$ its members are socially positioned as subordinate or privileged along some dimension (economic, political, legal, social, etc.), and the group is "marked" as target for this treatment by observed or imagined bodily features presumed to be evidence of ancestral links to a certain geographical region" (p. 236). This kind of hierarchical classification and division is inherently unjust—quite apart from the inequalities and disparities in various socio-economic domains arising due to it.

Can a phylogenetic conception of race account for racialization and its implications? On the face of it, a defender of a phylogenetic conception of race might think that knowing the genealogies of racial groups can contribute to understanding at least some of these social aspects of racialization. For example, a phylogenetic conception of race might be used to help us detect race-specific diseases, and thus aid us in finding ways to cure these. However, this kind of phylogenetic approach towards the social roles of race is in fact implausible.

On the one hand, there are, to date, no known race-specific diseases which are independent of socioeconomic conditions.[23] In identifying race-specific diseases, it is crucial not to disregard the socioeconomic factors that racialization creates: it is invalid to infer a causal relationship between being a member of race X and having a specific disease from observing disproportionately high distribution of that specific disease in race X in comparison to the rest of the society.[24] For instance, it is well-known that, in the US, the blood pressure of African descent persons is higher than that of other racial/ethnic groups (Cooper, 2013; Cooper et al., 2015; Cooper & Rotimi, 1997; Cooper et al., 1997). However, as shown by Cooper et al. (2015), this trait is best explained as the

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[23] At this point it should be qualified what I mean with there is no race specific diseases. Of course, there are genetic diseases that vary among populations: Tay-Sachs disease, cystic fibrosis, hemoglobin anomalies, and so on are present in some populations but absent in others. For instance, people of Jewish descent, not "white," share a risk of Tay-Sachs disease; the frequency of cystic fibrosis varies within Europe; and sickle cell anemia is distributed from sub-Saharan Africa to the Mediterranean (Cooper, Kaufman, & Ward, 2003). It is critical to flag that these chronic diseases are not specific to "races," though.

[24] See, e.g., Cooper et al. (2003) and Maglo, Mersha, and Martin (2016).

result of being placed in an environment where race plays a critical role (and not as the result of some racial genetic predisposition, say). They conduct research in the African diaspora in distinct regions: Chicago, Kingston, Jamaica, rural Ghana, Cape Town, South Africa, and the Seychelles. They find that African populations with lower socioeconomic status in racially heterogenous societies, such as the US and South Africa, experience more hypertension than the rest of the African populations in the study (Cooper et al., 2015). This, and other similar studies[25], show that socioeconomic factors play a more critical role than biological factors in determining the existence of disparities in multiracial societies.

On the other hand, phylogenetic conceptions of race will anyway be silent in explaining many of the major social consequences of racialization. For instance, phylogenetic conceptions of race cannot explain why there are large gaps of wealth and income between "black" and "white" in the US today.[26] Moreover, phylogenetic conceptions cannot explain why there is "a significant bias in the killing of unarmed black Americans relative to unarmed white American, in that the probability of being (black, unarmed, and shot by police) is about 3.49 times the probability of being (white, unarmed, and shot by police) on average" (Ross, 2015). These are just some instances of social consequences of racialization, which cannot be explained or given an account with having more information about genes or knowing that races are clades, or isolated breeding populations.

At this point, the defender of the phylogenetic views of race might argue that it does not matter if their concepts cannot account for the social role of racial categorization, such as

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[25] For instance, Cooper and David (1986); Cooper and Rotimi (1997).

[26] While the median household income was $44,100 among blacks, it was $75,100 for whites in 2015 (Bialik & Cillufo, 2017).

racialization, as they are trying to understand the *nature* of race but *not* the normative implications of racial categorization. They might agree on the fact that racialization has negative social and institutional affects, and it may cause disparities among racial groups. However, these problems arise due to various social dynamics but not due to the biological reality of race, and the social reality and impact of racialization do not change the fact that, at bottom, race is a biological entity, i.e. races are phylogenies.

To some extent, this is a fair response. However, there are two problems with it. First, it is irresponsible for biological racial realists not to realize that they usually equivocate socially defined races with biological conceptions of race; they treat social races as legitimate biological races.[27] Biological racial realists tend to think that, at the most general level, there are five major races—Africans, Caucasians (European and Non-European), Northeast Asians, Southeast Asians, and Pacific Islanders (including New Guineans and Australians) (Andreasen, 2004; Spencer, 2014). Both Andreasen (2004) and Spencer (2014) argue that these five biological races overlap nicely with the social races in the US.[28] However, biological racial realists do not realize that biological and social conceptions of race go apart, and even where they do not, the dynamics giving rise to them are very different. While the biological races are the result of the evolutionary dynamics of our species, such as migration, genetic isolation, and genetic drift, the social races have to do with social and cultural dynamics, such as colonialism, slavery, and genocide. For instance, as noted in section 3, the phylogenetic views of race disagree with typical social racial classifications: while "Asian" is a race according to social racial classifications (e.g. US Census),

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[27] For instance, see Graves (2010, 2015) and Friedman and Lee (2013).

[28] While Andreasen (2004) refers to the US Census 2000, Spencer (2014) refers to the US Census 2010 to argue for the overlap between biological races and social races.

it is not a race according to the phylogenetic views of race. Therefore, even though the biological and social races have the same, or very similar, extensions, the construction of, or making of, social and biological races are the result of different dynamics.

Second, an account of "race" that fails to account for the social aspects of racialization is too impoverished.[29] Phylogenetic accounts of race characterize, at best, the biological races. However, if these biological races have nothing to do with social conceptualizations of race, it is not clear why we should care about them (especially given the biological problems surrounding the biological conceptualizations of race).[30] If the phylogenetic views of race cannot make any contribution to explaining the roles of racialization, it becomes much less interesting. Our curiosity about the nature of race is socially loaded: our scientific concerns is guided by a concept that is inherently social, not biological. What we want to know is why African-Americans earn less than Whites in the US, or why people in African countries do not experience as much hypertension as African descent people do in the US.[31] Explaining the critical roles that race plays, and thereby eliminating the detrimental consequences of racialization, such as racism, are what most research on race should be about. Normative concerns should guide our questions about race. We should seek ways of treating people with fairness and justice and should find solutions to the harms done by racialization.[32] If phylogenetic conceptions of race are silent on these matters, there is little reason to hold onto them.

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[29] See Stacey (1992), Resnick (2000), Benjamin H Isaac (2006), Nirenberg (2014).

[30] Note also that the position here differs from an account like that of Spencer (2014), which explicitly tries to connect socially defined races and biological races. Spencer (2014) argues that socially constructed races are legitimate biological races.

[31] See Cooper et al. (2015).

[32] At this point, I agree with Mallon (2006) that the problem of race is a normative one, i.e. what do we want our concept(s) of race to do in this world.

6. Conclusion

In this chapter, I have argued that one of the most promising views to defend the biological reality of race, i.e. phylogenetic conceptions of race, fails to prove that races are biologically real. I have argued against two phylogenetic views presented by Kitcher and Andreasen. I have developed and defended my argument against the phylogenetic conceptions by relying on current research in population genetics, human evolution, and social science. All in all, races are not biologically legitimate. Thus, philosophers should direct their resources to understand problems that arise due to racialization, and thereby they should find solutions to those problems.

Chapter 2:

The Biological Reality of Race does not underwrite the Social Reality of Race

Quayshawn Spencer (2014) defends the biological reality of race. He argues that race, as used in the current US racial discourse, picks out a biologically real entity. He lays out his argument in two steps: first, he argues that race, in the US racial discourse, is a proper name for a set of human population groups, and second, by relying on recent data from human population genetics, he says that the set of human population groups matches the Blumenbachian partition, i.e. the US meaning of race is the set of populations at the K = 5 level of human population structure: Black Africans, Caucasians, East Asians, Amerindians, Oceanians. Therefore, Spencer argues that race, in its US meaning, picks out a biologically real entity.

However, I argue that Spencer's argument fails to prove that race is a biologically real entity in a *broader* sense, i.e. broader than the US meaning of race. Moreover, this broader sense of race is much more interesting than the US sense and does much better justice to the social reality of universal race discourse. Apart from this, there are internal worries with Spencer's argument, in that the kind of genotypic clustering (K = 5 level of human population structure) he relies on is not the only biologically interesting way of clustering human populations.

In the following chapter, first, I will lay out Spencer's argument. Second, I will present two criticisms of Spencer argument. Finally, I conclude.

1. Spencer's Argument

Before presenting the criticism of Spencer's argument, let me summarize Spencer's view. Spencer thinks that folk racial classification has a biological basis—in particular, he argues that the current US meaning of race is a proper name for a biologically real entity. First, Spencer states that the current US census classification yields five different races. Second, he argues that recent human population genetic research also yields an interesting level of genetic clustering at the K=5 level. Thus, he contends that the current US racial discourse matches nicely with recent genetic population clustering results, i.e. K=5 level of human population structure. (Spencer calls the K=5 level of human population structure ‘the Blumenbach partition’ in honor of J.F. Blumenbach.) Therefore, he argues that race, in its US meaning, picks out a biologically real entity, i.e. US racial categories are biologically real.

Spencer relies on recent findings of human clustering analysis to support the biological reality of race. He relies on Rosenberg et al.’s (2005; 2002) studies to demonstrate that the US census races overlap with five genetic clusters when *K* was set to 5. Rosenberg et al. (2005; 2002) use a Bayesian clustering program, *Structure*, to determine the number (*K*) of clusters in a given population genetics data set. *Structure* utilizes multi-locus genotype data to estimate the *K* of genetic clusters in a given data set and to assign individuals probabilistically to those *K* clusters. It yields the number *K* of clusters that is requested by the user. Rosenberg et al. (2002) analyzed 377 genetic markers in 52 populations around the world (they used HGDP-CEPH Human Genome Diversity Cell Line Panel), and they identified five genetic clusters that correspond to five major geographic regions when *K* was set to 5. Rosenberg et al. (2002) think that there is an interesting level of genetic clustering at the K = 5 level, and K = 5 best represents the genetic variation in the data set used.[33] Thus, Spencer argues that current US census classification, which yields 5 different races, match up with the results of genetic clustering research (when K is set to 5).

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[33] However, as I will discuss below, K = 5 is not the only number which yields interesting clustering results. Moreover, Rosenberg et al.’s (2002) data set produce other clusters when K was set to numbers between 2 and 20. Therefore, Bolnick (2008) argues that the comparison between K=5 and other number K of clustering does not suggest that K = 5 best represents the genetic variation in Rosenberg et al.’s (2002) data set. I will not go into details of these

This is the general structure of Spencer's argument. I will go into the details of Spencer's argument below.

2. The Social Reality of Race: Going Beyond the US

I find limiting the racial discourse to the US Census problematic. Why do we need to care only about what the US racial discourse tells us about human population groups? I think that Spencer, by limiting the racial discourse to the US race, does not do justice to the culturally diverse social reality of racial discourse. Racial discourse can be found in many parts of the world.[34] Hence, any theory supporting the biological reality of race needs to somehow acknowledge this diversity. I argue that if Spencer wants to vindicate the biological reality of the social concept of race, then he needs to vindicate his account in various cultures and societies, rather than only in the US, or alternatively, he needs to argue that the current US census classification of race is particularly interesting; however, neither of these options is promising. In this section, I will raise a criticism against Spencer by showing how racial categorization changes with respect to socio-economic developments over the time, and how states involve in race making. The main aim is to demonstrate that races are not biological concepts, but they are socio-historically constructed.

Spencer argues that race is a proper name for the following population groups: "Black," "White," "Asian," "Amerindian," and "Pacific Islander". However, this categorization does not apply globally: racial categorization of human populations differs cross-culturally. I argue that

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issues here since this not the aim of this chapter. See Bolnick (2008), Fujimura et al. (2014), and Morning (2014) for further discussion of *Structure*-based and PCA-based analyses of clustering.

[34] For an interesting discussion of racial discourse in China, see Dikötter (2015).

race, if it is real, is a social kind[35], not a biological kind or a biological entity. There is good socio-political and historical evidence that supports social construction of races (e.g. Hacking, 2005; Benjamin H. Isaac, 2004; J. E. Smith, 2015). Moreover, Brubaker, Loveman, and Stamatov (2004), by relying on recent research in social psychology and anthropology, contend that "cognitive perspectives provide resources for conceptualizing ethnicity, race, and nation as perspectives on the world rather than entities *in* the world" (p. 31).[36,37] Furthermore, recent studies show that racial categorization differs not only among countries but also within a nation over the time (Bailey, Fiahlo, & Loveman, 2018; Loveman, 1999, 2007, 2009, 2013; Loveman & Muniz, 2007).

For instance, Edward Telles (2003, 2004, 2015) compares the US racial discourse with the Brazilian racial discourse. He notes that there are crucial differences of racial classifications in the US and Brazil. For instance, while people with African origin are categorized as "black" in the US, even if they have "white" ancestors, people who are classified and identify themselves as "white" (*branco*) have African ancestors in Brazil. So, "white" and "black" racial categories refer to different population groups in the US and Brazil.[38] The differences in racial classification between the US and Brazil demonstrate that if socio-cultural and political realm change, then the referents of the racial categories change accordingly.

Moreover, Loveman and Muniz (2007) have examined how Puerto Rico became "white" over the years. According to official census results, the Puerto Rican population became

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[35] I do not go into metaphysical discussion of what is a social kind. When I argue that race is a social kind, I mean that it is socially constructed and has no or very little biological reality, i.e. physical features of a human being, e.g. skin color, hair, etc. are biologically real but racial categories do not follow these facial features.

[36] My emphasis.

[37] Please see the "Racial Cognition" chapter of this dissertation for a detailed discussion of this.

[38] Race in Brazil, unlike in the US, refers to skin color (black-white color spectrum) and physical features rather than ancestry.

significantly whiter in the first half of the twentieth century. According to the US Census in 1899, 61.8 % of Puerto Ricans were classified as whites. However, there was a significant increase of the white population in 1950 Census: 79.7% of the Puerto Rican population is classified as "white"; in the 2000 US Census, 80.5% of the Puerto Ricans self-identified themselves as white. Loveman and Muniz (2007) agree that racial boundaries are socially constructed. However, to explain the whitening of Puerto Rican population over time, they examine how the category of "white" has changed its social meaning, i.e. how social definition of whiteness broadened over time. This study is a good example of how racial classification schemes differ in a specific population over a time through political, social, and cultural processes. (Notice that this study does not appeal to "biological" racial differences to examine the change in the white population in Puerto Rican population.)

The racial category "Asian" also represents an interesting case. For instance, there are 56 ethnic groups in China (Myers, Xiaoyan, & Cruz, 2013). Majority of the Chinese population consists of Han Chinese (92%), and there are 55 nationally recognized minorities in China, comprising less than 9% of China's population. The major racialized ethnic groups rank in the following way: Zhuang, Machu, Hui, Miao, Uyghur, Tujia, Yi, Mongolian, and Tibetan (Myers et al., 2013; Wang, Štrkalj, & Sun, 2003). However, all of these minorities of China are grouped under the population partition of "Asian", and as Chinese in 2010 US Census (Hoeffel, Rastogi, Kim, & Hasan, 2012). However, Han Chinese, for example, might see themselves as just as different to Hui Chinese, Tibetans, Japanese, or Koreans as to Whites (or even more so).[39] Since

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[39] This is an assumption that I am making. There was the concept of "Chineseness" as a racial concept in China. "Chineseness" is seen to be a matter of biological descent, physical appearance, and congenital inheritance. According

all of these ethnic groups see themselves as different races or as racialized ethnic groups[40], i.e. they are socially and culturally different from each other. Therefore, it is a mistake to classify all these populations under the Blumenbach partition of "Asian" in the US Census: "Asian" just does not track what race means to Asians in Asia. In short: The Census racial discourse in the US does not map to the racial discourse in different countries.[41]

Moreover, it is highly unlikely that the current US meaning of race will remain unchanged in the future. Note that when we look at previous US censuses, we do not see the same 'Blumenbach partition' in those censuses, i.e. we do not see the same extensions of "race" in the old US censuses. Although some human groups were racialized in the US in the past, such as the Italian, the Irish, and the German, this is not the case anymore (Barrett & Roediger, 1997; Bayor & Roediger, 2014; Ruggles et al., 2010). Similarly, the "white" category in the US racial discourse has expanded to include or exclude Jews, Irish people, Laplanders, Hispanics, South Asians, Middle Easterners, and Ethiopians (Jacobson, 1999; Morning, 2014).[42] Also, the 1890 Census race categories were white, black, mulatto, quadroon, octoroon, Chinese, Japanese, and Indian. The 1940 race/color categories were white, Negro, Indian, Chinese, Japanese, Filipino, Hindu, and Korean. The 1950 Census race categories were white, Negro, American Indian, Chinese, Japanese,

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to this idea, all the socio-cultural properties, and cultural differences are grounded in nature, i.e. "Chineseness" is a 'biological' concept. See Dikötter (2015) and Myers et al. (2013).

[40] I talk more on this concept of "racialized ethnic groups/populations" below.

[41] For the history of Chinese racial discourse, see Dikötter (2015).

[42] In similar veins, some researchers, for instance Risch, Burchard, Ziv, and Tang (2002) include North Africans and Middle Easterners in their Eurasian cluster. This accords with the official US federal racial categorization. However, this categorization conflicts with popular notions of "whiteness" in the US and Western Europe (Compton, Bentley, Ennis, & Rastogi, 2010; Kayyali, 2013; Morning, 2014; Samhan, 1999). Similarly, for instance, Kayyali (2013) notes that the rise of multiculturalism and ethnic pride, and diverse immigrants "has created large segments of Arab Americans who do not feel 'white' and who perceive themselves as persons of color" (p. 1299) Therefore, it is a mistake to consider Arabs in the Eurasian cluster, because they do not identify themselves as "white".

and Filipino. Also, the “Pacific Islander” category does not appear in the previous US censuses. The Office of Management and Budget (OMB), in 1997, makes an adjustment in its racial categorization. The OMB removed Pacific Islanders and native Hawaiians from the “Asian” category and created a new category of “Other Pacific Islander/Native Hawaiian”. These changes in racial categories of the US censuses show that there are likely to be changes in the race categories in future US censuses as well.[43]

For instance, the category “Hispanic” might be accepted as a race, rather than an ethnicity, in the U.S Census soon.[44] Hispanics make up 17% of the US’ population and even though they check “some other race” in the census, they still write “Mexican,” “Hispanic,” and “Latin American” as their race in the provided box.[45] In other words, a significant portion of the Hispanics consider being Hispanic a race. If Hispanic is accepted as a race in the forthcoming US censuses, this will have unpalatable implication for Spencer’s account: there will only be a partial match between Spencer’s “Blumenbach partition” and U.S. Census races because Hispanic is not one of the population groups of Rosenberg et al. (2002)’s study. Therefore, race should cease to be biologically real in the U.S racial discourse as the biological reality of race will not underwrite the social reality of race in the U.S or vice versa: while the population genetics data discover five “meaningful” populations, there will be six, maybe more, racial categories in the US Census. This shows that the *current* US race categories are not special in any way. Therefore, Spencer cannot

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[43] The structure and results of the 2020 US Census will be a good demonstrator of these changes soon.

[44] Although the Census Bureau seriously considered to deem “Hispanic” as a racial group in the 2020 US census, rather than an ethnic group, it did not move on in this direction; and Hispanics will still be considered as an ethnicity for the next U.S. census (Telles, 2018)

[45] 37% and 42% of Latinos did this in the 2010 and the 2000 Censuses respectively (Parker, Menasce Horowitz, Morin, & Lopez, 2015).

hope to have vindicated racial discourse in general—for the latter differs from the current US racial discourse.

Given this, the question becomes: what is so interesting about the US-concept of race? Spencer identifies his task as identifying the national meaning of race in the US—but why is this an important task to accomplish? To determine the current US meaning of race by relying on human population genetics research is a wanting and a misguided task. This is for two reasons: first, human population clusters (the number K) "may not necessarily correspond to "real populations" (Pritchard, Stephens, & Donnelly, 2000, p. 956) and these inferred clusters should be thought as "theoretical populations" (Serre & Paabo, 2004); second, the supposed "Blumenbach partition" picks out different populations in different contexts.[46] The category "white", for instance, does not apply to same populations in different countries (e.g. Brazil and the US). The category "Asian" just does not track what race means to Asians in Asia, and so on. If Spencer's account is not going to yield a nice and crisp "solution" to the race problem in different contexts, then I find his task, *viz*. to determine the current US meaning of race with respect to genetic clustering of human population, parochial.

Sally Haslanger's (2012) account of race further supports this point. She says: "A group is racialized [in context C] iff_{df} its members are socially positioned as subordinate or privileged along some dimension (economic, political, legal, social, etc.), and the group is marked as a target for this treatment by observed or imagined bodily features presumed to be evidence of ancestral links to a certain geographical region" (Haslanger, 2012, p. 236). Haslanger's account shows that racial

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[46] I will talk more about the first reason below.

distinctions are drawn on different characteristics in different contexts. According to this account, "White," "Black," "Asian," "Amerindian," and "Pacific Islander" are racialized groups in the US currently. Similarly, Han Chinese, Mongols, Tibetans, and so on, are racialized in China at this time. Both racial classifications, and racial discourses, are equally valid. Note also that it is irrelevant that racial discourse or the existence of racial categories cannot be reduced to "observed bodily features" of the racialized ethnic minorities in China: this does not change the status of racialized ethnic groups in China, since these groups, socially and politically, are subordinate to Han Chinese.[47,48] Thus, Haslanger's account demonstrates that the meaning of race is not same everywhere. While race picks out certain groups of people in the US, it picks out totally different human groups in China. Therefore "race" is fluid and racialized groups change according to context.

All in all: it is not clear why we need to care about the US meaning of race. If Spencer's US racial discourse analysis is not going to map nicely to racial discourse universally, then why do we need to care if the US meaning of race is just the set of the populations at K=5 level of human population structure? It seems clear that if Spencer genuinely wants to biologically support racial discourse, he must vindicate it universally. However, he clearly cannot do this: racial discourse outside of the US does not match the K=5 clustering of human population groups.

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[47] People of China may "differentiate" members of different minorities form each other or from Han Chinese, or vice versa. However, this classification is not same as classifying people in a white-black color spectrum.

[48] Of course, both Han Chinese and other ethnic minorities think that they differ from each other via their ancestral links. This could cause people of China to classify the minorities according to their imagined bodily features—considering that Chinese do not differ on a White-Black color spectrum, i.e. all of them are members of "yellow" race (see Dikötter (2015)).

One can argue against in the following way: the fact that the current US racial discourse[49] matches an important way of biologically classifying humans, and this can be used to support the claim that the US racial discourse is particularly important. In fact, I do not reject this possibility. However, I argue that this match is just not theoretically interesting. As I have argued and demonstrated, race is a moving target in the US context and the US race categories change accordingly with the US censuses. Since the race categories in the US change over the time, and they change in an interactive fashion with political, cultural, and institutional movements, relying on genetic data to prove the biological reality of race is not (and will not be) able to give an account for the sociological reality of race. That is because, as Fujimura et al. (2014) say, "[Social] rules, not biological ancestry, have played the primary role in structuring racial membership in the United States" (p. 219). As I have mentioned above, and will talk more below, the population clusters of K = 5 are inferred clusters. The researcher infers the presence of K clusters, "but the inferred number K is not biologically interesting, as it was determined purely by the sampling scheme" (Pritchard et al., 2000, p. 956). However, the match between K=5 clustering and the US census racial categories seems just a sheer coincidence, which really does not tell us much about the biological reality of race but highlights how social reality of race affects scientific research. Even if there is a real match between K=5 clustering and the US racial categories, the geneticists emphasize that those five population clusters do not refer to five biological races (Rosenberg et al., 2005). I think that trying to give a biological basis for social categories of race is loaded with the influences of 18th century scientific theories of race, i.e. race is based on continental ancestry. The lingering influences of racialism of 18th century predetermine the "objective" clusters of the

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[49] I refer to the US census racial categories with "the US racial discourse."

human populations that population geneticists aim to "discover" in their analysis of global human population structure. (More on this in the following sections.)

3. Biologically Classifying Humans

However, there is a second criticism of Spencer's argument. Recall that Spencer (2014) argues that race, as understood in the US racial discourse, is a "biologically real set of population groups" (p. 1029). Spencer (2014) relies on recent data from population genetics to support his argument. Population geneticists have been conducting worldwide genetic clustering analyses on humans using HGDP-CEPH Human genome Diversity Cell Line, and they ended up with a certain robust result, i.e. K = 5 level of human population structure.[50] Spencer says that this result "indicate that the K = 5 partition of human genetic clusters is a partition of human populations", given the type of genetic data used in human genetic clustering. I have three criticisms of Spencer's use of population genetics studies to construct his argument for the biological reality of race and how the US racial discourse maps onto this genetics studies.

First, I argue that if other characteristics rooted in DNA, such as lactose resistance, are considered in racial classifications, then we would end up with a different taxonomy of races. Second, I argue that Spencer's 'Blumenbach partition' does not successfully represent human genetic variation and the structure of human racial groups. For small discontinuities in DNA marker frequencies that the population genetics studies that Spencer relies on do not represent biological differences between human groups. Therefore, those genetic population studies, i.e.

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[50] For more information on the results, see Rosenberg et al. (2005; 2002) and McEvoy et al. (2010).

Rosenberg et al. (2002) and Rosenberg et al. (2005), do not provide a basis for the biological reality of race.

More specifically, there can be other ways of biological clustering rooted in DNA. For instance, we can take other characteristics such as blood type, resistance to malaria, and lactose intolerance into account to racially classify humans. If such kind of biologically important characteristics were factored into our racial classifications, then they would produce a different taxonomy of races, i.e. we would end up with different clusters of races. Moreover, these other ways of clustering seem to be just as biologically meaningful. For instance, clustering human populations according to hemoglobin concentration and production seems extremely useful as well, given the importance of hemoglobin in structuring human lives. For instance, abnormalities in hemoglobin give us information about gene flow, i.e. admixture and migration about populations, mutation, and natural selection (e.g. sickle cell disease), and so on.[51] This information can give us good grounds to cluster human populations in a biologically meaningful and interesting way, unlike 'Blumenbach partition'.

In a recent study, Huerta-Sánchez et al. (2014) found a hypoxia pathway gene, EPAS1, which was previously identified as having the most extreme signature of positive selection in Tibetans and was shown to be associated with differences in hemoglobin concentration at high altitude. They re-sequenced the region around EPAS1 in 40 Tibetan and 40 Han individuals, and they found that this EPAS1 gene "has a highly unusual haplotype structure that can only be convincingly explained by introgression of DNA from Denisovan or Denisovan-related

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[51] For a classical discussion of how hemoglobin is used and analyzed to discover population specific diseases see Livingstone and Marks (2019).

individuals into humans" (Huerta-Sánchez et al., 2014, p. 194). After scanning a larger set of worldwide populations, they found that the selected haplotype is only found in Denisovans and in Tibetans, and at very low frequency among Han Chinese. This research illustrates that admixture with other hominin species has provided genetic variation that helped humans to adapt to the conditions of new environment. The results of this research are biologically significant—in other words, hemoglobin production/ concentration is useful as a way of clustering human populations.

Moreover, one of the research lines of the Reich Lab is to search for a new history and geography of human genes informed by ancient DNA. In a recent study, Reich et al. (2011) found that Aboriginal Australians, Near Oceanians, Polynesians, Fijians, east Indonesians, and Mamanwa (a "Negrito" group from the Philippines) have all inherited genetic material from Denisovans, but mainland East Asians, western Indonesians, Jehai (a Negrito group from Malaysia), and Onge (a Negrito group from the Andaman Islands) have not. The result of this study demonstrate that the population of Southeast Asia and Oceania is an admixture. As said above, Huerta-Sánchez et al. (2014) found that Tibetans have a region of DNA, haplotype, around the *EPAS1* gene—this region is also found in the Denisovan genome. So, both Reich et al. (2011) and Huerta-Sánchez et al. (2014) demonstrate that modern human populations in Southeast Asia, Tibet, and Oceania have Denisovan DNA. Then, why do not we cluster these populations accordingly? Why do not we think of human populations that share Denisovan DNA as one type of human race, as opposed to Blumenbachian partition, if we would like to make race a biologically real entity? In this case, there will be two different races: populations with and without Denisovan genome. This classification is biologically meaningful because it relies on the genetic structure of populations; and it is also useful because it helps us to detect what type of diseases that the Denisovan genome might cause for people who have Denisovan genes in their genome (see Reich et al. (2010)). Therefore, I argue that there are biologically other meaningful and useful ways of clustering human populations, and this means that K = 5 human population classification is not necessarily the only correct way to cluster human populations biologically.

There is a second point that I need to emphasize about geneticists' clustering of human populations into racial categories: clustering is always done with certain theoretical presuppositions in the background. In other words, population geneticists' preconceptions can affect their analyses of human population structure: which clusters, or how many clusters characterize our species? Geneticists generally test the efficacy of clustering methods "by comparing their results to 'known' population or racial classifications" (Morning, 2014, p. 199). For instance, Rosenberg et al. (2005) set the *K* between numbers 2 and 6, which is consistent with today's conception of number of existing human races. This is, interestingly, concordant with US federal racial categorization: "white," "black," "Amerindian," "Asian," "Native Hawaiian and Pacific Islander". In another study, Paschou et al. (2007) manually set the number of clusters to four. Even though the developers of *Structure* and PCA methods argue that their approaches are objective since they allow the researcher to estimate the number of clusters found in the genetic data rather than simply invent them, the researcher just dictates the clusters that (s)he feels/thinks that exist independent of genetic data (Morning, 2014, p. 199). In other words, researchers, after their analysis of data, "find" certain numbers of clusters that they pre-theoretically determined, or expected, to "find".

In population genetic software programs, such as *Structure*, which is a Bayesian clustering program, the scientist needs to specify the number of the clusters or population groups in advance (i.e. the number *K* of clusters). The scientist's understanding of history of human evolution, her presumptions about the origins of the current landscape of human genetic variation, her preconceptions about which population clusters characterize human species, and her research design factor in and influence the scientist's choice of the numbers of the clusters that she wants

Structure to yield.[52] All of these variables play crucial roles in the results of population genetics studies. Results of genetic clustering research reminds us Hacking's (1992) thesis of "the self-vindication of laboratory sciences", in which "ideas," "things," and "marks" can be adjusted in the laboratory accordingly with the cultural elements and with the number of the human clusters that we could like to come up with.[53] Researchers' presumptions and preconceptions about which clusters best represent the genetic variation in human species (i.e. their presumptions about the major population groupings of interest) influence their interpretations of the number *K* of clusters that they would like to "discover". In short: population geneticists, implicitly or explicitly, bring their own biases to clustering analysis; and they try to vindicate those biases with "objective" methods.[54]

I do not argue that population geneticists cannot tell us anything interesting about the population structure of our species. However, I argue that their research has the traces and influences of social structure. Genetics researchers bring their subjective preconceptions about racial classifications of populations into their studies to get the desired results. For instance, Rosenberg et al. (2002) could have divided populations according to completely different geographical criteria—for example, they could have chosen "Icelanders," "New Zealand Maoris,"

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[52] It should be noted that *Structure* does not only yield "meaningful" results when *K* is set to 5. Number K of clusters is requested by the user. Number K of clusters is set to 5 by Rosenberg et al. (2005; 2002). They think that their data suggest that K=5 best represents the genetic variation in their data set. However, their data set yielded interesting results when *K* was set numbers between 2 and 20. Moreover, Rosenberg et al. (2005) analyzed 993 genetic markers and they found slightly different set of genetic clusters at K = 6. The sixth population is turned out as the Kalash in Pakistan. More on this below.

[53] Please see Morning (2014) for a great discussion of how culture affects population genetics research in human clustering.

[54] A note to clarify. I do not argue that population genetics cannot objectively cluster populations—this would be absurd to argue for. However, I argue that the programs, such as *Structure*, that populations geneticists use, or the way that they use them, may be algorithmically biased. It is now known that algorithms can be biased in various ways (Lachance & Tishkoff, 2013; Obermeyer, Powers, Vogeli, & Mullainathan, 2019).

and “Mayans” as major ancestral populations instead of “African,” “Caucasian,” “East Asian,” “Oceanian,” and “Amerindian” (see Weiss and Fullerton (2005)). Although the clusters in the first group would not look as natural as the ones in the latter group, however, they would be equally good and valid categories. In other words, it is possible to categorize human beings according to any geographic criteria that we see fit, and one is not necessarily better, or biologically more meaningful, than the other.

For instance, one can argue that while the clusters of “Icelanders,” “New Zealand Maoris,” and “Mayans” may not be very useful racial categories in medical research, the clusters of “African,” “Caucasian,” “East Asian,” “Oceanian,” and “Amerindian”, which happen to nicely match with the US census racial classification too, can be medically relevant and useful to determine if some ethnic/racial group is prone to specific diseases. There is plenty of research supporting this argument (Burchard et al., 2003; Risch et al., 2002). To count a few examples: while susceptibility to Crohn’s disease is associated with three polymorphic genetic variants in the *CARD15* gene in whites (Hugot et al., 2001), these variants do not exist in Japanese patients with Crohn’s disease (Yamazaki, Takazoe, Tanaka, Kazumori, & Nakamura, 2002). 25% of white people, specifically northern Europeans, are heterozygous for CCR5-*delta32* variant, which protects them against HIV infection and progression. An allele that causes a disease can be shared by all ethnic and racial groups, such as *APOE*, and especially the variant *APOE ϵ4* increases the risk for Alzheimer’s diseases. It increases the risk from 9% in Japanese populations to 14% in white populations to 18% in black American populations (Burchard et al., 2003; Farrer et al., 1997). These examples can be multiplied. In short, it can be argued that while the latter grouping, i.e. “African,” “Caucasian,” “East Asian,” “Oceanian,” and “Amerindian,” may not be, biologically, the only meaningful way to categorize human beings, it has a pragmatic value for medical research.

It may look like the US census races are useful in medical research to diagnose, treat, and research race specific genetic diseases. However, this objection only goes so far.[55] This is for two reasons. First, as researchers have emphasized and showed time and again that most of the genetic variation (90 to 95%) occurs within, not among, races (Halushka et al., 1999; Romualdi et al., 2002; Rosenberg et al., 2002; Stephens et al., 2001; Templeton, 1998). Therefore, it is safe to argue that variation is continuous, and there is very limited systematic variation between human populations according to continent. Moreover, there is no good evidence to prove that specific races might have alleles which either make them prone to or protect them against genetic diseases. For instance, in the previous paragraph, I mentioned that if Europeans are heterozygous for CCR5-*delta32* variant, then they are protected against HIV. Although this situation applies to a very small subset of Europeans, some researchers rather than accepting the results as is, i.e. a very small subset of Europeans are protected against HIV, they interpret it as “whites” are protected against HIV. However, in this situation, a continental population is not of our interest, but persons of northern Europe are. Moreover, Esteban Gonzalez Burchard, for more than twenty years, conducts research to answer why asthma disproportionately affects Hispanics, and finds out that asthma is more prevalent among Puerto Ricans (18.4%), in comparison to Mexican Americans (4.8%) (Burchard et al., 2004; Mak et al., 2018; Naqvi et al., 2007; Pino-Yanes et al., 2015). These results show that Puerto Ricans, not Hispanics are prone to asthma—this, of course, is not only because of genetic reasons but also because of social, environmental, and dietary reasons. Therefore, our category of interest should not be “Hispanic,” but persons of Puerto Rican ancestry. As

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[55] Although I am skeptical of the value of the use of racial classification in medical genetics, I will not discuss this here as this topic requires a paper of its own.

epidemiological research shows, “race specific” diseases, or some races’ “susceptibility” to specific diseases, do not match with the racial categorization of the US Census. Therefore, it would be more useful to use more specific categorizations, such as Puerto Ricans living in the US, rather than relying on racial categories of the US census, to diagnose, understand the causes, and cure diseases.

The final point worth noting here is that Rosenberg et al. (2005; 2002)—which are the studies that Spencer relies on to support his argument—explicitly argue against the interpretations of their results as buttressing the biological reality of race. So, they do not even use the word race in their study and instead talk about “self-reported population ancestry” (Rosenberg et al., 2002, p. 2383). Moreover, their clusters do not map nicely on traditional races because they identified six main genetic clusters, and one of them correspond to the Kalash people of Pakistan at K=6. In their subsequent study, Rosenberg et al. (2005) found out that “the sixth cluster sometimes corresponds to a subdivision of native Americans into more northerly and more southerly populations rather than to a separation of the isolated Kalash population of Pakistan” (p. 662).

Furthermore, J. F. Wilson et al. (2001) argue that “commonly used ethnic labels are both insufficient and inaccurate representations of the inferred genetic clusters” (p. 265). In their analysis, which is done by using *Structure*, they find out that individuals can be partitioned into four clusters ($K = 4$), which correspond to four geographical areas: Western Eurasia, Sub-Saharan Africa, China, and New Guinea (p. 266). They also find out that China and New Guinea are placed almost entirely in separate clusters, which indicates “that the ethnic label ‘Asian’ is an inaccurate description of population structure” (J. F. Wilson et al., 2001, p. 267). In addition, for instance, Pritchard et al. (2000) say, “[C]lusters may not necessarily correspond to ‘real’ populations” (p.956). Similarly, Serre and Paabo (2004) say that “the inferred populations yielded by *Structure* do not match continents or geographical regions but represent theoretical "populations" in which all individuals show admixture to at least two such 'populations'" (p. 1682).

In short: Rosenberg et al. (2005) say that their "evidence for clustering should not be taken as evidence of our support of any particular concept of "biological race"" (p. 668). The talk about clines and clusters has been useful because these concepts facilitate research into human evolutionary history, human biology, genetic causes of diseases, and they help to identity medically important genotypes in different populations. However, Rosenberg et al. (2005) emphasize that "the arguments about the existence or nonexistence of "biological races" in the absence of a specific context are largely orthogonal to the question of scientific utility" (p. 668). In other words, they think that their genetic clustering studies are unrelated for discussions of the existence or nonexistence of biological races and argue that their results cannot be utilized to determine whether there are biological races or not. Most of the important population genetics studies in fact just *reject* the inference that population genetic clusters should be understood as biological races.

4. Conclusion

In this chapter, I have criticized Spencer's 'radical' solution to the race problem. First, I laid out Spencer's argument. Second, I raised two important criticisms against Spencer's account. I, first, argued that limiting the racial discourse according to current US Census is not the right way to talk about race. That is because, I argued, race is a fluid concept and it takes different shapes in different cultural and historical contexts. Second, I argued that there are other biologically interesting ways to classify human populations into different groups as opposed to K = 5 clustering that Spencer defends (such as classifying human populations according to their hemoglobin production, or whether humans have any Denisovan gene etc.) All in all, therefore, Spencer needs to answer the following two questions if he wants to argue the biological reality of race in the US racial discourse. First, how is it even possible to biologically support an inherently social category like race? Second, what makes the Blumenbachian partition better than hemoglobin production (or any other biologically interesting classification) for social clustering of human populations? Unless this is done, his account cannot be considered successful.

Chapter 3:

It Just Looks the Same: Differences in Racial Cognition among Infants and Older Humans

(with Armin Schulz)

1. Introduction

There is now considerable developmental psychological data suggesting that, starting from about 3 months onwards, humans are attuned to racial differences among people: in particular, there is now a wealth of evidence for the contention that many 3-month olds prefer looking at faces of their own race to those of another race (D. J. Kelly et al., 2005). There is also considerable evidence—from many different sources—that adult humans often think in racial terms (Gil-White, 2001; Haslanger, 2012; Kurzban, Tooby, & Cosmides, 2001). These facts raise (at least) three questions. First: why is it that humans think in racial terms at all? Second: why is it that humans think in racial terms from about 3 months onwards? Third: do all forms of racial cognition—whether in infants or adults—stem from the same set of psychological mechanisms, or are different such forms the results of quite different such mechanisms? In this chapter, we propose answers to these questions.

Specifically, we argue for a pluralistic account of racial cognition. Racial cognition, as we understand it here, concerns thinking in terms of racial categories in general; this obviously includes racial categorization, but it also incorporates racial facial, social, or other preferences. Given this, we suggest that (a) infants do notice and care about racial categories, but (b) they only do so because they track visual familiarity in faces: they are driven to attend preferably towards types of faces that they regularly see by the workings of an evolutionary relatively old mechanism that most likely evolved to track potential caregivers. However, we further argue that it is plausible that (c) as humans get older, the nature of racial cognition changes and becomes psychologically richer, in line with some of the prominent accounts of the nature and evolution of racial cognition already in the literature—such as those of Hirschfeld (1996), Kurzban et al. (2001), and Gil-White (2001).

In the chapter, we proceed as follows. In section 2, we present some key empirical findings concerning early human racial cognition. In section 3, we present three existing accounts of the evolution and nature of racial cognition—those due to Hirschfeld (1996), Kurzban et al. (2001), and Gil-White (2001)—and show why, given these accounts, the data concerning infant racial cognition are a bit of a puzzle. In section 4, we present an account of racial cognition for very young infants that can solve this puzzle. In section 5, we show how our account of infant racial cognition can be combined with the accounts of section 3 to yield a pluralist picture of racial cognition. We conclude in section 6.

2. Early Human Racial Cognition

It has now been fairly well documented that there is an own-race bias in early infant cognition: in particular, infants show a bias towards looking at faces of their own race (Anzures, Quinn, Pascalis, Slater, & Lee, 2013; Anzures, Quinn, Pascalis, Slater, Tanaka, et al., 2013; Bar-Haim, Ziv, Lamy, & Hodes, 2006; D. J. Kelly, Liu, et al., 2007; D. J. Kelly et al., 2009; D. J. Kelly, Quinn, et al., 2007; D. J. Kelly et al., 2005; Liu et al., 2015; Sangrigoli & De Schonen, 2004; Vogel, Monesson, & Scott, 2012).[56] Three important further facts concerning this finding need to be noted.

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[56] A word about the term "race": we do not think that this term picks out a meaningful natural—as opposed to socially constructed—kind (for some supporting arguments, see, e.g., Appiah, 1992; Appiah, 1996; Haslanger, 2012). What the research surveyed in this section shows, therefore, is that infants show preferences that range over a purely socially constructed kind. See also note 70.

1. The own-race preferences are, at least initially, quite labile. For example, even brief visual exposure to faces from different races during infancy is associated with a lack of own-race preferences for faces (Bar-Haim et al., 2006; Sangrigoli, Pallier, Argenti, Ventureyra, & Schonen, 2005). In particular, the own-race face perception bias has been shown to be eliminated in Caucasian 3-month-old infants after only 2 minutes of visual exposure to photos of three different Asian faces (Sangrigoli & De Schonen, 2004). However, as children get older, this lability decreases, and longer exposure to other races is necessary to attenuate own-race facial preferences (Anzures et al., 2012). [57]

2. In order for human infants to be able to successfully discriminate faces from other races, they need significant exposure to other-race faces, and the more so the older they are. Put differently, there is "perceptual narrowing" when it comes to the faces of other races: many infants lose the ability to perceptually discriminate faces from other races (Pascalis, de Haan, & Nelson, 2002). So, while Sangrigoli and De Schonen (2004) showed that brief two-minute exposure to other-race faces was sufficient for 3-month-old infants to successfully individuate other-race faces, Anzures et al. (2012) showed that visual exposure of a longer duration of time is needed to reverse the effects of perceptual narrowing and to attenuate own-race face biases among 9- to 10- month olds (100 to 155 minutes).[58]

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[57] While this lability thus decreases with age, there is evidence that it remains relatively strong even into adulthood: for instance, Kurzban et al. (2001) were able to deflate the tendency to categorize by race in adults simply by exposing them to an alternate social world for about 4 minutes.

[58] Similarly, D. J. Kelly, Quinn, et al. (2007) found that while 3-month-old Caucasian infants could discriminate other-race faces (i.e. African, Middle Eastern, and Chinese), 6-month-old infants could only discriminate Caucasian and Chinese faces, and 9-month-old infants only discriminated among own-race faces. Note that infants also need time to acquire the ability to distinguish the identity of faces (e.g. Chien, Wang, and Huang (2016)). Still, what matters here

3. Newborns do not demonstrate any racial facial preferences (D. J. Kelly et al., 2005).

What needs to be considered next is how these facts can be explained.

3. Three Evolutionary Psychological Accounts of Racial Cognition

In order to explain the existence and nature of human racial cognition, several different authors have proposed—mutually consistent—accounts of the evolutionary biological pressures that have led humans to have minds that think in racial terms (D. Kelly, Machery, & Mallon, 2010). Three of the most widely discussed of these accounts are those of Hirschfeld (1996), Kurzban et al. (2001), and Gil-White (2001). While (as we make clearer in section 5 below) these accounts significantly contribute to our understanding of the evolution and nature of human racial thinking, they do not make sense of the data concerning infant racial cognition (which they were not designed to do either). Bringing this out is the aim of this section.

First, Hirschfeld (1996) argues for an innate adaptation for folk sociological thinking—i.e. for detecting and essentializing social groups in a given social environment. He then argues that racial cognition results from the interaction between this innate capacity and the social structure that this capacity works in: when there are racial differences in a society, the folk sociological mechanism guides humans to identify and essentialize the properties of the relevant social groups. In short: according to Hirschfeld (1996), race-encoding is a byproduct of a module for tracking and essentializing social groups.[59]

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is just that, with more exposure to own-race faces and little exposure to other-race faces, infants cease to have the ability to recognize other-race faces while they retain their ability to recognize own-race faces.

[59] We use the term "byproduct" in the sense standard in evolutionary biology and evolutionary psychology: as traits that have evolved not because they have been specifically selected for, but because they are connected to other traits

Second, Kurzban et al. (2001) argue that racial categorization is the result of a cognitive system whose function is to track coalitions, i.e. groups of people who cooperate with each other in a given social environment. (Note that this differs from Hirschfeld's account, as not all of the coalitions in a given environment need to map onto stable, essentialized social groups.) This will lead to racial categorization, as "coalition detectors may perceive (or misperceive) race-based social alliances, and the mind will map race onto the cognitive variable *coalition*" (Kurzban et al., 2001, p. 15388). Put differently, encoding by race is a byproduct of a cognitive system that evolved to detect coalitions, within-group cooperation, and between-group competition.

Third, Gil-White (2001) argues that, in humans, a cognitive system for identifying "ethnies" has evolved. Ethnies are groups of people which consist of several hundred or thousand culturally homogenous members, and whose members share various essential properties which determine their behavior. According to Gil-White, evolution encouraged the development of such an "ethnies module", as "processing ethnic groups as species solved adaptive problems having to do with interactional discriminations and behavioral prediction" (Gil-White, 2001, p. 515): in the ancestral social environment, "interaction with out-group members [would have been] costly because of coordination problems due to different norms between ethnic groups" (Gil-White, 2001, p. 515). So, the ability to track ethnies allowed early humans to lower the "frequency of fruitless interactions across ethnic boundaries" (Machery & Faucher, 2005, p. 1213). According to Gil-White, then, racial categorization is a byproduct of this ethnicity module, because skin color,

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that have been selected for. Relatedly, it is useful to note that Hirschfeld (1996) and Kurzban et al. (2001) refer to modules as characterized by the massive modularity hypothesis (Carruthers, 2006), rather than Fodor's (1983) notion of a module. For more on both of these points, see e.g. Tooby and Cosmides (1992) and Buss, Haselton, Shackelford, Bleske, and Wakefield (1998).

hair type, and other morphological properties can be interpreted as ethnic markers by our minds (though they are not necessarily fully reliable as such). In short: according to Gil-White (2001), race-encoding is a byproduct of an ethnicity module, whose primary function is to track ethnic groups.

For present purposes, there are two key points about these accounts that need to be noted. First, all three of these accounts agree on the claim that there is no "race module" in the mind that has evolved to track races and racial membership as such. Instead, they all propose to explain the facts of racial cognition by seeing the latter as underwritten by a mental module that has another primary function—i.e. one that has not primarily been selected for detecting racial membership—but which leads to racial cognition as a byproduct. Where the accounts differ is in the nature of this module.

Second, in virtue of the fact that these accounts are learning accounts, they will, in principle, make a disjunctive prediction about racial cognition in infancy.[60] On the one hand, and most straightforwardly, these accounts can predict that young infants will not think in racial terms at all: 3-month olds, for example, may be thought to lack the data (and perhaps the cognitive abilities) with which to track coalitions, essentialized social groups, or ethnies, and hence should not be expected to have racial concepts. On the other hand, these accounts can predict that, if infants do have the data (and perhaps the cognitive abilities) with which to track coalitions, essentialized social groups, or ethnies, they will racially categorize, form racial preferences, etc.

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[60] A quick remark about nativism and learning is useful here. These accounts combine nativist and empiricist elements: they posit the existence of innate structures that facilitate the learning of certain facts—namely, facts about the prevailing coalitions, social groups, or ethnies.

for the same reasons that adults do. In short: these accounts predict that infants *either* do not think in racial terms at all, *or* that they think in racial terms for the same reasons that adults do.

We think the most plausible reading of these accounts is that they favor the first of these disjuncts: the purpose of these accounts is to make sense of the evolution of racial cognition among mature human beings—that is why they appeal to factors (social living with non-kin, competitive interactions with other human groups, etc.) that plausibly have shaped the evolution of the thought processes of adult humans. Certainly, we think that the most *charitable* interpretation of these accounts is that they favor the first of these conjuncts.

For this reason, it becomes clear that, as far as these accounts are concerned, the above findings concerning infant racial cognition are a bit of a puzzle. It is just not clear why we should expect infants to think in racial terms at all: if racializing evolved to facilitate the demands of (near-) adult human social living, it is not clear why infants would racialize. Note also that we cannot appeal here to the idea that these accounts would predict that infants merely collect the data on which mature racial cognition draws. This may well be true—a point to which we return in section 5 below—but this kind of data collection, by itself, should either lead to the absence of racial cognition in infancy (as the data are still in the process of being collected, as it were), or it should lead to the same kinds of racial preferences and categorizations that we find with adults. However, as we make clearer in the next section, neither of this is the case. Hence, another account is needed that explains the disposition towards (apparently) racial cognition specifically of infant humans. The next section spells out and defends such an account.

4. Race encoding in early infancy as a byproduct of a facial familiarity tracker

We think that a plausible explanation of the nature of early racial cognition can be found in the idea that that it is the result of the operation of a (probably evolutionarily relatively ancient) facial familiarity tracking mechanism.[61] To bring this out, note the following three points.

First, in general, newborns and young infants prefer looking at faces or face-like objects or configurations over non-faces or non-face-like objects or configurations (Cassia, Simion, & Umiltaà, 2001; Fantz, 1963; Goren, Sarty, & Wu, 1975; Hoehl & Peykarjou, 2012; Johnson, Dziurawiec, Ellis, & Morton, 1991; Johnson & Morton, 1991; Maurer & Young, 1983; Mondloch et al., 1999; Valenza, Simion, Cassia, & Umilta, 1996). For instance, Mondloch et al. (1999) found that newborns' visual preferences are influenced both by the visibility of a given stimulus and its resemblance to a human face. Equally, they found that 6-week-old infants demonstrate a visual preference for schematic face structures over non-face structures.[62]

There are some obvious reasons for why such a preference for seeing faces might have evolved. Human infants are extremely dependent on adult human help and care (Boyer & Bergstrom, 2011; Churchland, 2011; Hrdy, 1979; Pascalis & Kelly, 2009; Scarr & Salapatek, 1970; Simion & Di Giorgio, 2015); given the fact that humans are also primarily visual creatures (Marr, 1982), this makes it plausible that there is a lot of adaptive value in a tendency to attend to

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[61] A version of this idea is also being hinted at in Pascalis and Kelly (2009), D. J. Kelly et al. (2005), Bar-Haim et al. (2006), and Sangrigoli and De Schonen (2004) (among others). However, these other publications are first and foremost experimental papers, and they do not spell out in any detail an account of the evolution of infant racial cognition.

[62] Further relevant here are the findings concerning "face blindness" (see, e.g., Damasio, Damasio, & Van Hoesen, 1982; Farah, Wilson, Maxwell Drain, & Tanaka, 1995), which also suggest that humans track faces in a way that is quite different from how they track other shapes and objects. Moreover, a face selective electrophysiological activity has been observed in event-related potential (ERP) studies, which is particular to human face stimuli and has been observed neither for animal faces (de Haan, Pascalis, & Johnson, 2002) nor for objects (Rossion et al., 2000).

face-like structures (Alvergne et al., 2009; Baron-Cohen, 1995; Bruce & Young, 2012; Leopold & Rhodes, 2010; Pascalis & Kelly, 2009). In particular, doing so allows infants to locate and communicate with possible sources of help and care. This is also supported by the fact that a similar preference for seeing faces has been documented in a number of other species, all of which are predominantly visually orienting organisms whose offspring are heavily dependent on adult help: for example, this preference for seeing faces has been found in Japanese macaques (Kuwahata, Adachi, Fujita, Tomonaga, & Matsuzawa, 2004), gibbons (Myowa-Yamakoshi & Tomonaga, 2001), and sheep (Kendrick, da Costa, Leigh, Hinton, & Peirce, 2001).

Second, note that infants prefer familiar faces over unfamiliar faces (e.g. D. J. Kelly et al., 2005). As they get older and obtain more experiences with faces, infants prefer not just faces to non-faces, but also familiar faces to non-familiar faces (Bar-Haim et al., 2006; Hayden, Bhatt, Joseph, & Tanaka, 2007; D. J. Kelly, Liu, et al., 2007; D. J. Kelly et al., 2005; Rennels & Davis, 2008; Sangrigoli & De Schonen, 2004; Simion & Di Giorgio, 2015; Sugden, Mohamed-Ali, & Moulson, 2014).

The evolution of this preference plausibly was driven by the adaptive value of tracking potential caregivers: not all human adults are equally likely to provide help to a human infant—e.g. this might be more likely for kin than for non-kin (Boyer & Bergstrom, 2011; Churchland, 2011; Hrdy, 1979; Kaminski, Dridi, Graff, & Gentaz, 2009; Pascalis & Kelly, 2009; Scarr & Salapatek, 1970; Simion & Di Giorgio, 2015). In turn, this suggest that the more frequently an infant sees a face, the more likely it is that this face belongs to a member of the group of its caregivers—and thus, the more adaptive it is to attend to this face in the future. This reasoning is supported by several lines of evidence. For example, Quinn, Yahr, Kuhn, Slater, and Pascalis (2002) found that 3-month-old infants prefer to look at faces that match the gender of their primary caregiver (see also Field, Cohen, Garcia, & Greenberg, 1984).[63] Also, Rosa Salva, Farroni, Regolin, Vallortigara, and Johnson (2011) found that newly hatched chicks attend towards patterns similar to the head region of their caretakers. What these findings show is that the dependent offspring of a number of visually orienting organisms develop a preference for looking at faces that match those of their caretakers in significant ways.

Third and relatedly, there is reason to think that human infants do not just track familiar face *tokens*, but also familiar face *types*. Put differently: they assess how similar a given face is to the set of faces that they see often. So, for example, as the findings of Quinn et al. (2002) make clear, infants type caregivers by gender (at least).[64] To understand this better, though, it is important to note that "similarity" is not an objective notion: as such, there is no fact of the matter how similar two faces are to each other. The similarity among any two things is purely a matter of the similarity measure used—and there are many such measures (Sober, 2000, chap. 6). We return below to the question of what, exactly, the features are that should be seen to underlie the similarity measures used by infants; for now, it is just important to note that the fact that infants track familiar face *types* as well as familiar face *tokens* implies that infants *somehow* assign faces into similarity classes.

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[63] Interestingly, Quinn et al. (2008) further found that racial facial preferences trump gender-based facial preferences: 3-month-old Caucasian infants who were reared by Caucasian caregivers were shown to prefer female over male Caucasian faces, but did not show any preference of female over male Asian faces. See below for more on this.

[64] This is also supported by the Liu et al. (2015) studies: although 3-month-old infants look longer at own-race faces, 9-month-olds look longer at other-race faces. This suggests that infants' visual preferences shift from familiarity preferences (for own-race faces) to novelty preferences (for other-races) as they grow up. This is in line with previous work with nonface objects, which demonstrated that infants have a tendency to shift their preferences from a familiar to a novel stimulus with increasing exposure to the familiar stimulus (Houston-Price & Nakai, 2004). Underlying these findings is thus the fact that infants group faces into "familiar" and "unfamiliar" classes.

The evolutionary reason for this tendency to create similarity classes of faces—i.e. to track familiar face types as well as tokens—is not fully clear, but may have something to do with allowing for more efficient storage of important face-related information, or for quick inferences as to which unfamiliar faces to attend to. For example, if it is in particular kin that are important for providing help to an infant, and if kin look somewhat similar in their facial features, then being able to track that similarity can be adaptive, as it would allow an infant to predict whether a novel face is likely to be kin or not—and thus, whether it is likely to provide help or not (see also Field et al., 1984; Kaminski, Gentaz, & Mazens, 2012). Fortunately, for present purposes it is not greatly important to specify this reason in detail, and so we will not discuss it further here.[65]

Combining these three points leads to the following. There is reason to think that human infants are born with a "facial familiarity tracker"—"FFT" in what follows. (Given the fact that this mechanism has likely evolved due to its allowing infants to attend to potential caregivers, we could also call it "caregiver tracker".)[66] This is a mechanism that (a) directs attention to face-like structures in the environment, (b) directs attention especially to familiar faces, and (c) determines whether a given face is "familiar" by comparing it to known faces using some kind of similarity

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[65] There is some comparative psychological evidence that is worth mentioning here, though. Sugita (2008) conducted a deprivation study with Japanese macaques who were separated from their parents and reared by human caregivers who wore masks—i.e. they had no exposure to any faces for 6-24 months. The monkeys, before they were being allowed to see a face, showed a preference for human and monkey faces in photographs, and they were able to individuate human faces as well as monkey faces. After the deprivation period, they were exposed to either human or monkey faces for a month. After this exposition, the monkeys demonstrated preference for the category of faces to which they were exposed over the other category (and they were able to discriminate individual faces only within their familiar category of faces). Therefore, this study indicates that these monkeys have a predisposition to group faces into similarity classes of "familiar" and "unfamiliar" (D. J. Kelly et al., 2009; Sugita, 2008). This thus speaks at least for the fact that generating similarity measures among faces has evolved a relatively long time ago.

[66] Note that this differs from the suggestion of, e.g., Pascalis and Kelly (2009) that the FFT evolved to track potentially dangerous others. Given the findings of, e.g., Quinn et al. (2002), Rosa Salva et al. (2011), and Kaminski et al. (2009), we think that it is more plausible to see the evolutionary function of the FFT as the tracking of potential caregivers, though this may be more of a difference in emphasis.

metric.[67] Further, there are some good reasons to think that this FFT is a relatively ancient adaptation for obtaining help from caregivers (see also Kaminski et al., 2009; Pascalis & Kelly, 2009).

Acknowledging the existence and nature of the FFT is important, as it can be seen as a possible—and, as we argue momentarily, plausible—source of racial cognition in infants. So, racial facial preferences (in particular) could simply stem from many infants' large amount of experience with own-race faces and lack of experience with faces from other-races (see also Bar-Haim et al., 2006; D. J. Kelly et al., 2005; Sangrigoli & De Schonen, 2004). This can be made clearer by noting the following.

As newborns, infants lack enough data to group faces into similarity groups of familiar and unfamiliar faces: in order to tell which sorts of faces the infant sees a lot, it needs to have access to a number of different faces—for only then can it compute any kind of similarity metric between them. For this reason, it is not surprising that we do not see racial facial preferences in newborns.

However, as they grow older, infants do obtain the needed data: they gain experience with more different faces, and thus are able to group these faces into similarity classes of familiar and unfamiliar face types. Now, since (as noted earlier) there are no objective facts about similarity, any grouping of faces into similarity classes would be possible in principle. In practice, though, it appears that the similarity measure that infants rely on focuses on features that are also relevant for some contemporary racial classifications. Put differently, infants seem to assign a face to the

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[67] There are various ways to measure similarity in faces: for example, using morphometrics, quantitative genetic studies, or faciometrics (see, e.g., Cox & Cox, 2000, for an overview). For present purposes, though, these details do not matter.

"familiar" or "unfamiliar" category by assessing (among other things) whether the face is morphologically similar to known faces, with the morphological similarity considering, among other things, some currently accepted racial markers (such as skin pigmentation).[68] Three further points are important to realize about this account.

First, our claim is not that infants decide whether a face is familiar or not by considering its "racial features" *alone*—race is just one dimension in a multi-dimensional face-space (see Valentine, 1991; Valentine & Endo, 1992). Rather, our claim is that the infant compares a given face to known faces using a similarity measure that focuses on a certain set of morphological features which includes, among others, some currently accepted racial markers.[69] Thus, if an infant mostly sees faces from a given race, it will consider other faces of that race as more familiar than faces from a different race. If the infant often sees faces of many different races, however, this same similarity measure will lead to a different, non-racial class of "familiar" and "unfamiliar" faces. We return to this point below; for now, though, it is sufficient to note that we do not claim that infants only classify faces into the familiar vs. unfamiliar category by considering their racial features (or even that racial features are the major determinant of this classification).[70]

Second, one might wonder about why "racial" features (such as skin color)—rather than, say, whether there is a speck of dust on a person's cheeks—form *any* part of the basis of the

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[68] Here, it is important to recall that (a) racial classifications differ across time and space (e.g. "Irish" was a racial classification in the 19th Century in the US, and "Han Chinese" is a racial classification in contemporary China; see e.g. Roediger (1999, 2002) and Dikötter (1997, 2015), and (b) biologically, there is little to underwrite any of these racial classifications (Appiah, 1996; Haslanger, 2012; though see also Spencer, 2014).

[69] For further discussion of face-spaces, see Valentine (1991); Valentine and Endo (1992); Valentine, Lewis, and Hills (2016).

[70] This is further made implausible by the fact (noted earlier) that infants also consider the gendered features of faces to group them into similarity classes of familiar faces (Quinn et al., 2002).

similarity measure underlying the FFT. In response to this question, we note two points. On the one hand, the direction of causality between the similarity measure underlying the FFT and the nature of many contemporary racial classifications is not clear. In particular, it is plausible that much racializing happens along psychological fault lines of familiarity. When deciding whether to racialize a given group, we might well—though most likely subconsciously—consider whether this group corresponds to the output of our innate similarity measure for familiar faces. If so, then *any* of the similarity measures that could underlie the FFT would match racial classifications at least some of the time. (We return to this point in section 5.)

On the other hand, for a set of facial features to be a good marker of potential caregivers, it has to be sufficiently invariable among the caregivers and sufficiently variable between caregivers and non-caregivers to be a reliable cue with which to distinguish one from the other (Alvergne et al., 2009; Green & Swets, 1966; Kaminski et al., 2009; Kaminski et al., 2012). Many potential facial features fail this test: for example, it is implausible to think that human populations ever faced conditions in which whether there is a speck of dust on a person's cheeks was a good indicator of who is a potential caregiver. By contrast, while we do not want to claim that features like skin color are *always* good markers with which to distinguish caregivers from non-caregivers, we do want to argue that they are at least potential such markers: they are sufficiently heritable and sufficiently easily detectable, at least in some cases, to differentiate caregivers from non-caregivers (Alvergne et al., 2009; Kaminski et al., 2009; Kaminski et al., 2012). This is enough to make it plausible that (so-called) racial facial features would be included in the set of features to attend to when constructing a similarity class of familiar faces.[71]

The third point to note about the FFT account of early racial cognition is that it can be seen as providing the evolutionary underpinnings of the widely accepted face-space accounts of perceptual narrowing (Valentine et al., 2016). These latter accounts are proximate: they note that infants seem to rely on a multi-dimensional face-space to classify faces. What the FFT account adds to this is the ultimate explanation that underlying this face-space is an evolved mechanism for tracking familiar faces that was most likely selected for allowing infants to attend to potential caregivers. In this sense, the FFT account deepens face-space accounts of racial perceptual narrowing by providing an ultimate, evolutionary explanation for the latter: one in terms of a mechanism that has evolved to track caregivers.

In short: the important point to note here is that we think it is very plausible that infants group faces into similarity classes of familiar and unfamiliar faces, and that there are some good reasons to expect that these similarity classes are at least partly based on features that match the features relevant for current racial classifications. So far, though, this merely shows that the existence and nature of the FFT *might* underlie infant racial cognition—why think that it *actually* does so? In response, we note three sources of support for the FFT-based account.

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[71] This account is also supported by the work of Quinn, Lee, Pascalis, and Tanaka (2016), who have found that while 6-month-old White infants categorically represent the distinction between Black and Asian faces, 9-month-old White infants form a broader other-race category which includes both Black and Asian faces. This suggests that as infants get older, the race of their primary caregiver gets elevated as a marker of which sorts of faces should be included in the "familiar" group, while other "racial" differences get downgraded as bases for similarity groupings of familiar faces.

First, this account fits well to the empirical findings sketched in section 2, as well as to a number of other findings not yet sketched. In particular, as just noted, our account can easily make sense of the facts that (1) newborns do not show racial facial preferences, and (2) 3-month-olds do. Further, we can easily account for the fact that (3) racial facial preferences are quite labile, though less so as children get older. The reason for (3) is that, if racial preferences are just similarity judgments among what faces an infant is familiar with, then, as one changes the base of familiar faces—by exposing the child to more other-race faces—the sorts of faces that are classified as similar to each other changes. Moreover, it is true that, the bigger the base is—i.e. the older the child is—the longer the exposure to other-races needs to be to sway the initial similarity-judgments—after all, the base-line set of data is larger for older children. The same goes for the fact that (4) there is perceptual narrowing in facial recognition (which causes the "other-race effect"). The less experience an infant has with races of a given similarity-type, the less able it will be to discriminate these faces from each other (D. J. Kelly et al., 2009; D. J. Kelly, Quinn, et al., 2007). Given that something similar holds for a number of other animals, this kind of perceptual narrowing should thus be seen to be a part of the nature of the FFT.

However, there are also several other findings that are well accounted for by the FFT-based account.[72] In particular, there is the fact that (5) if 3-month-old infants are living in a heterogonous racial environment in which they have regular exposure to individuals from other races as well as faces from their own-race, they do *not* demonstrate visual preferences for faces belonging to either

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[72] Here, it is also interesting to note that Heron-Delaney et al. (2017) found that Caucasian 3.5- and 6-month-old infants have a preference for upright Caucasian adult over Caucasian infant faces, but no preferences among upright Asian adult and infant faces. This preference is also well accounted for by the fact that these Caucasian infants were mostly familiar with adult Caucasian caregivers.

group (Bar-Haim et al., 2006).[73] So, Bar-Haim et al. (2006) tested a group of Ethiopian infants who had been raised in an absorption center in Israel. These infants had exposure to both Ethiopian and Israeli adults, and they did not demonstrate preference for either African or Caucasian faces when presented simultaneously (Bar-Haim et al., 2006). Similarly, Gaither, Pauker, and Johnson (2012) found that monoracial Caucasian and Asian infants exposed to a racially diverse social environment do not seem to develop an other-race effect by 3 months. Indeed, they found that biracial 3-month olds even showed a *novelty preference* for Caucasian faces, and that they scan faces differently from monoracial children. Gaither et al. (2012), thus, conclude that their "data are consistent with a differential-experience model of face processing, which argues that cognitive specialization develops in infancy due to environment interactions and inputs during critical developmental time points" (p. 6). In short: the first source of support for our account is that it can make sense of a wide variety of empirical findings concerning early racial cognition.[74]

The second source of support for the FFT-based account of early racial cognition comes from the fact that it predicts that infants employ racial categories in their thoughts *independently* of their tracking coalitions, essentialized social groups, or ethnies. This matters, as the latter prediction also has some empirical support. So, while it is true that Rhodes, Hetherington, Brink,

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[73] Similarly, Pauker, Williams, and Steele (2016) found that contextual factors—both of the infants' cultural background and the experimental setting—influence their propensity towards racial categorization. Again, this is very much in line with our account here.

[74] Relatedly, it is also worthwhile noting that our account makes some as yet untested predictions that can be used to further distinguish it from rivals. For example, our account predicts that infants growing up in a racially heterogeneous environment will still categorize humans into different groups—corresponding to the familiar and the unfamiliar—but that this categorization will be highly specific to the facial features of the caregivers these infants have been in contact with. For example, some infants growing up in racially heterogeneous environments might categorize heavily by gender, whereas others might categorize heavily by the presence or absence of facial ornaments (earrings etc.). While this prediction of relatively great diversity in facial preferences among infants growing up in racially heterogeneous environments has not yet been tested, we think it is noteworthy here, as it shows that our account is empirically fruitful.

and Wellman (2015) showed that 16-month-old infants are able to track social allegiances, Rhodes and Gelman (2009) found that young children do not essentialize racial cues. So, although young children are aware of racial markers, physical appearance-based categories, and social coalitions, and although they treat physical markers as indicative of race as inherited, they do not view racial features as having social significance; instead, children treat these cues as flexible and subjective markers of social categories (Kinzler, Shutts, Dejesus, & Spelke, 2009; Rhodes & Gelman, 2009; Shutts, Kinzler, Katz, Tredoux, & Spelke, 2011). Also, Kinzler and Spelke (2011) found that infants do not demonstrate *social* preferences, i.e. preferences about who to interact with, for own-race individuals.[75]

Third and finally, the FFT-based account gains support from the fact that a mechanism similar to the FFT is widely accepted to be an evolutionarily relatively ancient part of our minds (and those of many other animals) (see, e.g., Kaminski et al., 2012; Pascalis & Kelly, 2009; Sugita, 2008). In turn, this implies that it should be taken seriously as a driver of racial cognition especially among young infants (who have had relatively little exposure to their wider social environment): it should *somehow* be taken into account in our theorizing about the development of racial cognition, and not simply be ignored.

All in all, therefore, we think that the FFT-based account provides a plausible explanation of the evolution and nature of racial cognition in early infancy. Importantly, furthermore, this

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[75] For example, they observed that 10-month-old infants accepted toys equally from own and other-race individuals. In fact, Kinzler and Spelke (2011) did not detect race-based social preferences until 5 years of age: even 2.5-year-old children gave toys equally to White and Black individuals. They did find that 5-to-6-year-old children expressed race-based social preferences in the same events. See below in section 5 for more on this.

account can be combined with the accounts of section 3 to yield a heterogeneous picture of human racial cognition in general. The next section makes this clearer.

5. The Heterogeneous Nature of Human Racial Cognition

It is crucial to note that the account presented in the previous section does not make the claim that humans *never* track social-groups, coalitions, or ethnies by relying on racial features. In fact, it does not even make the claim that much about human racial cognition is not well accounted for by the postulation of modules for tracking social groups, coalitions, or ethnies. Rather, all that we have argued for so far is that it is implausible and unnecessary to see *very young* children as using racial features to track social groups, coalitions, or ethnies. This, though, is consistent with there being another mechanism that explains the existence of racial cognition *later in life*—both when it comes to facial preferences and when it comes to other psychological attitudes or ways of thinking.[76]

In particular, we think it is uncontroversial that, as infants get older, they learn lots of things from their social environment (what to wear, how to talk, etc.). Because of this, we think that it is very plausible that older children have the cognitive and evidential resources to track social groups, coalitions, or ethnies, and that doing this was selected for. Indeed, we think that the much-acknowledged fact that racial classifications are often heavily socially driven. For instance, Anzures, Quinn, Pascalis, Slater, and Lee (2013), Appiah (1996), and Haslanger (2012) give strong support to the idea that, among older humans, racial cognition is underwritten by the sorts of

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[76] Scherf and Scott (2012) also hint at a pluralist picture of racial cognition, but for very different reasons.

mechanisms suggested by Hirschfeld (1996), Kurzban et al. (2001), and Gil-White (2001) (even if they do not necessarily consider the last three in detail).

For this reason, we think that racial cognition needs to be seen to change its nature over time. While racial cognition in early infancy is just driven by familiarity, it gains another aspect in addition to this later in life. Graphically, this can be represented like this:

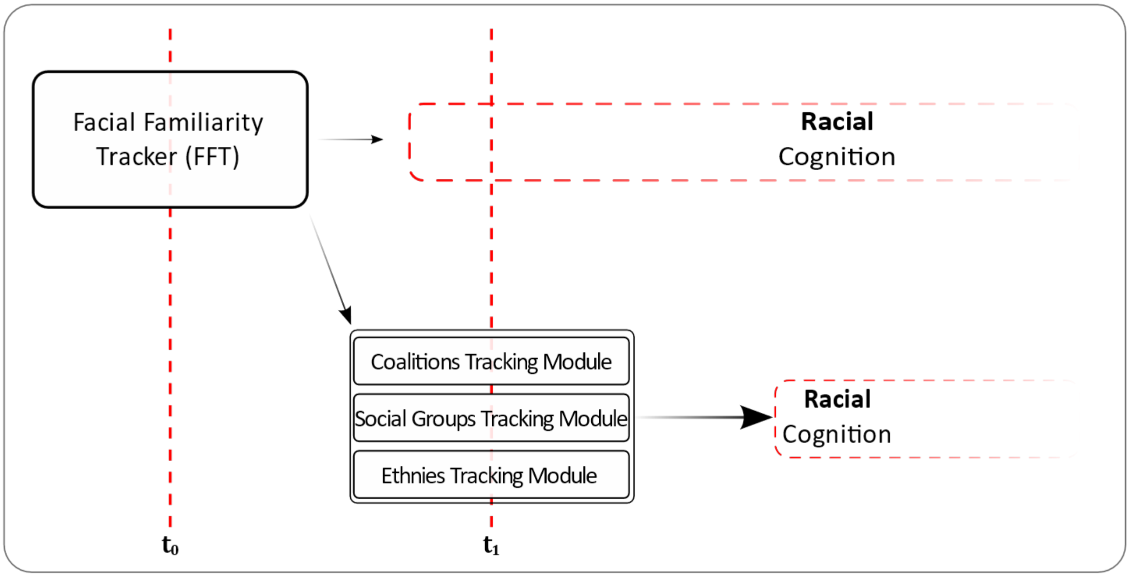

Figure 3: Changes in the Nature of Racial Cognition

According to Figure 3, from about 3 months of age to sometime later in life, racial cognition is just a byproduct of the FFT. Infants, by this age, track races (to the extent that they do so at all) only in so far as they track familiarity in faces. However, later on in life, another cognitive system—such as a coalitions-tracking module—might well have enough information to become active. After that point, "racial" cognition will no longer be a product of just the FFT: another cognitive system also becomes active (and might in fact be the sole source of the racial cognition).[77]

There is much more that can and should be said about the nature of this later kind of racial cognition, and about the switch to it from the earlier, familiarity-driven kind.[78] However, for present purposes, the key point to note is just that the picture developed here is deeply *heterogeneous* in nature. That is, we think that it is plausible that (a) early racial cognition exists (in a way), but also that (b) it differs from later racial cognition and should be explained in a different manner. We think that this two-sided nature of racial cognition is important to emphasize: while it may *appear* that infants think in racial terms in a similar way to older humans, this is a mere surface similarity. Underneath these similarities lie major differences in the psychological mechanisms that bring about these forms of racial cognition. Indeed, a case can be made for the conclusion that infant racial cognition is not actually "racial" at all—the "racial" nature of their thoughts is really just a by-product of their tracking similarity groups of familiar faces. In short: we think that accepting our account of racial cognition in early infancy should lead to the appreciation that the nature of human racial cognition changes over time—away from cognitively relatively shallow familiarity tracking towards more cognitively complex social group tracking.[79]

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[77] See e.g. Lam, Guerrero, Damree, and Enesco (2011) on some of the changes in racial cognition around age 4.

[78] So, for example, Pauker, Xu, Williams, and Biddle (2016) have shown that the propensity for out-group racial stereotyping and for the essentializing of social groups in 4-year olds was culturally variable (greater in Massachusetts and lower in Hawaii). Thus, more research is needed to understand how, when, and in what contexts the switch from the FFT-based to a more complex form of racial cognition occurs.

[79] We also think this conclusion has some major policy implications (see, for example, Lee, Quinn, & Heyman, 2017; Lee, Quinn, & Pascalis, 2017, for how perceptual training—i.e. exposure to other race-faces in infancy—would reduce implicit racial bias against other races). However, bringing these out in detail calls for a paper of its own.

However, it is critical to flag that we are not arguing that the FFT mechanism does not feed into racial cognition later in life. On the one hand, there is no reason to think that the FFT will cease to be operative in mature humans. For this reason, our account predicts that even adults can be expected to group faces into familiar and unfamiliar categories—a prediction that has some empirical plausibility (Zebrowitz, White, & Wieneke, 2008). On the other hand, as noted earlier, the FFT may well feed into the mechanisms underlying racial cognition in mature humans: for example, familiarity considerations may influence what sorts of coalitions, social groups, or ethnies we expect to encounter. Our point is just that racial cognition gets significantly enriched as humans mature: whereas it initially *just* consists of tracking familiar faces, it becomes more socially focused later in life. This, too, has some empirical support (Telzer, Humphreys, Shapiro, & Tottenham, 2013).

6. Conclusion

We have developed and defended a new account of early racial cognition: this account is centered on the operation of a facial familiarity tracker. Given this, we have shown how our account can be combined with the existing accounts of the nature of racial cognition to yield a heterogeneous picture of racial cognition, according to which early and later racial cognition are similar only on the surface, and in fact driven by radically different psychological mechanisms.

In this way, we seek to (a) provide evolutionary biological underpinnings to the existing work on infant racial cognition, and (b) connect this work to the existing evolutionary psychological accounts of racial cognition. We thus hope to be able to push forward our understanding of the evolution and development of racial cognition.

Conclusion

In my dissertation, I responded to the new biological racial realism and showed it to be unconvincing. Then, I provided a novel account of racial categorization by looking towards evolutionary biology.

I began by arguing against two recent attempts to save biological racial realism, which interprets race as a biologically real category. In Chapter 1, I argued against phylogenetic conceptions of race, which consider races as branches on a human evolutionary tree. I argued that there is little-to-no reason to think that different races can be traced back to different ancestors. Therefore, I argued, on both empirical and theoretical grounds, that the reality of race cannot be supported with biological arguments. In Chapter 2, I argued against the view that races are genetic natural kinds, according to which humans can neatly be categorized into genetic population clusters that correspond to "racial differences." I showed that, genetically, race is not an interesting category: there is no empirical reason to think that there are major genetic continuities between "races." Then, in Chapter 3, I turned to evolutionary and developmental psychology for a proper account of race that can underwrite racial discourse. I questioned what psychological mechanisms underlie racial thoughts in humans, and why these mechanisms have evolved. I argued that there is no specific psychological mechanism that has evolved to track "races" in humans: racial cognition, i.e. thinking in terms of racial categories, is, at least in the first instance, the result of a psychological mechanism that humans have evolved to assess similarities/differences in human faces. In this way, my dissertation research sought (1) to further the discussion beyond the question of "What is race?"; (2) to understand problems that arise due to racialization; and (3) to find solutions to those problems.

There is a fundamental schism, which hampered the progress in the area of philosophy of race, between social constructivists and race naturalists on the nature of races. They disagree on the ontological status of races: whether races are biologically real (naturalists), socially real (social constructivist), or not real at all (eliminativists). Scholars in either of these camps argue for a monistic view about races. However, as I have shown in this dissertation, however you carve the nature, the answer to the question of "what race is" and the referents of racial groups will differ depending on the context. Therefore, I argue that a pluralistic approach should be taken to underwrite racial discourse, and that thereby the gap between social sciences and evolutionary biology can be closed.

After I completed writing the main chapters of this dissertation, two other attempts have been made in this direction. David Ludwig (2019) and Quayshawn Spencer (2019) also present novel accounts of pluralistic account of racial discourse. These are steps in the right direction, and I look forward to continue to work towards freeing discussions in philosophy of race from the yoke of the stale question of "What is race?"—and to moving it towards solving the problems that arise due to racialization.

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