Received: 6 June 2016 | Revised: 21 July 2017 | Accepted: 20 September 2017
DOI: 10.1111/phc3.12468

WILEY

ARTICLE

Racial realism I: Are biological races real?

Quayshawn Spencer

University of Pennsylvania

Correspondence
Quayshawn Spencer, University of Pennsylvania, Department of Philosophy, 249 South 36th Street, Philadelphia, PA 19104, USA.
Email: qspencer@upenn.edu

Abstract

In this article, I discuss and critique how metaphysicians of race have conceived of and defended racial realism according to how biologists use "race". I start by defining "racial realism" in the broadest accepted way in the metaphysics of race. Next, I summarize a representative sample of recent attempts from metaphysicians of race and biologists to defend racial realism and the main criticisms against each attempt. I discuss how metaphysicians of race have defended racial realism according to how ordinary people use "race" in Part II.

1 | INTRODUCTION

In Joshua Glasgow's influential book *A Theory of Race*, he clearly and succinctly defines "racial realism" as the view that "race is real," where "something is real just in case it exists" (Glasgow, 2009, 5).[1] While there is variation among metaphysicians of race with respect to what gets called 'racial realism', Glasgow's definition nicely captures the core of what all metaphysicians of race accept.[2] Now, given this thin notion of racial realism, racial realism might seem to be trivially true. For example, it is widely accepted in the natural sciences that if you can show that even one member of a kind exists, then that kind exists.[3] For instance, that is the strategy chemists use to identify new elements, and it is the strategy that biologists use to identify new species. Given this assumption, and given that, say, Asians, Blacks, Native Americans, and Whites are paradigms of races in current American English, is not it trivially true that *race* itself exists? Well, it is not that simple.

First, we need to do some metaphysics. To be specific, we need to know what is sufficient for existing in order to say that Asians, Blacks, Native Americans, and Whites exist. This may sound strange. But think about this. Is not it true that *Tyrannosaurus rex* is a paradigm species of the genus *Tyrannosaurus*? But does that fact make it true that the genus *Tyrannosaurus* exists? Of course not, because we need to show that the instances of a kind exist in order to use those instances as evidence that the kind itself exists. Furthermore, showing that anything exists requires adopting some standards for existing.

Second, we need to do some linguistics. In particular, we need to know what "race" means in the relevant context in order to say that any particular group exists as a race in that context. This investigation is needed because while it may be true that Asians, Blacks, Native Americans, and Whites exist, it may turn out to be false that each one is a race. For example, Blum (2002, 137–146) has argued that Asians, Blacks, Native Americans, and Whites exist, but do not exist as races given the high bar for what counts as a race in current American English.[4] Only after one completes both of these investigations can one use the existence of Asians, Blacks, Native Americans, and Whites, as evidence for the reality of race.

As you might have guessed, the metaphysical exercise of answering whether race is real has churned out many different answers. For instance, when the linguistic context of asking whether race is real is restricted to "race" as understood among biologists (e.g., "race" as a synonym for "subspecies" or "ecotype"), then some philosophers and biologists have argued that race isn't real.[5] However, some philosophers and biologists have argued that race is real in a biological sense of "race".[6] When the linguistic context of asking whether race is real is restricted to some ordinary language or dialect (e.g., English, American English, etc.), the most common answer among metaphysicians of race is that race is real.[7] However, more than a few metaphysicians of race have argued that race is not real in the relevant ordinary sense.[8]

Now that I′ve discussed how metaphysicians of race define "racial realism," I'll move on to a discussion of the major attempts to defend racial realism as "race" is understood among biologists, as well as the major objections to each attempt in the literature. I will save my discussion of major attempts to defend racial realism as "race" is understood among ordinary people for Part II.

2 | IS RACE REAL IN ANY BIOLOGICAL USE OF "RACE"?

2.1 | Races as Subspecies

In the last twenty years, there have been five major attempts to defend the reality of race when "race" is understood in a purely biological way. I will group them into two types of defenses. Some of them are defenses of the reality of race when "race" is understood as a synonym for "subspecies". The rest are defenses of the reality of race when "race" is understood as a synonym for "ecotype". I will discuss attempts to defend the reality of subspecies first. But before I begin, I should clarify a few things about subspecies.

In *systematics* (the study of biodiversity), organisms are sometimes classified into subspecies in addition to species, genera, and orders. In the most general sense, a *subspecies* is a subgroup of a species that is an "incipient species" (Mayr, 1942, 155).[9] Moreover, incipient species are groups of organisms that are not quite species, but are well on their way to becoming species (Mayr, 1969, 44). After Darwinian evolutionary theory was incorporated into systematics, systematists have felt the need to classify many species into subspecies. This is because Darwin not only made popular the idea that almost all species originated from evolution, but also that species tend to originate from gradual evolution due to the dominance of natural selection as the process of *speciation* (species evolution).[10] Thus, if natural selection is the dominant cause of speciation, we should expect to find that many past and present species had or have incipient species (a.k.a. subspecies).

In the last 20 years, one major attempt to defend *subspecies realism*, as I will call it, was Ernst Mayr's defense of the reality of geographic race.[11] According to Mayr (1969, 41; 2002, 90), a "geographic race" or "subspecies" is "an aggregate of phenotypically similar populations of a species inhabiting a geographic subdivision of the range of that species and differing taxonomically from other populations of that species." Mayr (2002, 90) argued that it is "a biological fact" that geographic races exist in many animal species, and so, from induction, it is "a biological fact" that the geographic race itself exists. While Mayr (2002, 91) thought that geographic races exist in humans (*Homo sapiens*), the case for the existence of geographic races is best made using non-human animals.

For instance, in a groundbreaking study, Gonder et al. (2011, 4767) identified three phenotypically similar subgroups of common chimpanzees (*Pan troglodytes*), each of which occupy a subdivision of the geographic range of common chimps, and whose genetic variation is large enough to pass conventional tests of "differing taxonomically". To be specific, some biologists today use a threshold of $\sigma_a^2 \geq 0.25$ in an analysis of molecular variance (or "AMOVA") to test whether the genetic variation among two or more conspecific groups is taxonomically significant (Templeton, 2013, 263).

An AMOVA is a genetic analysis that divides the total genetic variation in a species (σ^2) into genetic variation among its organisms (σ_c^2), genetic variation among its local populations of organisms (σ_b^2), and genetic variation among its groups of local populations (a.k.a. population groups) at a single level of grouping (σ_a^2); where a *local population* is a randomly mating group of organisms. The equation that guides the analysis is below:

$$\sigma^2 = \sigma_c^2 + \sigma_b^2 + \sigma_a^2 \tag{1}$$

Gonder et al. showed that the total genetic variation among common chimps can be divided in such a way that its population groups differ taxonomically in virtue of exceeding the $\sigma_a^2 \geq 0.25$ threshold. The AMOVA equation that Gonder et al. (2011, 4768) found is below:

$$1 = 0.642 + 0.057 + 0.301 \tag{2}$$

The population groups that Gonder et al. (2011, 4768) used to calculate (2) were Upper Guinea chimps, Gulf of Guinea chimps, and equatorial Africa chimps. Given that $\sigma_a^2 = 0.301$ and that these three chimp populations exemplify the other essential properties of being a geographic race, it seems unquestionable that geographic races exist in common chimps, and thus, that the geographic race exists. For a bit of context, the reader might be interested to know that $\sigma_a^2 = 0.043$ for humans when we are subdivided into our most genetically different population groups (Rosenberg, Pritchard, et al., 2002, 2,382).

While the case for geographic race realism might seem airtight, there are some leaks. In particular, some biologists and philosophers of biology have complained for years that the geographic race is not biologically real because the threshold used to identify taxonomic difference is biologically arbitrary or subjective.[12] For example, there is no biological theory that justifies picking $\sigma_a^2 \geq 0.25$ as a threshold for subspecific difference. It just as well could have been 0.15, 0.35, or anything else. Furthermore, even if most systematists agree that $\sigma_a^2 \geq 0.25$ is an appropriate threshold to use, that would give the geographic race a subjective reality at best, as opposed to an “objective” reality (Templeton, 1998, 632–633; Andreasen, 1998, 205).

While this line of attack has been persuasive to many in the literature, I am not convinced. For one, any quantification of genetic difference in this context is merely a measure of taxonomic difference, not what constitutes taxonomic difference. In the case of subspecies, what constitutes taxonomic difference is being an incipient species. So, even if a threshold of genetic difference is biologically arbitrary, that fact does not imply that the geographic race itself is biologically arbitrary, just that our quantitative tests for subspecific difference are biologically arbitrary. And they are!

Instead of focusing on the quantity of genetic difference among population groups to measure taxonomic difference, systematists should look at the quality of genetic difference among population groups. This is because the genetic difference between two population groups can be very small but biologically important if that difference is relevant to reproductive compatibility. A good example is the genetic difference among humans and common chimps. On average, a human's genome differs from a common chimp's genome in only 1.229% of total nucleotides, however, the small genetic difference between humans and common chimps is enough to sustain a biological species boundary between the two because humans and common chimps cannot produce viable and fertile offspring (Yu, Jensen-Seaman, Chemnick, Ryder, & Li, 2004, 1381).[13]

In the case of subspecies, a good qualitative genetic test for subspecific difference would be identifying genes for incomplete hybrid sterility. When two groups can produce viable and fertile hybrids, but viable and fertile hybrids are limited to a particular type (e.g., a particular sex), that is known as *incomplete hybrid sterility*. If incomplete hybrid sterility exists among a set of population groups within a species and the phenomenon has a genetic basis, that is much better evidence than the current quantitative genetic standard for these groups “differing taxonomically”.

However, a more decisive objection against the biological reality of the geographic race is that geographic races are not required to be genealogical groups—and by a *genealogical group* I mean a *monophyletic group* (or *clade*), which is a group containing all and only an ancestor and all of its descendants, or a *paraphyletic group*, which is a group containing all and only an ancestor and some, but not all, of its descendants (Wiley & Lieberman, 2011, 9).[14] Since Darwinian evolutionary theory was incorporated into systematics, most systematists agree that real taxa must be genealogical groups. The reason why is twofold.

First, most systematists have always agreed that "real" or "natural" taxa are the groups of organisms that nature has produced (Darwin, 1859/1999, 338; Wiley & Lieberman, 2011, 9). Second, most systematists agree with Darwin's (1859/1999, 109–110) hypothesis in *The Origin of Species* that the groups of organisms that nature has produced are genealogical groups, all of which are genealogically connected in a "great Tree of Life". So, for most systematists today, to not require taxa to be genealogical groups is tantamount to not requiring taxa to be *real*. Moreover, we now have empirical evidence that geographic races sometimes systematically mismatch the genealogical groups that nature has produced.

For example, in a surprising meta-analysis, Zink (2004, 561) discovered that 97% of the geographic races that systematists have identified in birds (*Aves*) are not monophyletic groups. Also, it might interest the reader to know that two of the three geographic races that Gonder et al. (2011, 4768) identified in common chimps are neither monophyletic nor paraphyletic groups (Kaessmann, Wiebe, & Pääbo, 1999, 1161). Due to the worry that geographic races are not the groups of organisms that nature has produced, the majority of the remaining defenses of subspecies realism in the past 20 years have advanced genealogical conceptions of subspecies. Below are the views about what race is from three of the most discussed defenses of subspecies realism in the past 20 years.[15]

1. "[R]aces" or "subspecies" are "the smallest population units that function as an evolutionary lineage within a species" (Templeton, 1998, 632; 2013, 263).
2. "Cladistic subspecies" or "cladistic races" are "monophyletic groups" of "breeding populations" in "well-defined species" (Andreasen, 1998, 209; Andreasen, 2005, 95–96).
3. "[R]aces" are "inbred lineages" within a species that originated from "populations once geographically separated" and that "as a result of the separation, there are differences in superficial phenotypic traits," and "the distinct phenotypes" are maintained when conspecifics from different inbred lineages are brought together due to "incipient isolating mechanisms" that developed during the period of geographical isolation (Kitcher, 1999, 97; 2007, 303).

Due to space constraints, I will not discuss all three of the major defenses of subspecies realism in the past 20 years. Rather, I will just discuss Andreasen's as representative of the group. Andreasen's argument for the reality of cladistic race is slightly different from Mayr's argument for the reality of geographic race. Remember that Mayr claimed that geographic races exist in many animal species, and used that claim to infer that the geographic race exists as well. In contrast, Andreasen (1998, 200) claims that cladistic races "once existed" in the human species, and she uses that historical fact to infer that the kind *cladistic race* has "biological reality".[16]

Something that's key to appreciating Andreasen's defense for the biological reality of cladistic race is understanding why she thinks that something that satisfies the essential properties of a cladistic race is biologically real. Basically, she thinks this because she thinks that cladistic races are groups of organisms produced by nature—in this case by the natural process of evolution—as opposed to merely being a product of "our classifying activities" in systematics—as she thinks is the case with geographic races (Andreasen, 1998, 207–209). But even so, Andreasen owes us some empirical evidence that humans once had cladistic races. For that evidence, Andreasen turns to a well-known phylogenetic tree first constructed by the population geneticists Luigi Cavalli-Sforza, Paolo Menozzi, and Alberto Piazza, which I have presented in Figure 1 below.

While the details of how Cavalli-Sforza, Menozzi, and Piazza (1994) constructed the tree in Figure 1 are complex, all you need to know for this discussion is how to interpret the tree and that the tree has been reproduced over and over again using different background assumptions.[17]

As for how to interpret the tree in Figure 1, interpret each edge as a breeding population, each internal vertex as a point in time when a parent population split into two daughter populations, the root as the time when our species

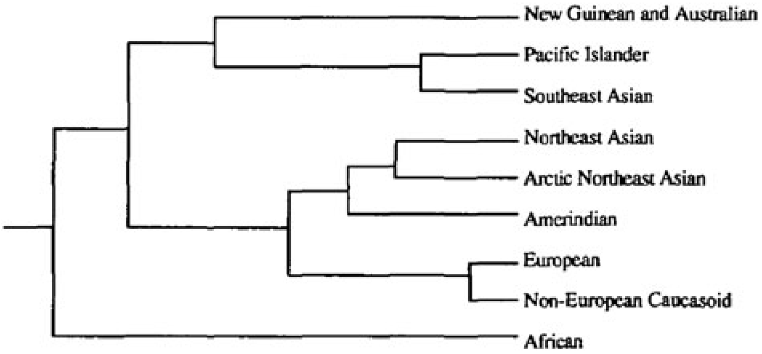

FIGURE 1 A Phylogenetic tree for nine human breeding populations from Cavalli-Sforza et al. (1994, 80)

originated, and each leaf as a more modern (but unspecified) time.[18] Furthermore, interpret each edge incident to a leaf as representing one of nine breeding populations that Cavalli-Sforza, Menozzi, & Piazza, 1994, 77–79) have previously determined to be monophyletic groups of breeding populations. Thus, if Cavalli-Sforza et al.'s tree is accurate, the human cladistic races that once existed were the following: New Guineans and Australians, Pacific Islanders (excluding New Guineans), Southeast Asians, Northeast Asians (excluding Arctic Northeast Asians), Arctic Northeast Asians, Amerindians, Europeans, non-European Caucasoids, Africans (excluding North Africans), non-Africans, and six other monophyletic groups of breeding populations that I will leave as an exercise for the reader to identify.[19]

In the literature, there have been three major objections to Andreasen's racial realism. The first is *the semantic mismatch objection*. Roughly, this objection states that cladistic subspecies are not races because what constitutes a cladistic subspecies deviates too much from "the folk concept of race" and "our folk taxonomy" of races (Glasgow, 2003, 459–460).[20] For instance, notice that according to Figure 1, neither Asians nor Hispanics (a.k.a. Latinos) were ever human cladistic races. However, some critics consider these omissions to be a "central flaw" of Andreasen's racial realism (Glasgow, 2003, 459; Glasgow, 2009, 96). In addition, according to Figure 1, there were many human cladistic races that ordinary people have never recognized as races. One example is Pacific Islanders, Southeast Asians, and the parent population of these two. Finally, notice that, according to the concept of a cladistic race, cladistic races need not be distinguishable by visible phenotypes. However, that is also a fatal flaw of Andreasen's racial realism for many critics since they see races to be distinguishable by visible phenotypes by definition (Glasgow, 2009, 94 Zack, 2002, 76).

Unfortunately, Andreasen wavered in her response to the semantic mismatch objection. Sometimes she responded to it by saying there is "quite a bit of agreement" between the human cladistic races that once existed and some ordinary racial schemes, especially the one used on the 2000 US census questionnaire (Andreasen, 2004, 437). Other times, Andreasen (2005, 105) responded to it by saying that human cladistic races need not match folk races or folk concepts of race in order to be races because systematists are simply using "race" differently from ordinary people. The correct response to the semantic mismatch objection is Andreasen's second response.

As Sally Haslanger (2012, 299) has rightly pointed out, there are no "language police" for the word "race" or any other word. Words get their meanings from linguistic communities conventionally assigning meanings to them, and as such, any word can have a different meaning across different linguistic communities that intend to use the word differently. Furthermore, and as I have discussed previously, systematists do intend to use "race" differently from ordinary people. They intend to use "race" as a synonym for "subspecies". So, how ordinary people use "race" is irrelevant to whether Andreasen's defense of racial realism succeeds.

A much stronger objection to Andreasen's racial realism is *the treeness objection* (Gannett, 2004, 330; Templeton, 2013, 264). Remember that Andreasen relies entirely on Cavalli-Sforza et al.'s phylogenetic tree as evidence that any cladistic races ever existed. However, this is a controversial source of evidence because it's controversial that the evolutionary history of human populations has a *tree* structure. In graph theory, a *tree* is a connected graph with no loops or cycles (Diestel, 2000, 12). Since Cavalli-Sforza, Menozzi, & Piazza, 1994, 80) represented each human breeding population as a single *edge* before the time *t* represented by the leaves, that assumption seems to presuppose that (T1) each population was reproductively isolated at *t* and was reproductively isolated at all times from *t* to when it evolved (Gannett, 2004, 329). Since Cavalli-Sforza, Menozzi, & Piazza, 1994, 80) represented the evolutionary relationships among human breeding populations before *t* with a *tree*, that assumption seems to presuppose that (T2) before *t*, no population evolved from fusion or hybridization, and every population evolved from branching or anagenesis (Gannett, 2004, 329).

Together (T1) and (T2) constitute the necessary and sufficient conditions for an evolutionary history of populations having a tree structure, and *the treeness objection* states that human cladistic races have never existed because the evolutionary history of human breeding populations has never had a tree structure (Gannett, 2004, 330; Templeton, 2013, 264). Furthermore, if human cladistic races have never existed, then Andreasen lacks the evidence to say that the cladistic race exists. Also, the critics here do more than make bold claims.

One notable critic, Alan Templeton, devised a test for detecting whether an evolutionary history of populations has a tree structure—a test called "Multi-locus nested clade phylogenetic analysis (ML-NCPA)"—and used that test on a sample of human breeding populations similar to Cavalli-Sforza et al.'s sample (Templeton, 2013, 269).[21] His result was that "ML-NCPA strongly rejects the null hypotheses of no gene flow and no admixture under the null hypothesis that isolated lineages did exist [in humans]" (Templeton, 2013, 269). In other words, Templeton found that (T1) is false for every breeding population represented in Figure 1.

While the treeness objection is relevant and formidable, it is not the fatal blow that many race scholars take it to be against Andreasen's racial realism.[22] This is for two reasons. First, it can be true that the evolutionary history of human breeding populations has never had a tree structure and false that human cladistic races have never existed. Second, Cavalli-Sforza et al. do not need to presuppose that the evolutionary history of human breeding populations has a tree structure in order to reliably use a tree to reconstruct the evolutionary history of human breeding populations. Both of these claims may sound unbelievable, so let me explain.

Suppose that the evolutionary history of human breeding populations has never had a tree structure. Then, that implies that there has never been a time when both (T1) and (T2) were true for human breeding populations. But even if the latter is true, why does that matter for knowing whether human cladistic races ever existed? Andreasen (1998, 209) defines a "breeding population" as "a set of local populations linked to one another by reproductive ties that are, for the most part, reproductively isolated from other such populations." Thus, breeding populations can exist without being completely reproductively isolated from one another. In that case, (T1) being false does not imply that human breeding populations never existed.

But also, a monophyletic group of breeding populations can exist even if some of its constituent breeding populations evolved from fusion or hybridization. For instance, some evolutionary biologists take Cavalli-Sforza et al.'s tree to be evidence that East Asians evolved from fusion between Northeast (including Arctic Northeast) and Southeast Asians (Karafet et al., 2001, 625). If that is true, and if Southeast Asian is an extinct breeding population and East Asian is an extant breeding population, then {Southeast Asian, East Asian} is a monophyletic group of breeding populations where one population in the group (East Asian) evolved from fusion. So, (T2) being false for human breeding populations does not imply that monophyletic groups of breeding populations never existed in humans. Provided that *H. sapiens* is a well-defined species, all of this shows that it is possible that monophyletic groups of breeding populations in a well-defined species (cladistic races) once existed in our species even if the evolutionary history of human breeding populations never had a tree structure.

Of course, even if human cladistic races *could have* existed without the evolutionary history of human breeding populations being a tree structure, the question now becomes how can Andreasen reliably use Cavalli-Sforza et al.'s tree as *evidence* that human cladistic races once existed? The latter is especially perplexing since we now know (from Templeton's analysis) that the evolutionary history of human breeding populations *does not* have a tree structure. The worry here is that since Cavalli-Sforza et al.'s use of a tree to reconstruct the evolutionary history of human breeding populations appears to presuppose a tree structure for that history, and since the evolutionary history of human breeding populations doesn't have a tree structure, it seems to be a mistake to use Cavalli-Sforza et al.'s tree as reliably representing the underlying evolutionary history.

However, Andreasen's reliance on Cavalli-Sforza et al.'s tree to infer that human cladistic races once existed is not problematic simply because we know that the evolutionary history of human breeding populations does not have a tree structure. The latter is because Cavalli-Sforza et al.'s tree is an idealization that is strictly speaking inaccurate, but accurate enough to be useful in detecting major branchings in the evolutionary history of human populations.[23] For instance, the split on Cavalli-Sforza et al.'s tree that separates Africans from non-Africans is very robust across phylogenetic studies and was 98% robust in Cavalli-Sforza et al.'s bootstrap analysis (Cavalli-Sforza, Menozzi, & Piazza, 1994, 80; Cavalli-Sforza & Feldman, 2003, 269).[24] As such, it is not a bad inference at all to say that, at some point in the past, non-Africans and Africans were two human breeding populations (in Andreasen's sense) that evolved via branching from a single parent population. Furthermore, if at least that much is true, then Andreasen can say with confidence that humans once had at least two cladistic races: Africans and non-Africans. With that said, the more recent splits on Cavalli-Sforza et al.'s tree were less robust in their bootstrap analysis and are less robust across phylogenetic studies, and so, should be viewed with skepticism.[25]

Perhaps the strongest objection to Andreasen's racial realism is that she hasn't provided a convincing case for any cladistic races being biologically real (and thus, real) even if it's true that humans once had groups of populations that satisfy the essential properties of a cladistic race. We can call this *the biological reality objection* against Andreasen's racial realism.[26] There are a number of concerns that one can have about the biological reality of cladistic races, but here is one.

Andreasen (1998, 209) has given us no reason to believe that "for the most part, reproductively isolated" is not merely a "conventional" boundary for breeding populations that she invented as opposed to a biologically real boundary (Andreasen, 1998, 209; Mncube, 2015, 168). In particular, there is nothing about Andreasen's boundary for breeding populations that guarantees that breeding populations will be genealogical groups.[27] For example, suppose that *A*, *B*, *X*, and *Y* are all distinct local populations that exist throughout a time period *t*. Also, suppose that the genealogical relationships among them are as follows: *A* budded from *B* and *X* budded from *Y*.[28] Now suppose that these are all of the gene flow events that occurred throughout *t* that involved at least one of these local populations: there were four gene flow events between *B* and *X*, three gene flow events between *X* and *Y*, and four gene flow events between *A* and *Y*.

Given the above assumptions, it follows that, during *t*, ~57% of all gene flow events involving a member of {*B*, *X*} occurred with another member of {*B*, *X*}, and ~43% of all gene flow events involving a member of {*B*, *X*} occurred with a member of {*A*, *Y*}. Furthermore, an analogous pattern holds for the members of {*A*, *Y*}. Since both {*B*, *X*} and {*A*, *Y*} are "for the most part, reproductively isolated" groups of "local populations" that share "reproductive ties," each one counts as a distinct breeding population during *t* according to Andreasen (1998, 209). However, neither {*B*, *X*} nor {*A*, *Y*} are genealogical groups of local populations! Rather, the genealogical groups of local populations in this scenario are {*A*, *B*} and {*X*, *Y*}. Furthermore, the above scenario is not just an imaginative hypothetical. This very systematic error has been discovered in one of the most popular computer programs that population geneticists use to detect breeding populations (Kalinowski, 2011).

Since there is nothing about Andreasen's boundary for breeding populations that guarantees that breeding populations are genealogical groups, the cladistic race suffers the same fate as the geographic race. Neither is *real* from the viewpoint of systematics after the Darwinian revolution. So far, I hope I have shown how difficult it has been for scholars to defend subspecies realism. The difficulty is essentially that we have not yet been able to find a way of dividing a species into *naturally occurring* incipient species as opposed to merely *conventional* groups.[29] However, even if it turns out that the subspecies is not real, it could be true that the ecotypic race is real.

2.2 | Races as Ecotypes

In ecology (the study of interactions among living things), "race" is sometimes used as a synonym for "ecotype," where an "ecotype" or "ecotypic race" is a group of organisms "(within a species) genetically adapted to a certain environment" (Pigliucci & Kaplan, 2003, 1163). The term "ecotype" was coined by Göte Turesson in 1922, but the idea of an ecological race was introduced by Benjamin Walsh in 1864.[30] In the race theory literature, Massimo Pigliucci, Jonathan Kaplan, and John Dupré have all argued that the ecotypic race is real.[31] However, I will focus on Pigliucci and Kaplan's (2003) defense as representative of the group.

In Pigliucci and Kaplan's (2003) defense, they use Mayr's strategy for defending the reality of the geographic race. In other words, since ecotypic races are biologically real (and thus real) in many species, the ecotypic race is real as well. In particular, Pigliucci and Kaplan (2003, 1162–1163, 1170) argue that ecotypic races are found in an evergreen species, a bacterial species, two butterfly species, a wasp species, and even humans. Furthermore, according to Pigliucci and Kaplan (2003, 1163, 1169), ecotypic races are biologically real (and thus real) because they are "biologically meaningful" conspecific groups in virtue of being "ecologically distinct," and this is so despite the fact that ecotypes are not necessarily "incipient species" or even "phylogenetically distinct". Pigliucci and Kaplan (2003, 1168) use "fair-skinned people" as an example of an ecotypic race in the human species.

We now know, largely due to the work of Nina Jablonski and her colleagues, that lightly pigmented skin is an adaptation in the human species. It turns out that lightly pigmented skin makes surviving to reproductive age easier for humans in environments with low ultraviolet B (UVB) sunlight (e.g., Alaska, Northern Europe, Greenland, Siberia, etc.) because it allows human skin cells to produce more vitamin D_3 (a vital nutrient) from sunlight than they would be able to produce being heavily pigmented (Jablonski & Chaplin, 2010, 8962). Even though humans in low UVB sunlight environments have always obtained significant amounts of vitamin D_3 from their diets, it still helps to have light skin.[32]

Thus, over time, lightly pigmented skin spread widely among people residing in low UVB sunlight environments as an adaptation for survival (Jablonski & Chaplin, 2000, 74). Some examples of human populations with high frequencies of people with lightly pigmented skin are the Saami people of Scandinavia, the Chukchi people of Siberia, and the Greenlandic Inuit (Jablonski, 2012, 57, 207). In addition to these evolutionary facts, we also know that lightly pigmented skin originated as a genetic mutation in the indigenous people to low UVB sunlight environments thousands of years ago (Jablonski, 2012, 42–45).[33] Thus, Pigliucci and Kaplan (2003, 1168) take "fair-skinned people" to be a clear example of a group of organisms in the same species who are genetically adapted to a specific environment (an ecotypic race), and thus, as evidence that the ecotypic race is real.

But is it? There have been more than a few worries presented in the literature about the reality of the ecotypic race. For one, some critics worry that there is no biologically non-arbitrary reason to use some genetic adaptations to identify ecotypic races, like skin color, but not others, like, say, lactase persistence (Andreasen, 2007, 471; Templeton, 2013, 269).[34] Furthermore, some critics say that replying to the latter objection by saying that *each* genetic adaptation to a particular environment can, in principle, be used to identify a distinct ecotypic race amounts to "trivializing the concept of race" (Andreasen, 2007, 471). In addition, some critics worry that since many animal and plant traits are continuous (e.g., stem height) as opposed to discontinuous (e.g., finger number), thinking in terms of ecotypes will lead to unnatural ecological classifications. For example, Templeton (2013, 269) points out that since skin color is a continuous trait in humans, there is no biologically non-arbitrary way to divide people into discrete skin color ecotypes, such as "fair-skinned people".

While these objections appear to be fatal to ecotype realism, they are not. I will handle the continuous trait worry first. Templeton is absolutely right that "fair-skinned people" is not an ecotype and we should be worried about any attempt to divide a species into ecotypes based on continuously varying traits. However, all that objection does is problematize one example that Pigliucci and Kaplan provide for the existence of ecotypes. There are plenty more to choose from, even in humans. For example, consider the sickle cell trait in humans. It is a discontinuous trait, and it is a genetic adaptation (due to balancing selection) to a specific environment—namely, environments where malaria is endemic.

With respect to the first two objections, the mistake here is thinking that there is some common "concept of race" among biologists that makes it a problem that ecotypes can be based on any genetic adaptation. Sure, this may seem weird from the viewpoint of a subspecies conception of race. For instance, a single organism can be wholly a member of many different ecotypes at the same time due to simultaneously possessing many different genetic adaptations, but a single organism cannot be wholly a member of more than one subspecies at a time given how biologists think of subspecies.[35] However, all that shows is how different an ecotype is from a subspecies, not that there is something conceptually confused about the idea of an ecotype! In fact, biologists allow a single organism to be wholly a member of many different homozygotes at the same time, so why not ecotypes?[36]

A better worry about the ecotype is whether it is a kind of thing that nature produced (a natural kind) as opposed to a kind of thing that ecologists simply made up. I am sympathetic to this worry for the simple fact that it is far from clear that the species category itself is a natural kind as opposed to a kind of thing that systematists simply made up.[37] So, any attempt to present an infraspecific division of organisms (e.g., subspecies, ecotypes, etc.) as "natural" should be met with skepticism. With that said, there are deflationary ways to identify biologically real things, and according to those ways, the strongest arguments for the biological reality of race in a biological use of "race" come from Pigliucci, Kaplan, and others on behalf of the ecotypic race.[38]

3 | CONCLUSION

In this article, I have summarized what "racial realism" means among metaphysicians of race and I have discussed a few representative attempts to defend racial realism of a particular type in the last 20 years. The type of racial realism I focused on was racial realism from the viewpoint of biologists' use of "race". Now, let us move on to exploring the landscape of racial realism defenses when "race" is understood in an ordinary way.

ENDNOTES

[1] As is customary in the metaphysics of race, I will use the term "exists" as synonymous to the phrase "actually exists". Thus, what's real from the viewpoint of metaphysicians of race is just what actually exists. However, note that this practice is not uncontroversial in metaphysics. For instance, Lewis (1986) has defended the position that reality consists in what actually exists and what possibly exists.

[2] For example, in a series of articles, Robin Andreasen defends "the biological reality of race" but remains "agnostic" about "the existence of races today" (Andreasen, 2000, S653, S659). However, note that Andreasen's biological realism about race still accepts Glasgow's core notion of racial realism.

[3] In metaphysics, a kind is usually understood to be a traditional kind or a cluster kind. A "traditional" kind is a group whose members are determined by a set of "necessary and sufficient membership conditions" (Boyd, 1999, 142). An example would be the element *gold*. Any atom with exactly 79 protons is an instance of gold. A "cluster kind" is a group whose members are not determined by a set of necessary and sufficient membership conditions, but rather, by possessing "most" of a family of non-accidentally co-occurring properties (Boyd, 1999, 143). For example, there is no set of necessary and sufficient membership conditions for being a member of the species *Escherichia coli* (a.k.a. *E. coli*). Rather, something is a member of *E. coli* if it exemplifies most of the following properties: gram-negative, facultative anaerobic, rod-shaped, non-spore forming, and lactose fermenting.

[4] See Appiah (1992) for a similar line of reasoning for rejecting racial realism.

[5] For some examples, see Wilson and Brown (1953), Mishler (1999), and Maglo (2011).

[6] For some examples, see Andreasen (1998), Templeton (1998), Kitcher (1999), Mayr (2002), Pigliucci and Kaplan (2003), Dupré (2008), and Coyne (2009).

[7] For examples, see Outlaw (1996), Sundstrom (2002), Alcoff (2006), Haslanger (2012), Taylor (2013), Spencer (2014), and Hardimon (2017).

[8] For examples, see Appiah (1992), Blum (2002), Corlett (2003), and Glasgow (2009). However, it's worth noting that Glasgow has since changed his mind. See Glasgow and Woodward (2015) for Glasgow's new realist stance.

[9] Subspecies are also called "species in statu nascendi," which amounts to the same thing as incipient species (Dobzhansky, 1943, 441).

[10] I say "almost all" because Darwin (1859/1999, 395) was agnostic about how the original species (or species) originated. Also, please read all of my remarks about Darwinian evolutionary theory as contextualized to earth. Darwinian evolutionary theory is a theory about the origin of terrestrial species.

[11] However, see Coyne (2009) for another defense of geographic race realism. Also, it's worth pointing out that Theodosius Dobzhansky was a huge defender of geographic race realism in the twentieth century. See Gannett (2013) for a thorough discussion of Dobzhansky's many different defenses of racial realism.

[12] This objection was first made by Wilson and Brown (1953). But for reiterations, see Andreasen (1998) and Templeton (1998).

[13] This point has been made before by Mosley (1999, 80) and Boxill (2004, 211).

[14] For example, see Andreasen (1998, 204–205) for this objection.

[15] While Kitcher never explicitly calls his definition of "race" a definition of "subspecies," he does appeal to "incipient isolating mechanisms" in his definition of "race" (Kitcher, 1999, 97). Kitcher (1999, 92) also claims to be capturing "how biologists employ the notion of race" and engages with the geographic race concepts of Theodosius Dobzhansky and Ernst Mayr (Kitcher, 1999, 90–91). So, Kitcher's concept of race is at least close enough to the notion of a subspecies that it's reasonable to classify his work on race with the work of subspecies realists.

[16] Interestingly, and as I said earlier in this article, Andreasen (2000, footnote 4) is "agnostic" about the existence of human cladistic races today.

[17] For a detailed discussion about how this tree was built, see Cavalli-Sforza et al. (1994, 7–9, 24–30, 73–81). For a discussion of this tree's robustness, see Cavalli-Sforza and Feldman (2003).

[18] This last point is important. As Andreasen (1998, 200) rightly points out, it's implausible that these leaves represent the present day due to the rampant gene flow among present-day human populations. However, it's more believable that these leaves represent the time when previously isolated human populations began interbreeding, which could be, say, 1492.

[19] See Cavalli-Sforza, Menozzi, & Piazza, 1994, 79) for textual evidence that this is how one should interpret each of these population terms.

[20] For critics who launch a semantic mismatch objection against Andreasen's defense of racial realism, see Zack (2002, 76) and Glasgow (2003, 2009, 91–97). Also, see Glasgow (2003, 2009, 97–102) and Appiah (2006, 366) for semantic mismatch objections against Kitcher's defense of racial realism.

[21] The reason why it's prudent to conduct a test for tree structure on a data set is because some tree reconstruction methods, such as the very one that Cavalli-Sforza et al. (1994) used, will produce a tree from a data set regardless of whether the data set represents an evolutionary history with a tree structure.

[22] Besides Gannett and Templeton, see Maglo (2011, 378–379), Hochman (2014, 84–85), and Kopec (2014, 1060–1063) for more race scholars who see the treeness objection to be a fatal blow to Andreasen's racial realism.

[23] The type of idealization that I think Cavalli-Sforza et al. are using is what Michael Weisberg (2007, 640) calls a *"Galilean idealization,"* which is the deliberate introduction of a distortion into a theory in order to make it "computationally tractable". See Cavalli-Sforza, Menozzi, & Piazza, 1994, 81) for textual evidence that this is what's going on.

[24] A *bootstrap analysis* for a phylogenetic tree is an analysis of the degree of confidence one has in each branching event represented by the tree being accurate. See Cavalli-Sforza, Menozzi, & Piazza, 1994, 80–81) for an example of bootstrap analysis.

[25] For instance, the split between European and non-European Caucasoids has been rejected by Li et al. (2008, 1101) and Tishkoff et al. (2009, 1036).

[26] For examples of critics who have entertained this worry about Andreasen's racial realism, see Spencer (2012, 202–203) and Mncube (2015).

[27] This concern can be extrapolated from Spencer (2012, 203). Also, for a general objection to using breeding relations instead of genealogical relationships to define biological taxa, see Velasco (2008).

[28] *Budding* and *splitting* are the two types of branching evolution. In a *splitting*, the parent does not survive the evolution of its offspring. An example is when an *E. coli* bacterium undergoes binary fission to produce two new bacteria. However, in a *budding* the parent survives. An example is when a fallen branch from a California redwood sprouts into a new tree. Of course, for each of these examples, some modification must occur (e.g., mutation) in order for the branching to count as evolution.

[29] Actually, see Kitcher (2007) for a retraction that there ever were any naturally occurring races out there. He's now a pragmatist about which biological kinds are *real*.

[30] For a discussion of the history of the idea of an ecological race, see Spencer (2009, 14).

[31] For evidence, see Pigliucci and Kaplan (2003), Dupré (2008), and Pigliucci (2013).

[32] For example, the traditional diet of Greenlandic Inuit relies heavily on eating the blubber of marine mammals (e.g., seals, walruses, etc.) which is rich in vitamin D_3 (Jablonski, 2012, 56).

[33] With that said, human skin pigmentation is controlled by multiple genes and we don't yet know the identity of all of the genes involved (Jablonski, 2012, 42–45).

[34] *Lactase persistence* is the trait in humans of being able to digest lactose up to and throughout adulthood.

[35] This is one major conceptual problem for the idea of an ecotypic race according to Andreasen (2007, 471).

[36] A *homozygote* relative to a locus *L* is any organism that possesses alleles at *L* and only the same alleles at *L*.

[37] For some defenses of the unnaturalness of the species category, see Mishler (1999) as well as Barker and Velasco (2013).

[38] For some deflationary notions of biologically real kinds or particulars, see Glasgow (2009, 82), Spencer (2012, 2014, 1036), and Hardimon (2017, 94).

ORCID

Quayshawn Spencer http://orcid.org/0000-0001-6896-164X

WORKS CITED

Alcoff, L. M. (2006). *Visible identities: Race, gender, and the self*. Oxford: Oxford University Press.

Andreasen, R. O. (1998). A new perspective on the race debate. *The British Journal for the Philosophy of Science*, *49*(2), 199–225.

Andreasen, R. O. (2000). Race: Biological reality or social construct? *Philosophy of Science*, *LXVII*(3S), S653–S666.

Andreasen, R. O. (2004). The cladistic race concept: A defense. *Biology and Philosophy*, 425–442.

Andreasen, R. O. (2005). The meaning of ‘race’: Folk conceptions and the new biology of race. *The Journal of Philosophy*, *102*(2), 94–106.

Andreasen, R. O. (2007). Biological conceptions of race. In M. Matthen, & C. Stephens (Eds.), *Philosophy of biology* (pp. 455–481). Amsterdam: North Holland.

Appiah, K. A. (1992). *In my father's house*. Oxford: Oxford University Press.

Appiah, K. A. (2006). How to decide if races exist. *Proceedings of the Aristotelian Society*, *106*, 365–382.

Barker, M., & Velasco, J. (2013). Deep conventionalism about evolutionary groups. *Philosophy of Science*, *80*(5), 971–982.

Blum, L. (2002). *I'm not a racist but…: The moral quandary of race*. Ithaca: Cornell University Press.

Boxill, B. (2004). Why we should not think of ourselves as divided by race. In M. L. Pataki (Ed.), *Racism in mind* (pp. 209–224). Ithaca: Cornell University Press.

Boyd, R. (1999). Homeostasis, species, and higher taxa. In R. Wilson (Ed.), *Species: New interdisciplinary essays* (pp. 141–186). Cambridge: MIT Press.

Cavalli-Sforza, L., & Feldman, M. (2003). The application of molecular genetic approaches to the study of human evolution. *Nature Genetics*, *33*, 266–275.

Cavalli-Sforza, L., Menozzi, P., & Piazza, A. (1994). *The history and geography of human genes*. Princeton: Princeton University Press.

Corlett, J. A. (2003). *Race, racism, and reparations*. Ithaca: Cornell University Press.

Coyne, J. A. (2009). *Why evolution is true*. New York: Viking Penguin.

Darwin, C. (1859/1999). *The origin of species by means of natural selection or the preservation of favoured races in the struggle for life*. New York: Bantam.

Diestel, R. (2000). *Graph theory* (Second ed.). New York: Springer-Verlag.

Dobzhansky, T. (1943). The species concept. *Revista de Agricultura*, *18*, 441–442.

Dupré, J. (2008). What genes are, and why there are no genes for race. In B. A. Koenig, S. S.-J. Lee, & S. S. Richardson (Eds.), *Revisiting race in a genomic age* (pp. 39–55). New Brunswick: Rutgers University Press.

Gannett, L. (2004). The biological reification of race. *The British Journal for the Philosophy of Science*, *55*(2), 323–345.

Glasgow, J. (2003). On the new biology of race. *The Journal of Philosophy*, *100*(9), 456–474.

Glasgow, J. (2009). *A theory of race*. New York: Routledge.

Glasgow, J., & Woodward, J. M. (2015). Basic racial realism. *Journal of the American Philosophical Association*, *1*(3), 449–466.

Gonder, M., Locatelli, S., Ghobrial, L., Mitchell, M., Kujawski, J., Lankester, F., … Tishkoff, S. (2011). Evidence form Cameroon reveals differences in the genetic structure and histories of chimpanzee populations. *Proceedings of the National Academy of Sciences*, *108*(12), 4766–4771.

Hardimon, M. (2017). *Rethinking race: The case for deflationary realism*. Cambridge: Harvard University Press.

Haslanger, S. (2012). *Resisting reality*. Oxford: Oxford University Press.

Hochman, A. (2014). Unnaturalised racial naturalism. *Studies in History and Philosophy of Biological and Biomedical Sciences*, *46*, 79–87.

Jablonski, N. (2012). *Living color: The biological and social meaning of skin color*. Berkeley: University of California Press.

Jablonski, N., & Chaplin, G. (2000). The evolution of human skin coloration. *Journal of Human Evolution*, *39*, 57–106.

Jablonski, N., & Chaplin, G. (2010). Human skin pigmentation as an adaptation to UV radiation. *Proceedings of the National Academy of Sciences*, *107*(2), 8962–8968.

Kaessmann, H., Wiebe, V., & Pääbo, S. (1999). Extensive nuclear DNA sequence diversity among chimpanzees. *Science*, *286*, 1159–1162.

Kalinowski, S. (2011). The computer program STRUCTURE does not reliably identify the main genetic clusters within species: Simulations and implications for human populaiton structure. *Heredity*, *106*, 625–632.

Karafet, T., Xu, L., Du, R., Wang, W., Feng, S., Wells, R., … Hammer, M. (2001). Paternal population history of East Asia: Sources, patterns, and microevolutionary processes. *American Journal of Human Genetics*, *69*, 615–628.

Kitcher, P. (1999). Race, ethnicity, biology, culture. In L. Harris (Ed.), *Racism: Key concepts in critical theory* (pp. 87–117). Amherst: Humanity Books.

Kitcher, P. (2007). Does ‘race’ have a future? *Philosophy & Public Affairs*, *35*(4), 293–317.

Kopec, M. (2014). Clines, clusters, and clades in the race debate. *Philosophy of Science*, *81*(5), 1053–1065.

Lewis, D. (1986). *On the plurality of worlds*. Oxford: Blackwell.

Li, J., Absher, D., Tang, H., Southwick, A. M., Casto, A. M., Ramachandran, S., … Myers, R. M. (2008). Worldwide human relationships inferred from genome-wide patterns of variation. *Science*, *319*, 1100–1104.

Maglo, K. (2011). The case against biological realism about race: From Darwin to the post-genomic era. *Perspectives on Science*, *19*(4), 361–390.

Mayr, E. (1942). *Systematics and the origin of species: From the vewpoint of a zoologist*. Cambridge: Harvard University Press.

Mayr, E. (1969). *Principles of systematic zoology*. New York: McGraw-Hill.

Mayr, E. (2002). *The biology of race and the concept of equality* (pp. 89–94). Winter: *Daedalus*.

Mishler, B. (1999). Getting rid of species? In R. A. Wilson (Ed.), *Species: New interdisciplinary essays* (pp. 307–315). Cambridge: MIT Press.

Mncube, Z. (2015). Are human races cladistic subspecies? *South African Journal of Philosophy*. https://doi.org/10.1080/02580136.2014.998854

Mosley, A. (1999). Negritude, nationalism, and nativism: Racists or racialists? In L. Harris (Ed.), *Racism: Key concepts in critical theory* (pp. 74–86). Amherst: Humanity Books.

Outlaw, L. (1996). *On race and philosophy*. London: Routledge.

Pigliucci, M., & Kaplan, J. (2003). On the concept of biological race and its applicability to humans. *Philosophy of Science*, *70*(5), 1161–1172.

Pigliucci, M. (2013). “What Are We to Make of the Concept of Race? Thoughts of a Philosopher-Scientist.” *Studies in History and Philosophy of Biological and Biomedical Sciences*, *44*(3), 272–277.

Rosenberg, N. A., Pritchard, J. K., Weber, J. L., Cann, H. M., Kidd, K. K., Zhivotovsky, L. A., & Feldman, M. W. (2002). Genetic structure of human populations. *Science*, *298*(5602), 2381–2385.

Spencer, Q. (2009). *Is cladistic race a genuine kind?* Ann Arbor: ProQuest LLC.

Spencer, Q. (2012). What ‘biological racial realism’ should mean. *Philosophical Studies*, *159*(2), 181–204.

Spencer, Q. (2014). A radical solution to the race problem. *Philosophy of Science*, *81*(5), 1025–1038.

Sundstrom, R. (2002). Race as a human kind. *Philosophy & Social Criticism*, 91–115.

Taylor, P. (2013). *Race: A philosophical introduction* (Second ed.). Cambridge: Polity Press.

Templeton, A. R. (1998). Human races: A genetic and evolutionary perspective. *American Anthropologist*, *100*(3), 632–650.

Templeton, A. R. (2013). Biological races in humans. *Studies in History and Philosophy of Biological and Biomedical Sciences*, *44*(3), 262–271.

Tishkoff, S. A., Reed, F. A., Friedlaender, F. R., Ehret, C., Ranciaro, A., Froment, A., … Williams, S. M. (2009). The genetic structure and history of Africans and African Americans. *Science*, *324*, 1035–1044.

Velasco, J. (2008). Species concepts should not conflict with evolutionary history, but often do. *Studies in History and Philosophy of Biological and Biomedical Sciences*, *39*(4), 407–414.

Wiley, E., & Lieberman, B. (2011). *Phylogenetics: Theory and practice of phylogenetic systematics*. Hoboken: Wiley-Blackwell.

Wilson, E., & Brown, W. (1953). The subspecies concept and its taxonomic application. *Systematic Zoology*, *2*(3), 97–111.

Yu, N., Jensen-Seaman, M., Chemnick, L., Ryder, O., & Li, W. (2004). Nucleotide diversity in gorillas. *Genetics*, *166*, 1375–1383.

Zack, N. (2002). *Philosophy of science and race*. New York: Routledge.

Zink, R. (2004). The role of subspecies in obscuring avian biological diversity and misleading conservation policy. *Proceedings of the Royal Society of London, Part B*, *271*, 561–564.

Quayshawn Spencer received his PhD in philosophy and an MS in biology from Stanford University in 2009 and 2008, respectively. His dissertation questioned whether the cladistic race was biologically real using a novel way of identifying scientifically real kinds. His master's project in biology was to investigate whether certain *Eurema* butterfly species have been misclassified by systematic entomologists using mitochondrial DNA and newer phylogenetic tree reconstruction algorithms. Spencer is currently an Assistant Professor in the department of philosophy at the University of Pennsylvania. His research in the philosophy of race, philosophy of biology, and philosophy of science has primarily appeared in *Philosophy of Science*, *Philosophical Studies*, and *Studies in History and Philosophy of Science*. Spencer also has two books under contract with Oxford University Press that engage with topics in the metaphysics of race.

How to cite this article: Spencer Q. Racial realism I: Are biological races real? *Philosophy Compass*. 2018;13: e12468. https://doi.org/10.1111/phc3.12468