Biological Race Realism and the Legacy of Racial Pseudoscience

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Abstract: As much contemporary work in biology and philosophy has shown, disagreements between biological race realists and biological race anti-realists are primarily normative. Yet despite the well-recognized normative nature of the debate, contemporary versions of biological race realism continue to be built on empirically questionable background assumptions that are centrally motivated by historical ideologies of racial pseudoscience rather than by pragmatic or normative considerations. I consider the case studies of Andreasen's (2000, 2004) and Spencer's (2018) arguments, showing how some of their background assumptions stem from pseudoscientific racial ideologies. Even when philosophers and biologists purport to accept the normative nature of the question of race as a genetic population-level category, their views remain susceptible to the influence of said ideologies in ways that may continue to uphold their harmful legacies. The stakes of these positions are significant, as they connect to contemporary issues of racial equity in science and medicine.

Keywords: Racial classification, population genetics, scientific racism, geographic ancestry, human migration and evolution, race and medicine

1 Introduction

The debate over whether race is biologically real shows no sign of relenting. As data on genomics and geographic ancestry become ever-more sophisticated, biological race realists and their opponents continue to clash over whether these developments provide scientific evidence for a biological conception of human races. The concept of race is continually reinvented to keep up with changing science and be more in line with the picture of human biological diversity painted by data on population genomics. Many philosophers recognize that there is no way to answer whether race exists as a biological entity independently of normative considerations and that disagreement between biological race realists and biological race anti-realists is primarily normative, residing in the value-laden background assumptions and definitional terms that constitute the playing field on which the empirical engagement takes place (Hochman 2017, Lemeire 2016, Ludwig 2015, Mallon 2006). As Kaplan and Winther (2014: 1040) have argued, 'our best genomics forever underdetermines the existence of biologically real human races.' They propose a view they term *constructivist conventionalism*, which reflects that pragmatic and normative choices about how to collect and interpret data affect the conclusions drawn about the biological reality of race. They write, 'Either realism or antirealism can be justified given particular choices and norms about how to interpret the biological data and which mathematical methods to use' (2014: 1040).[1] Not only do scientific disagreements about biological race

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[1] It is worth noting that Kaplan and Winther take biological race realism as defined above to be unsupported by our best science.

realism primarily involve disputes over value-based background assumptions, such assumptions are frequently obscured or made invisible by the theoretical frameworks in which they reside.

Even when such concessions about the state of the debate are explicitly made, unnamed commitments to pseudoscientific racial ideologies continue to pop up in contemporary mainstream versions of biological race realism. As examples, I consider Andreasen's (2000, 2004) and Spencer's (2018) arguments for biological race realism. [2] An analysis of Spencer's methodology shows that some of his premises rely on empirically unmotivated views about race that align with pseudoscientific historical ideologies,[3] while Andreasen's background assumptions converge with colonial myths about Indigenous peoples.

For the purposes of this paper, biological race realism is the view that Kaplan and Winther (2014) call *biological racial realism*: that groups identified genomically or phenomically map stably onto social groups conventionally identified as races.[4] This is the best way to characterize the view that Spencer (2018) advocates when he suggests that the human continental populations mapped by programs like *structure* should be considered a vindication of popular and historical racial typologies. In 2002, Rosenberg et al published a landmark study showing that the software program *structure*, by using multilocus genomic analysis, was able to assign individuals to population groups without prior information about their origins. The program grouped individuals into clusters based on their genotypes at 377 loci, and the researchers showed that these groupings accorded with the individuals' continental and regional origins. Though the researchers never use the word 'race' in the paper and do not defend biological race realism, the view's advocates nonetheless marshalled the paper as evidence of race's biological reality, and many continue to cite it as such today.[5] Wills (2017) notes that, while the much-discussed Rosenberg et al (2002) study provides evidence only for the existence of population structure in *homo sapiens* assessed through genomic measures, many still interpret it as providing evidence for biological race realism (Sesardic 2013, Wade 2014, Spencer 2018). I focus on Spencer's (2018) work, as it contains his most recent arguments for biological racial realism. While Spencer is significantly more careful than Sesardic and Wade about the details of the *structure* results in Rosenberg et al (2002), he deploys shaky philosophical arguments in service of similarly undermotivated conclusions about race.

Before delving into Spencer's work, I turn first to Andreasen's (1998, 2000, 2004) arguments for what she calls an 'objective' biological view of race rooted in cladistics, and I identify their unspoken—and undefended—background assumptions that align with colonial myths about Indigenous peoples. I then turn to Spencer's (2018) arguments that there is a biological conception of race that is useful to medical genetics. I identify the background assumptions on which they depend and raise several objections to them, and I outline how some of Spencer's

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[2] Spencer now accepts what he refers to as a 'radically pluralist' account of race (2019: 27). His new view is not a rejection of his old view but an embrace of a pluralism that attempts to include the diversity of folk racial classification schemas reflected in ordinary language while also presuming the soundness of his past arguments for biological race realism.

[3] This issue remains important as Spencer's work continues to be taken to show that our best science can license a form of biological race realism.

[4] It bears emphasizing that dominant social schemas of race vary significantly across cultural and national contexts, periods of time, and geographic locations (Roberts 2011).

[5] See Hochman (2013) for a refutation of arguments that *structure* results support the views of "race naturalists."

(2018, 2015) background assumptions accord with tenets of a historically produced pseudo-scientific picture of race. Finally, I discuss the content of historical theories of scientific racism and trace their lineages in contemporary science and medicine to better contextualize both the vestiges of such theories within Spencer's and Andreasen's arguments and the costs of continuing to reinforce them.

2 Legacies of race ideology in human evolution and migration modeling: Andreasen's argument for the cladistic view of human races

A prominent area in which common yet unsupported assumptions about race have influenced research is population sampling. One example is the Human Genome Diversity Project (HGDP). Rather than randomly sampling a variety of populations across the globe, researchers often exclude populations from geographic regions with high levels of intermixture, such as the Middle East or the Balkans, because such populations can be fit into more than one genomic cluster. They also cherry pick groups that "best fit a priori racial classifications" (Roberts 2011: 66). As Roberts points out, Northern Africans such as the Mozabite people and Eastern Africans like Ethiopians and Somalis are rarely selected to represent the African continent 'because they do not fit the profile of 'black' Africans—they have mixed too much with Europeans, Arabs, and other non-Africans' (2011: 65). This suggests that researchers already have in mind some conception of race that they are, perhaps unconsciously, seeking to confirm. Genetic sampling methods frequently fit into and strengthen pre-determined notions of race. Researchers need not be acting fraudulently when cherry picking certain groups and excluding others. They may simply be subject to the influence of some of the assumptions at the heart of historical ideologies of race without explicitly subscribing to such theories.

In addition to pervading the HGDP, for which Luigi Luca Cavalli-Sforza was a lead researcher, these same sampling biases show up in Cavalli-Sforza's (2000) other research representing human migration and evolution as a branching tree structure. Cavalli-Sforza's sampling methods are relevant for our purposes, because Andreasen relies on his data analysis in her (1998, 2000, 2004) arguments for a cladistic view of race, causing his bias to percolate into her background assumptions. The populations that Cavalli-Sforza includes in his data set reflects an assumption about which groups are 'admixed' and which are 'pure.' He considers genetic samples only from what he refers to as 'the modern indigenous populations of the five continents' to map the genetic distances among each of these five populations (2000: 36). He admits to excluding from his data set 'the most obviously admixed populations of North Africa, Western Asia, and the Pacific islands smaller than Australia' (40), purportedly for the sake of simplification. These exclusionary sampling methods are reflective of the pattern Roberts identifies above of including only populations that are seen to fit within our pre-theoretic racial classification schema. Cavalli-Sforza's (2000) choice to use specific groups to represent whole continental populations further reflects one of the very underlying biases that population-level genetic research is supposed to counter. Roberts writes, 'Sampling a handful of ethnic groups to symbolize an entire continent mimics a basic tenet of racial thinking: that because races are composed of uniform individuals, any one can represent the whole group' (2011: 65). The sampling method in question tacitly endorses the assumption that racial groups, conceived of as continental populations, have some underlying form or set of features that members share. This is what licenses inferences from the small and apparently isolated sample population to the continental population group.

Cavalli-Sforza's methodology and background assumptions are significant for the investigation of the hidden influence of racial ideology on contemporary forms of biological race realism. While Cavalli-Sforza does not himself argue for biological race realism, his work forms the foundation for Andreasen's (1998, 2000, 2004) cladistic view of race, a prominent and purportedly 'objective' biologically realist account of race. Andreasen assumes that human evolution takes the form of a branching tree and then goes a step further by characterizing the population groups resulting from the presumed branching points as biological races. This, she contends, provides an objective biological basis for races, suggesting that races can be defined as reproductively isolated breeding populations that share a common origin. Specifying her view, she writes,

> A "breeding population" is a set of local populations that exchange genetic material through reproduction and are reasonably reproductively isolated from other such sets. For example, a tribe of bushmen might constitute a local population. When there is interbreeding among tribes, but no outbreeding, these local populations form a breeding population. A breeding population is "born" when a local subpopulation becomes separated from a parent population and there is limited gene flow between "parent" and "offspring" (Andreasen 2000: 659)

Here, Andreasen assumes that something like Cavalli-Sforza's branching tree or 'candelabra' model is the correct model of human evolution (Gannett 2004). While Andreasen allows that the details of the 'actual' tree representing human evolution may differ from the specifics of Cavalli-Sforza's, she nonetheless presumes that human evolution is indeed accurately represented as a branching tree and recognizes that her account depends on this being the case (2004: 431).[6] Cavalli-Sforza's representation of human evolution as a branching tree itself relies on the assumption that 'genetic distance,' the statistical measure of differences in gene frequencies between human population groups reflects geographic distance between groups and can be used to infer the chronology of branching points among populations. However, as Templeton (1999: 2013) points out, genetic distance is also compatible with a 'trellis' model that reflects recurrent gene flow and thus 'continuous admixture' among populations. The trellis model is consistent with the idea that most population groups were never isolated enough to develop into branching inbred lineages (Mncube 2015: 173). While Andreasen (2004) acknowledges in a footnote that there is such an 'opposing view', she does not provide evidence that her view is more strongly supported than the hypothesis that human evolution is most accurately represented by the trellis model (Hochman 2014).

Andreasen (1998, 2004) takes research in human evolution to support the idea that ancestral races evolved in the past after splitting into separate breeding groups due to significant

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[6] Templeton (2018, 214) observes that assumptions of treeness as opposed to network diagrams dominate the literature on human evolution and suggests that most investigators assume treeness for human population as a result of splitting and isolation without ever testing the legitimacy of this assumption.

reproductive isolation. To establish this claim, Andreasen (1998) cites the work of Stringer and Andrews (1988) and Nei and Roychoudhury (1993), among others. But these researchers argue for a cladistic single-origin view of human evolution *as opposed to a multiregional evolution hypothesis*. Their arguments are that contemporary evidence supports the view that *homo sapiens* share a common ancestor *over the view that homo sapiens developed independently in multiple regions* from *homo erectus* ancestors. They do *not* argue that there is more evidence for the accuracy of the branching model over the trellis model. As Templeton notes about Nei and Roychoudhury's (1993) work, 'no mention is even given to the trellis model interpretation' (1998, 640). Andreasen also cites their earlier work as providing evidence that human evolution can be represented as a branching tree. However, Templeton points out that Nei and Roychoudhury (1974, 1982) not only fail to test their data for the properties of treeness before representing them as a tree but that said data sets 'have long been known not to fit treeness' (1998: 639). As Templeton emphasizes in (2013: 12), 'The literature on hypothesis testing for a treelike structure for human populations is easy to summarize: the null hypothesis of a tree is almost always rejected' (2018: 217). He offers a discussion of the 'abysmal' results of the extensive empirical testing of the tree hypothesis on which the cladistic view of race depends (2018: 204-227). Using nested clade phylogeographic analysis (NCPA), Templeton ran a battery of tests against the null hypothesis that human populations have branched into mostly separate evolutionary lineages and consistently found no evidence for it. As one example, he tested the null hypothesis that there was no gene flow between sub-Saharan African and Eurasian populations from 600,000 – 50,000 years ago and was able to strongly reject it, finding that there was significant genetic interchange rather than isolation between these populations (209). Templeton concludes:

> The fit of human population data to an evolutionary tree is typically abysmal, yet the depiction of human population trees is widespread throughout the human genetic literature. There is no justification for this in terms of hypothesis testing, so despite the popularity of population trees, they are an inappropriate and misleading depiction of human evolutionary history (2018: 217).

Why would Andreasen assume that there was enough breeding group isolation to produce clades that could then be categorized as races? For one thing, Andreasen appears to associate a population's being Indigenous with its members staying in place and remaining cut off from other populations prior to European colonialism.[7] In describing how researchers can minimize the influence of evolutionary convergence of traits when attempting to infer phylogenies from genetic distance, Andreasen suggests that, 'geneticists can greatly reduce the problems posed by hybridization by studying *aboriginal populations*—breeding populations that occupied their present location before the great migratory waves that began with the voyages of discovery in the mid- to late fifteenth century' (1998: 211). Presumably, studying groups that Andreasen refers to as 'aboriginal populations' would protect against 'the problems posed by hybridization' only if they did not engage in mixing or interaction with other populations. Andreasen also pinpoints the

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[7] Of course, it could be the case that Andreasen's view that biological races are clades is true and also that there have never been any such thing as biological races. To be clear, Andreasen's cladistic view of race does not logically require a commitment to the claim that Indigenous populations prior to colonization, were, for the most part, insular and cut off from one another. Nonetheless, her work *does* rely on such an assumption, and that is what is of interest to this paper's argument.

beginning of European colonization as the time that the previously separate and distinct biological races started blending and thus “fading out of existence.” She writes, “Ever since the voyages of discovery, colonization and immigration have been blurring racial distinctness” (1998: 215). Andreasen’s picture is one in which initial migrations led to insular populations that were almost completely cut off from other populations until Europeans began traveling the globe to engage in theft and colonization of lands and peoples (Gannett 2004).

It is significant that Andreasen offers no evidence that “aboriginal populations” did not have long-running contact and gene exchange with other groups. The fact that Andreasen does not defend or offer evidence in favour of this clearly empirical assumption is suggestive that it appears to her to be ‘self-evident.’ However, the fact that a population group has occupied their present location since before the beginning of European colonization does not entail that they did not practice extensive travel, trade, or intergroup mixing prior to that time. Indeed, the diverse and storied histories of Indigenous internationalism that have long preceded European colonization indicate otherwise.[8] Gannett (2004) critiques Andreasen’s unsupported presumptions about ‘aboriginal populations’ for their proximity to a central tenet of colonial mythology. She writes, ‘Geographically-isolated “aboriginal populations” are presented as examples of persisting races, but other endogamous groups are ignored. This naturalistic approach to the study of human evolution runs the risk of perpetuating colonialist myths about people with, and people without, culture’ (2004: 331). Colonial mythology portrays Indigenous peoples as ‘primitive’ peoples who are a part of nature akin to non-human animal species and are therefore presumed to lack culture, agency, and technology. This portrayal of Indigenous peoples as ‘uncivilized’ was essential to promoting the doctrine of *terra nullius* and justifying early waves of colonial land dispossession and genocide. The presumption that, before the beginning of European colonization, Indigenous peoples did not have the knowledge, skills, or technology to engage in complex voyaging—such as over the open ocean—is rooted in a colonial notion of racial hierarchy that positions Indigenous peoples as ‘primitive’ and ‘less advanced’ than Europeans in order to license land theft, kidnapping, and enslavement.

Consider another place where the influence of colonial mythology about Indigenous peoples manifests in theories of evolutionary history and human migration. Thor Heyerdahl’s racist ‘drift theory’ of the settlement of the Pacific claimed that it was impossible that Austronesian voyagers intentionally and successfully navigated east against the winds and was more likely that American Indians accidentally drifted west with the wind from the coast of South America (Herman 2014). Heyerdahl’s theory took a major hit in 1976 from the successful voyage of the Hōkūleʻa from Hawaiʻi to Tahiti using only traditional Micronesian navigational practices (Arvin 2019). Led by Micronesian master navigator Mau Piailug of Satawal, the Hōkūleʻa’s

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[8] Following the publication of Andreasen’s papers, extensive empirical evidence of the “geographically widespread genetic interchange” or gene flow among ancient populations has become available. Studies of ancient DNA (sometimes involving the reconstruction of individual genomes from Neanderthal or Denisovan populations) in conjunction with samples from living populations have refuted the presumption of significant isolation among the populations that Andreasen refers to as “aboriginal” (Templeton 2018). As Templeton summarizes, “The evidence from both ancient DNA and modern populations clearly indicates that the modern human gene pool is derived from multiple geographical regions and represents a mixture of many ancient populations that made unequal contributions to the current gene pool” (2018: 227).

voyage definitively demonstrated what many had long known—that intentional and planned long-distance voyaging could be accomplished using Indigenous navigational knowledge and so-called 'non-instrument' techniques that long pre-dated computer technologies. The Hōkūleʻa later completed a successful journey around the world, continuing the long historical legacy of complex and sophisticated Indigenous astronomical knowledge that has allowed the peoples of the Pacific to navigate using the sun, stars, winds, and knowledge of birds, fish, and ocean swells to voyage throughout Oceania for thousands of years.

The presumption that early Pacific peoples could not have travelled among different lands and waters for trade, diplomacy, marriage, or simply the pleasure of voyaging has a long colonial history. When colonizer James Cook first arrived in the Hawaiian archipelago, he is said to have expressed shock when Kanaka Maoli (Native Hawaiians) and Tupaia, a Tahitian navigator and *arioi* from Raʻiātea who had travelled with Cook, began conversing and understanding one another in their respective languages (Herman 2014). The close lexical relationship was clear evidence of a shared lineage and pointed to the extraordinary navigational ability that had once allowed Tahitians to cross 2,500 miles of open ocean to make a home on the islands of the Hawaiian archipelago. Further, evidence such as the presence of the sweet potato and bottle gourd in the islands, both vegetables of South American origin, as well as the fact that mitochondrial DNA sequencing of Chilean chicken bones perfectly matched those from chicken bones found in ancient sites in Tonga and Samoa (Borrell 2007), points to cultural exchange between Pacific Islanders and Amerindian peoples well before 1492. The reasoning of James Cook, Thor Heyerdahl, and 'drift theory' proponent anthropologist Andrew Sharp all demonstrate the same assumption: that geographic barriers like vast expanses of ocean provide insurmountable obstacles to intentional voyaging for non-European peoples and thus prevent the possibility of cultural exchange as well as gene flow among them.

In a similar vein, Gannett (2004) critiques Andreasen (2000) for assuming that geographic barriers alone were responsible for producing reproductive isolation and overlooking the extent to which socio-cultural factors determine the meaning and consequences of geographic barriers among populations. Gannett notes that:

> The extent to which physical structures like mountain ranges and rivers really do serve as barriers to gene exchange is always a function of the cultural significance that neighboring communities attach to them and the effort they are prepared to put into traversing them (Gannett 2004: 331).

When scientific theorists fail to rule out or even provide evidence against the possibility that travel, outbreeding, and gene flow exchange could have been the norm among population groups prior to the beginning of European colonization, it is suggestive of the continuing influence of a conceptual framework of racial hierarchy that undervalues the knowledge and abilities of Indigenous and non-European peoples and civilizations.

Because of the insidious effects of generations of racial pseudoscience masquerading as legitimate science, we cannot assume that contemporary biological race realism is uninfluenced by these ideologies even when it purports to be. Clearly, some of these effects manifest in the subtle theoretical background assumptions upon which race scientists rely when constructing contemporary theories. Yet race scientists are not the only ones who fall prey to such confusions; philosophers of race science can be similarly affected. Biological race realism is the metaphysical account of race that is closest to the traditional ideologies of race. While this does not automatically make it false, we should expect its proponents to be more susceptible to the influence of these vestigial assumptions, as their view is the one licensed by these widely if sub-consciously held associations. It is thus imperative that we bring to the fore as many of biological race realism's background assumptions as possible and subject them to critique.

In the next section, I explore the ways that another contemporary philosopher of biology's commitment to a Blumenbachian view of races as continental populations influences his metaphysical interpretations of data from population genomics.

3 Spencer's arguments for biological race realism

Spencer (2018) relies on a pre-established notion of 'human continental populations' that is derived from Blumenbach's pseudoscientific racial classification system. He brings it to bear in his analysis of the *structure* results despite the fact that is not licensed by the data or model under consideration. That Spencer relies on such a notion is made clear both by his explicit acknowledgement of Blumenbach's influence on his own racial thinking and by his invocation of Blumenbach's racial terminology. Spencer uses Blumenbach's language to describe the results of a (2009) study by Tishkoff et al as returning a partition at *K*=5 consisting of 'Caucasians, Mongloids [sic], and three distinct clusters of black Africans!' (2014: 1034) despite the term Mongoloid' not appearing anywhere in the original paper. Spencer's application of Blumenbach's language to the results of a study that does *not* invoke such language gestures toward the influence that Blumenbach's typology has on Spencer's own. Spencer also refers to the *K*=5 partition as 'the Blumenbach partition' because 'that partition is roughly coextensive with J. F. Blumenbach's anthropological division of humankind' (2014: 1026) and because, in 1795, Blumenbach 'became the first person to (roughly) discover this partition' (1030). He goes so far as to say that 'the Blumenbach partition is just the US meaning of "race"' because 'the set that Americans call "race" is *identical* to the Blumenbach partition' (1031, emphasis added). While Spencer (2018) engages with important scientific details of modern population genetics, his analyses fall prey to some of the assumptions characteristic of traditional race ideologies.

In what follows, I show how the content of race ideology rushes to close the gaps between the data Spencer considers and the biological race realism that he takes them to warrant. To demonstrate this, I look closely at Spencer's support for some of the premises in his argument that there is a notion of biological race that is useful in medical genetics. His argument is as follows:

1. The set of 1997 U.S. Office of Management and Budget (OMB) races is a racial classification.
2. The set of 1997 OMB races is identical with the set of human continental populations.

3. There are medically relevant genetic differences among human continental populations.
4. If (1)–(3) are true, then there's a racial classification that's useful in medicine.
5. Thus, there's a racial classification that's useful in medicine.

In this argument, Spencer takes a sociological classification of race created by the United States Office of Management and Budget (OMB) and used in the U.S. census and ties it, via an identity relation, to a purportedly biological racial classification.[9] He goes on to make an apparently a priori claim that this racial classification is 'useful' to medical genetics, invoking a normative notion that does not appear in any of the other premises. There are several unspoken assumptions in this argument, and I take each in turn.

First, the way that Spencer invokes the Rosenberg et al (2002) study is an example of the phenomenon identified by Wills (2017)—namely, using data from this study to motivate the view that the groups identified map stably onto groups that are socially identified as races. However, rather than provide evidence for this claim, Spencer simply assumes that the relation between the socially determined groups (those racial groups identified by OMB) and the 'set of human continental populations' (presumably, those genomic groups identified by *structure* at $K=5$) is identity. This is a strong claim and it is hard to see how it might turn out to be true. In fact, it is not even likely to turn out to be *referential*, as there is no single set of entities the phrase picks out.

How ought we to make sense of the identity claim in Spencer's premise 2? Since Spencer formulates this identity claim in terms of sets, the axiom of extensionality appears to be relevant to establishing its truth-conditions. The axiom of extensionality is foundational in naïve set theory and Zermelo-Fraenkel set theory. Formally, this axiom states:

> Axiom of Extensionality: $\forall A \forall B(A=B \Leftrightarrow (\forall X\colon X\in A \Leftrightarrow \mathrm{X}\in B))$

This means that for any set A and any set B, A is equal to B if and only if they share all the same members. Thus, sets are uniquely determined by their members. This is important background for interpreting Spencer's second premise:

> 2. The set of 1997 OMB races is identical with the set of human continental populations.

Given the axiom of extensionality, the truth conditions of this premise are clear. This claim is true iff the set of OMB races contains all and only those elements that are contained in 'the set of human continental populations'. In what follows, I show that there is good reason to take the phrase 'the set of human continental populations' to be non-referring, and Spencer provides little reason to think otherwise. But for the sake of argument, let us briefly assume that there is a unique partitioning of human continental populations—that which *structure* returns at $K=5$—and that this phrase refers to it.

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[9] Spencer (2014) also claims that Americans engaged in 'race talk' are referring to the OMB race categories anytime they use race terms.

What then are the elements of each of these sets? We can interpret the left side of the identity claim as referring to the set that contains the racial categories ‘American Indian or Alaska Native’, ‘Asian’, ‘Black or African American’, ‘Native Hawaiian or Other Pacific Islander’ and ‘White’. Given our above stipulation about the referent of ‘the set of human continental populations’, we can interpret the right side of the identity claim as referring to the set that contains the populations sorted by *structure* into each of the following geographic regions: Eurasia, East Asia, Africa, America, and Oceania (Rosenberg et al 2002).

To adequately explicate premise 2’s identity claim, the racial and population groups from the OMB classification that Spencer takes to match up with each member of ‘the set of human continental populations’ returned by *structure* at K=5 must be made explicit. Something like the following schema with an OMB racial group on the left and a population group sorted by *structure* at K=5 on the right appears to be implicitly assumed in Spencer (2018):

i. American Indian or Alaska Native = people with genomic ancestry from the population of the Americas
ii. Asian = people with genomic ancestry from the population of East Asia
iii. Black or African American = people with genomic ancestry from the population of Africa
iv. Native Hawaiian or Other Pacific Islander = people with genomic ancestry from the population of Oceania
v. White = people with genomic ancestry from the population of Eurasia

What then are the truth conditions for these further identity claims, upon which the identity in premise 2 is based? The most obvious candidate is if each of the racial and population groups contained in the two sets are themselves sets made up of their members and these sets are coextensive. Suppose that the identity conditions of the racial and population groups are to be wholly determined by their set membership. With the set interpretation of *i*-*v* above, the relevant identity claims become the following:

i. {American Indian or Alaska Native} = {people with genomic ancestry from the population of the Americas}
ii. {Asian} = {people with genomic ancestry from the population of East Asia}
iii. {Black or African American} = {people with genomic ancestry from the population of Africa}
iv. {Native Hawaiian or Other Pacific Islander} = {people with genomic ancestry from the population of Oceania}
v. {White} = {people with genomic ancestry from the population of Eurasia}

In the Rosenberg study, at K=5 genetic data from South Asian regions are grouped into the Eurasian cluster rather than the East Asian one. However, in the OMB classification, people from the Indian subcontinent are grouped into the ‘Asian’ category. Since people with genomic ancestry entirely from the subcontinent have membership in the {Asian} set but not the {people with genomic ancestry from the population of East Asia}, the identity in *ii* fails. And since they have membership in the {people with genomic ancestry from the population of Eurasia} set but not the {White} set, identity *v* also fails. This interpretation of Spencer’s premise 2 will not make the identity claim true.[10] It is unclear what empirical or metaphysical considerations could justify Spencer's claim that 'the set of 1997 OMB races is identical with the set of human continental populations' besides the question-begging presumption that there are five human races and each classification schema is picking up on this. It is especially odd that Spencer identifies the *K*=5 grouping with what he refers to as 'the Blumenbach partition' given that, as he acknowledges in a footnote in (2014), 'Blumenbach divided humans into Malays instead of Oceanians.' However, Spencer fails to recognizes that Blumenbach's category of the 'Malay' race included peoples, such as Filipinos, who are not now included among 'Oceanic' peoples—or the purportedly corresponding census category of 'Pacific Islander'—in contemporary groupings. What supports this alleged correspondence to Blumenbach's groupings—other than the fact that they both number 5—remains a mystery.[11]

A further problem with Spencer's argument is that he buries philosophically relevant features of the *structure* software program and its results. One feature that Spencer ignores is that Rosenberg et al (2002) do not identify any single specific grouping as 'the set of human continental populations,' nor do any of the resulting data provide the tools for doing so. Here is how Spencer (2018: 1018) describes the study:

> The set of human continental populations was discovered to be a human population subdivision by the population geneticist Noah Rosenberg and his colleagues in 2002. . . For any level with *n* number of clusters, the authors referred to that level as '*K*=*n*' and they were able to divide humans into unambiguous genetic clusters from *K*=2 to *K*=6.

It should be noted that, when using *structure,* researchers must enter *as an input* the number of groups into which the program should divide the human genetic samples. For each number chosen as an input in the 2-6 range, the program returned a single way to divide the human population. For instance, when *K* is set to 2 (by hand, before the computer returns any results), the two geographic regions that the program divides the human population into are Africa and

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[10] Spencer (2014) suggests that racial groups are sets of particulars. He takes this to be a result of his position that the referents of folk race terms in the U.S. just are those of OMB census racial terms. On this assumption, the identity claim for Spencer would be an identity not between sets of sets but between sets of particulars. However, this route will still result in a failure of identity, as it does not eliminate the differences between members of the two sets, whether understood as sets themselves or as particulars.

[11] Spencer spends several pages listing geographic populations that are primary examples of each of the OMB racial classifications. He lists several groups strongly fitting the classification of the 'Caucasian population' (It should be noted that neither OMB nor Rosenberg et al. use the term 'Caucasian', itself a holdover from early pseudoscientific race ideology as first used in a racist anthropological typology by German philosopher Christoph Meiners. The relevant geographic region Rosenberg et al. refer to is that of Eurasia. Spencer simply takes the extension of the OMB classification of 'White' to be identical with the population group classed as Eurasian in the *structure* study). Spencer writes, 'Some examples of people with strong membership in this population are. . . Kalash Pakistanis' (2018, 1019). But Spencer sidesteps an important issue here. This group is only strongly classified as Eurasian when *K*=5. When *K* is set to 6 instead of 5, Kalash Pakistanis are the group that is separated out and classified as *their own unique population group*. If *structure* outputs Kalash Pakistanis as having 'strong membership' in the group that Spencer terms the 'Caucasian population' at *K*=5 but outputs them as their own unique population group at *K*=6, that ought to tell us something about the arbitrariness and instability of these groupings across different values for *K*. While Spencer (2018: 1023) acknowledges in a footnote that at *K*=6, 'the Kalash separated from Caucasians to form their own population structure', he does not consider any of the questions this raises either for the 'strength' of their membership in the 'Caucasian' group at *K*=5 or for the presumed naturalness of the human population group structure that results at *K*=5.

the Americas. These two regions represent the geographically farthest from one another in terms of the evolutionary history of human migration and thus the most genetically distinct. At *K*=5, the genetic clusters correspond to the major geographic regions of Africa, Eurasia, East Asia, Oceania, and America. As discussed, this subdivision appears to be what Spencer is referring to in premise 2 with his use of ‘the set of human continental populations.’

However, there is an equivocation between the claim that *K*=5 clusters are *a* real human population subdivision and the claim that they are *the* set of human continental populations. The former is a very weak claim. The latter, which Spencer presupposes in premise 2), is much stronger. Consider Spencer’s wording in (2): ‘The set of 1997 OMB races is identical with *the* set of human continental populations’ (emphasis added). What explains Spencer’s use of ‘the’ in this premise? Two potential explanations come to mind: 1) it is licensed by the fact that *structure* identified some privileged set of human population clusters, or 2) it is licensed by some folk notion informed primarily by the history of racial pseudoscience. I argue that it cannot be the former, as *structure* found no such privileged set of population groups. The only relevant claim that *structure* provides evidence for is that *K*=5 clusters are a way of subdividing human populations. This is something few would dispute. Even Spencer writes, ‘The set of human continental populations was discovered to be *a* human population subdivision by the population geneticist Noah Rosenberg and his colleagues in 2002’ (2018: 1018, emphasis added). This suggests that he is invoking a pre-established notion of what ‘the set of human continental populations’ is that was not produced or licensed by *structure*.

If there is not a single privileged set of human continental populations, then there is no candidate class to be the referent of the phrase ‘the set of human continental populations.’ In a context such as this one, the use of ‘the’ triggers the presupposition of uniqueness. If there is no unique class of human continental populations to be picked out by the phrase ‘the set of human continental populations’ because, for instance, human continental populations can be partitioned in multiple ways, then the phrase must be treated as empty and non-referring. This would similarly be the case if someone used the phrase ‘the prime number between 1 and 100,’ as there is no unique prime between 1 and 100 and thus no referent that such a phrase picks out.

In his discussion of the *structure* study, Spencer fails to engage with the fact that nothing in the results motivates choosing any of the values of *K* as the most natural or objective for producing racial taxonomy. The results do not privilege a unique taxonomic scale or grain of resolution at which the clusters returned can be non-arbitrarily designated as the ones that correspond with either the ‘races’ or even the ‘human continental populations.’ Importantly, *structure* itself *does* offer a criterion for identifying whether there is a privileged value for *K* for any given data set. Specifically, this is the value of *K* that maximizes the probability of observing the data set. In Bayesian terms, this would be the value for *K* that has the highest probability. However, no single value of *K* maximized the probability of observing the data set, and none was reported in the study. Even though *structure* does provide a way of identifying ‘the number of genetic clusters most likely represented in this data set,’ no such value for *K* emerged (Bolnick 2008: 77). The inability of *structure* to identify a single value for *K* as the most likely indicates that, while there may be objective clinal structure in human genetic populations reflected in allele distribution across geographic regions, there is *no single best way* to divide up human populations into continental subpopulations. Given that the study did not identify a best value for *K*, the choice of any single human population grouping as being licensed by the study is arbitrary. If Spencer is relying on a further background assumption containing a relevant condition for what it is for *structure* to pick out a metaphysically privileged partition that is separate from the Bayesian condition that privileges the value of *K* that maximizes the probability of observing the data set, he must both make it explicit and show that it is met (solely) by the *K=5* partition.

The second fact that Spencer fails to engage with is that the patterns of groupings we see at different values for *K* are exactly what we would expect to find if the best way to understand the patterns of population difference in the data are as those determined by isolation-by-distance. For any number greater than 6, *structure* was not able to determine a uniquely likely partitioning of the population data into that number of groups. This means that for any *K* where *K*>6, *structure* returned multiple possible clusters for the human genetic population data. The closest Spencer comes to acknowledging this is in the following passage: 'Some of the human genetic clusters that Rosenberg and his colleagues identified were idiosyncratic to their study (e.g. *K*=6 clusters) or not likely caused by underlying population structure (e.g. *K*=2 clusters).' Spencer does not engage with the possibility that what is reflected by *structure*'s inability to produce unique groupings at values for *K*>6 or to identify a single value for *K* as the most likely, is that there is objective clinal structure in human genetic populations reflected in allele distribution across geographic regions but no single best way to divide up human populations into continental subpopulations.[12] The *structure* results are just as compatible (arguably more so) with variations among populations following patterns of isolation by distance and no population partition being metaphysically privileged as they are with some partition being 'the' set of human continental populations or biologically real races.[13]

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[12] Most genetic human population diversity is clinal rather than discrete (Kopec 2014). This means that, for most population features, there are gradual shifts in allele frequency that occur as one moves geographically across continents. These line up approximately with the evolutionary history of human migration out of Africa (Bellwood 2013). Much human biological diversity is due to genetic drift (Ackermann and Cheverud 2004, Andrews 2010). More specifically, genetic bottlenecks created by serial founder effects are responsible for most of the patterns of observed variation across human populations (Ramachandran et al 2005).

[13] In the documentation manual for the *structure* software, Pritchard, Wen, and Falush (2009) explicitly warn against the suitability of the *structure* model for data that follow a pattern of isolation by distance—exactly what many population geneticists take human population data to be. They write, 'Isolation by distance refers to the idea that individuals may be spatially distributed across some region, with local dispersal. In this situation, allele frequencies vary gradually across the region. The underlying structure model is not well suited to data from this kind of scenario. When this occurs, the inferred value of K, and the corresponding allele frequencies in each group can be rather arbitrary. Depending on the sampling scheme, most individuals may have mixed membership in multiple groups. That is, the algorithm will attempt to model the allele frequencies across the region using weighted averages of K distinct components. In such situations, interpreting the results may be challenging.' The authors of the software manual directly state that an inference to a specific value for K in such a case is likely to be arbitrary. That human genetic diversity follows a pattern of isolation by distance and this is what accounts for the structure results (including the lack of a uniquely best value for *K* as determined by the program's own Bayesian criterion) is an alternative explanation of the results of *structure* in Rosenberg et al (2002) that Spencer must rule out but fails to.

Bolnick (2008) asks why the results for *K*=5 and *K*=6 have been so strongly emphasized in the popular media and scientific literature, despite there being very little evidence to suggest that these values for K are somehow more biologically or ontologically significant than many other values. She writes,

> I would suggest that these particular results have been emphasized simply because they fit the general notion in our society that continental groupings are biologically significant. This notion is a legacy of traditional racial thought and seems to persist even when not clearly supported by biological data (2008: 77).

Spencer's focus on *K*=5 appears to fit this pattern, as it is the grouping that accords best not only with the OMB practices of racial classification but with folk and historical pseudoscientific conceptions of race. His move from the claim that *K*=5 clusters are *a* real human population subdivision to the conclusion that they are *the* set of human continental populations seems to be one place where historical race ideology functions to close the gap between what the data show and the conclusion that there is a uniquely best way to divide humans into races.

Spencer further offers an inadequate response to what he takes to be the strongest version of the reification objection. This is the objection 'that the model assumptions of *structure-like* programs are too unrealistic to interpret the inferred genetic clusters of these programs as anything other than fictional—or at best—abstract objects' (Spencer 2018: 1023). DeSalle and Tatersall (2018: 146) explicate a version of this objection based on the 'rather paltry sample size' of genetic data used in the *structure* analysis, suggesting that 'applying its results to understanding human population structure was something of a stretch.' Spencer's response to this version of the reification objection focuses on the fact that scientists often use models that involve false assumptions or idealized background conditions but this does not necessarily prevent one from making justifiable inferences about the concrete reality of the objects posited by such models. While this is of course true, there are very specific cases and conditions under which scientists make justified inferences based on idealized models or models with false background assumptions. Spencer invokes one such case, the prediction of the existence and location of Neptune using Newtonian gravitation, without attending to these special conditions. In fact, there is a principled distinction between that case and the case of inferring the biological reality of race from *structure*-like programs. Namely, the former involves a theory that made empirically confirmed novel predictions, while the latter does not.

Spencer invokes the famous case of astronomers Adams and Leverrier discovering the existence of Neptune by inference from perturbations in Uranus's orbit and Newtonian mechanics. The astronomers noticed that the path of Uranus deviated from what would be predicted by Newtonian theory. Instead of rejecting the theory outright, they reverse engineered a prediction of where an unseen planet would have to be to exert gravitational effects on Uranus that would cause it to deviate from its orbital path. When they turned their telescope on the sky, they discovered Neptune in the exact location they had predicted. What is significant about this example is that Newtonian mechanics—a theory with some false assumptions—was able to make a novel prediction, in this case the existence of a new planet. Broadly, novel prediction occurs when theories designed with one set of data in mind turn out to predict some unforeseen result.

A theory's ability to make novel predictions which are then confirmed is perhaps the strongest evidence for the reality of the entities it posits. More specifically, the scientific realist need only commit to ontological realism about theories that have made novel predictions. Because explaining novel prediction is the motivation for ontological commitment to the entities posited by a theory or model with false background assumptions, Spencer's invocation of Adams and Leverrier cannot be employed in the service of reifying a biological ontology of race from the results of *structure*. If Spencer wants to use the results of such a program to draw lessons about the biological reality of race, he can only do so after providing evidence that using *structure* to generate $K = 5$ clusters of human populations generates empirically confirmed novel predictions.

Spencer's metaphysical inferences about race from models of population genetics involve moves that demonstrate an a priori commitment to biological race realism. These show up in his assumptions about reference, ontology, and modelling. Hochman's (2014) criticism of Spencer's (2014) attempt to defend a naturalist version of biological race realism by deferring to what 'the folk' mean by their racial terms applies equally to Spencer's (2018) arguments that the *structure* results at K=5 vindicate an ontology inherent in OMB's racial classification schema. Hochman writes, "This is indeed a creative response: Spencer turns the problem into the solution!" (2014, 13).[14] Many gaps remain between the data provided by the *structure* results and the realist conclusions Spencer draws.

It should further be noted that Spencer's reliance on the outdated Rosenberg et al (2002) paper is itself indicative of his pre-theoretic commitments. Behar et al (2010) ran a model similar to *structure* that used the same single-level clustering but had a larger sample size, better geographical coverage, and a higher-resolution genetic survey. This would have been a more appropriate study to use, because it is more recent and more precise than the 2002 *structure* study. Yet in contrast to the results of Rosenberg et al (2002), the results of Behar et al (2010) found greater evidence of genetic admixture across nearly all individuals (Templeton 2018: 182). Nonetheless, Spencer cites the older, Rosenberg (2002) study, which had sparser geographic sampling with larger distances between populations, rather than the more recent Behar (2010) study that had much finer sampling in Africa and Western Eurasia. While the results of Rosenberg et al (2002) do not provide evidence for biological race realism, they can be more easily contorted into a theoretical framework that is already committed to such a view than can the results of the more recent and more representative Behar et al (2010) study. This suggests the possibility that Spencer relies so heavily on the outdated Rosenberg study in part because it can be more easily framed as supporting his a priori commitments than can the most recent scientific modelling on genetic admixture in human populations.

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[14] Spencer (2014) does engage with what Hochman (2014) refers to as the 'grain-of-resolution problem,' and Hochman notes that Spencer's (2014) response involves a sleight of hand. Spencer defends the view that the race naturalist may appeal to what 'the folk' believe to justify the acceptance of K=5 as the correct grain of resolution at which to measure the number of human races. But while 'the folk' may believe that there are five human races, as Hochman points out, "the race naturalist can't ask the folk how many races there are, it is the race naturalist's job to work that out!" (2014: 15). Spencer's (2018) approach no longer involves *direct* appeal to 'the folk,' though his appeal to the purported ontology of OMB racial classifications is just another way to appeal to 'the folk', since he believes that the OMB semantically determines the referents for folk racial discourse in the U.S.

While Spencer plainly embraces a Blumenbachian vision of race, it is not uncommon for vestiges of historical race ideologies to continue to influence the beliefs and judgments even of those who explicitly reject such views. We see their effects across various domains of biological race research, including in the representation of data and the production of background assumptions. Linguistic and visual representations of genetic data can unwittingly promote unsupported assumptions about race. Wills' (2017) discussion of how Rosenberg et al (2002) chose to visually represent how *structure* sorted genomic data into population groups provides one fascinating example. Wills argues that, 'the study is presented with subtle linguistic and visual ambiguities that potentially predispose a reader toward the very interpretation that the authors deny' (2017: 2). While the authors eschew any connection between the results of their study and support for biological evidence of conventional notions of race, Wills analyzes how the researchers' choice to assign a colour to each of the five continents promotes the impressions that population clusters are more unified, less heterogeneous, and more distinct from one another than they really are (2017: 12). That subtle features of the figures included tacitly promote a view of race that the authors do not subscribe to and do not take to be licensed by the results of their study shows how powerful and resilient historical ideologies of race can be in the face of contemporary scientific evidence against them.

When an area of science creates justifications for oppressive social structures that serve the interests of dominant groups, it becomes necessary to interrogate its background assumptions, methodologies, and theoretical frameworks. We can and should expect areas of scientific research involving race to be among those most susceptible to the influence of long-standing pseudoscientific ideologies and their enduring afterlives.

4 On the dangers of pragmatic optimism: taking the history of scientific racism seriously

The influence of pseudoscientific racial ideologies on contemporary research in biology, medicine, and the social sciences is not negligible. Whether one thinks of race as an illusory notion that arises out of practices of racialization or a social kind that is inherently linked to racism, or whether one thinks of it as a biological kind that has its own reality and stability apart from or prior to structural racism and colonial white supremacy, will make a world of difference to what one takes to be the primary causes of inequalities in disease rates and health outcomes among racialized populations. This, in turn, will radically affect when, where, and how one looks for solutions to these inequalities. Reflecting on the powerful legacies of racial pseudoscience and their use of scientific authority to justify racial inequality makes it clear just how much structures of the past continue to breathe life into the present. In this section, I trace aspects of the historical ideology of race that continue to influence medical research and practice, and I draw connections among the historical and contemporary effects of scientific racism and the normative stakes of philosophical debates about the biological reality of race.

The function of scientific racism consists in naturalizing socially produced inequalities among racialized groups by postulating their origins in purported biological differences among 'races' (Berenstain forthcoming). Early race science, i.e. racist pseudoscience, originated from the practice of biological classification of organisms in rank-based taxonomies. Carl Linnaeus created a hierarchical system of classification which subsumed all living organisms under phylogenetic kinds such as order, family, class, genus, and species. Linnaeus also believed human population groups could be organized into four ‘varieties’ based on continental location, *Europaeus albus*, *Americanus rubescens*, *Asiaticus fuscus*, *Africanus niger* (Doron 2012: 85).[15] Influenced as he was by the medical theory of the humors, Linnaeus included in this classification system personality traits that he took to be characteristic of each human ‘variety’ based on their different quantities of biological fluids: irascibility and stubbornness for Native Americans, intelligence and creativity for Europeans, greed and contemptuousness for Asians, and sluggishness and caprice for Africans (Moore 2008).

Immanuel Kant, one of the intellectual progenitors of scientific racism, produced an even more powerfully racist classification scheme by entrenching African, Asian, and Native American inferiority to the European in a *metaphysical* hierarchy. For Kant, only Europeans were capable of rationality, morality, and higher thought. Non-European races were inferior not just as a contingent matter, but necessarily so, because of their imagined racial metaphysical essences. Whereas Linnaeus had posited mere patterns of trait variance among the groups, Kant posited that Africans and Native Americans were *by nature* inferior to Europeans. He offered pragmatic advice to enslavers: Use a split bamboo cane rather than a whip to beat enslaved Africans because otherwise their ‘thick skin’ would prevent their bodies from being wracked with sufficient agony to motivate obedience (Eze 1997: 116). This reflects that early racial pseudoscience and scientific racism were not solely about classification but rather served to naturalize a hierarchy of European peoples over non-European peoples in order to justify the former’s subordination and exploitation of the latter through enslavement, land theft, and colonization (Roberts 2011b).

This function of racial classification, to portray contingent social hierarchies as necessary and inevitable results of the natural order, would remain at the core of race science for centuries. In the nineteenth century, Josiah Nott, a physician and enslaver in the American South, argued that slavery was morally permissible on the basis of craniometry.[16] Dr. Samuel Cartwright also produced scientific justifications for racial oppression and enslavement by developing empirical methods for ‘confirming’ that African-descended peoples achieved optimal health under slavery. He made technical advancements to the spirometer, a medical instrument created during slavery to measure lung capacity. After finding differences in the lung capacity of white people and enslaved African and African-descended peoples, Cartwright claimed these differences were innate and used them to argue against the abolition of slavery. Specifically, he suggested that forced manual labour was beneficial to enslaved African and African-descended peoples because, without such physical activity, not enough oxygen would reach the brain due to their innately lower lung capacity. Nott’s and Cartwright’s work demonstrates the historically tight connection between race science and the political project of justifying systems of racist brutality as part of the natural and moral order.

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[15] As Hochman (2019) points out, ‘variety’ was intended as a ‘mere category of convenience, rather than a scientific category’ and had no genealogical component.

[16] He suggested that forced labor and bondage actually benefitted African and African-descended peoples, claiming that ‘the negro attains his greatest perfection, physical and moral, and also greatest longevity, in a state of slavery’ (Nott 1847, 281).

The presumption of natural biological differences in lung functioning among differently racialized populations—and its corresponding ability to uphold socially produced inequities—is still common today. The spirometer remains in use as a tool for the diagnosis and management of respiratory disease (Braun 2015). When using the tool, practitioners must enter the race of the patient resulting in an automatic 'race correction' on the instrument. This serves to normalize increased levels of symptomology in Black patients. Misconceptions about the established nature of a biological basis for race can prevent Black patients from receiving needed health treatments by presenting health disparities and inequities as the normal consequence of inherent dysfunction in Black bodies (Roberts 2011). This is one of many examples of how derivatives of pseudoscientific race ideology can operate in the tacit assumptions and practices of contemporary researchers and physicians who explicitly disavow such ideology.

The harmful legacy of presuming inherent racial differences in physiology extends well beyond the use of tools that measure lung capacity. The view that Black people feel pain less intensely than white people, for instance, is another major lingering legacy of scientific racism.[17] This belief, which remains widespread among white medical students today (Hoffman, Trawalter, Axt, and Oliver 2016), translates into tangible differences in quality of care. Todd, Deaton, D'Adamo, and Goe (1997) found that, among patients treated in emergency rooms, Black patients were significantly less likely than white patients to receive analgesics for an isolated long-bone fracture despite reporting similar levels of pain. It is especially important to note that, 'Racial bias in perceptions of pain (and possibly treatment) does not appear to be borne out of racist attitudes' (Hoffman et al. 2016: 2). *Aversive* racist attitudes among medical practitioners are not necessary for the propagation of the harmful effects of ideologies borne of scientific racism:

> Today, many laypeople, scientists, and scholars continue to believe that the black body is biologically and fundamentally different from the white body and that race is a fixed marker of group membership, rooted in biology (26–28) . . . Research suggests that people even believe that black people are more likely than white people to be capable of fantastical mental and physical feats, such as withstanding extreme heat from burning coals (17). These biological conceptions of race are only weakly if at all correlated with racial attitudes (27, 34). They are nonetheless consequential (Hoffman et al. 2016: 2).

This means that the group of scientific researchers and medical practitioners who are affected by these harmful myths (and who cause harm to patients because of them) does not show significant overlap with the group of scientists and clinicians who hold aversive racist attitudes. The consequences of these ideological afterlives of scientific racism are insidious: they affect the quality of care and pain management that Black patients can expect to receive, and they deflect attention away from to the socio-structural causes of Black patients' high rates of conditions like congestive heart failure and uterine fibroids. As Roberts puts it, these ideologies attribute health disparities 'to flaws inside black people's bodies rather than to flaws in the society they live in' (Roberts 2011b, 15). This has the effect of making the health disparities between Black and

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[17] Scientific racists such as Cartwright also claimed that Black people were significantly less susceptible to pain than white people. J. Marion Sims, known as the 'father of modern gynecology', invoked the myth of Black insensitivity to pain to justify his torture via forced surgical experimentation without anesthesia of Anarcha, Lucy, and Betsey, Black women he enslaved.

white populations produced by systems of white supremacy seem 'natural, normal, and inevitable' (Collins 2000: 5).

Debates in the metaphysics of science about the biological reality of race are not merely academic but are situated within a context structured by the insidious histories and enduring effects of pseudoscientific race ideologies. As Berenstain (forthcoming) shows, 'individual researchers need not consciously endorse racism and white supremacy in order for their work to uphold scientific racism.' What does this mean for philosophers working in these areas? Given the high stakes of questions about the metaphysics of race, and the negative relationship of race ideology to the ability of racialized populations to access quality medical care, I contend that Spencer's framing of the debate is inadequately attuned to the potential of biological race realism to naturalize contingently produced social inequities by portraying them as the inevitable result of biological racial difference. Spencer's rhetoric portrays some of most important normative questions of this debate as either irrelevant or subordinate to purportedly non-normative questions, construed as purely scientific or empirical. He closes the (2018) paper with was he calls 'a disclaimer and a dilemma.' The dilemma is that nothing in his argument 'implies that medical researchers or clinicians should actually use this racial classification in clinical practice or medical research, nor does this fact guide us in how we should use this racial classification in medicine if we should use it at all' (2018:1034). Despite purporting to give an argument for the existence of a racial classification that is useful in medical genetics, Spencer has no suggestion about whether such a classification ought to be used. Instead, he emphasizes that 'it really is a dilemma whether we should use any racial classification in a genetic way in medicine.' What Spencer ignores, however, is the dilemma about whether the classification system he offers should even be considered *racial* in the first place. The answer to the ethical dilemma Spencer presents as arising separately from the question of metaphysical interpretation must in fact inform our *initial* methodological choices about how we operationalize, measure, and interpret race.

While these initial choices are often passed over as trivial, unimportant, or even self-evident, they are in fact central to the conclusions drawn. As Weiss and Fullerton emphasize, research on race involves myriad factors that are 'not inherent to the data, but choices investigators make for a host of reasons, some so taken for granted that they we may not recognize them as choices at all' (2005: 167). Dotson (2018) describes the initial choices made within any epistemological framework as 'operative orienting variables'. She emphasizes that these choices are 'not a trivial matter' but rather 'an initial power play' (Dotson 2018: 131). This notion applies to metaphysical interpretations of population data, as different choices of operative orienting variables in the biology of race will be more or less efficacious at promoting and upholding harmful interpretations of race, such as those that normalize various racial inequalities in health by making them appear "natural" (Hardimon 2017: 63).

Spencer (2018) does recognize some possibility of harm resulting from the potential use of his suggested racial classification in medical or clinical practice. He writes, 'On the con side, new work from educational sociologists shows that, sometimes, just reading about human genetic diseases in recognizably racial terms (e.g. 'Black', 'White', 'Caucasian', etc.) significantly raises one's probability of developing an "essentialist" conception of race, which is itself correlated with developing racist attitudes' (2018: 1034). Yet he ignores significant evidence of the actual material harms that goes well beyond merely 'developing racist attitudes'. Perhaps the most significant harm is the misdirection of attention away from racism and racist environments as a cause of and contributing factor to disease and ill-health for populations of colour (Roberts 2011b). Spencer's recognition of the scope of potential harm from invoking a biological conception of race in medicine is thus severely limited.

Perhaps one plausible version of an argument for biological race realism is as follows: we should just take race to be geographic ancestry. Geographic ancestry plays a useful role in medical genetics. Therefore, there is a conception of race that is useful in medical genetics. But this argument masks several important features of reality. One might concede that if some biological property *must* be taken to play the role of race, that biological property ought to be geographic ancestry. But of course, it is not the case that some biological property *must* be taken to be race. It is question-begging to assume that something must be race and science has only to uncover what it is. Further, there is no reason to think that invoking a notion of *race as geographic ancestry* in medical genetics would be more useful than simply invoking the notion of geographic ancestry in the same research. What biological race realists must do is offer a reason to be committed to a notion of race *over and above* the notion of geographic ancestry that we already know may be useful in medical genetics.[18]

There are also significant reasons to think that using a notion of *race as geographic ancestry* in medical genetics would be worse than simply using geographic ancestry without construing it as race. Roberts (2011) catalogues them in her discussion of the extensive harms caused by medical stereotyping. These include the stereotypes that white patients are not candidates for sick-cell anaemia and Black patients are not candidates for cystic fibrosis, that Black patients seeking treatment for pain are engaging in drug-seeking behaviour (94), and that hyperactive behaviour in Black children and teens is evidence of oppositional defiance disorder or even schizophrenia (2011: 94-99). American medicine's presumption in the early-to-mid twentieth century that sickle-cell anaemia was a disease that was 'confined to a single race' and whose occurrence depended 'entirely on the presence of Negro blood' (JAMA 1947) held back the development of scientific research into sickle-cell trait for decades. While sickle-cell disease is still is popularly seen as a 'Black disease', the geographic distribution of sickle-cell trait actually aligns with the prevalence of malaria due to the resistance against the disease conferred by the heterozygous carrier state. The trait is thus common across many populations in the Mediterranean, the Middle East, and India, as well as parts of Africa (Piel et al 2010). The notion of race in medicine can activate assumptions left over from discredited racial theories as well as associations from contemporary social ideologies of race that are scientifically unsupported, and this has non-negligible consequences that are harmful both to racialized populations and to scientific progress.

Taking race to be membership in a group based on geographic ancestry does not clearly add anything beneficial or functional to medicine or medical genetics over and above the benefits that result from classifying patients according to their geographic ancestry. As Root (2003) has

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[18] This is not to say that the notion of geographic ancestry is or will be *generally* useful in medicine. There are certain contexts in which it is useful, such as in determining one's likelihood of carrying the gene for Tay Sachs. And while there are some indications that it could play a promising role in personalized medicine, such an approach also produces significant risks of harm, especially to Black populations (Root 2003).

pointed out, when facts about geographic ancestry are indeed useful in medical genetics, they are facts about ancestry at a much smaller scale than the scale of continental population groups. As this section has shown, tacking on a label of 'race' to such a property can lead to conceptual confusion and ultimately obfuscation and harm due to the concept's ability to trigger a set of confounding associations and false assumptions inherited from the long history of racial pseudoscience. For this reason, it is reasonable to predict that the general practice of invoking a biological conception of race (even one as thin as membership in a genomic grouping based on geographic ancestry) will likely do significant harm. And there is little reason to believe it will do any good *beyond* that which is done by its being a proxy for geographic ancestry.

5 Conclusion

Holdovers from early theories of scientific racism continue to influence contemporary researchers in biology and anthropology (Morning 2011). Such influence is also present in contemporary philosophical accounts of biological race realism. This paper has revealed how Spencer's (2018) and Andreasen's (1998, 2000, 2004) arguments for biological race realism may have been similarly influenced. After identifying some of the analytical gaps in their arguments for biological racial realism, I argued that the authors allow long-standing racial and colonial ideologies to fill these gaps. I have shown where their arguments depend on background assumptions that, at best, align with and, at worst, derive from the same pseudoscientific racial ideologies that scholars of race and science have worked for decades to reveal and undo. The question of whether to be biological realists about race involves a series of evaluative and pragmatic judgments that depend in part on induction over a long and ongoing history of racial harm and oppression produced and upheld in part by the purported science of race. And the costs of making the wrong call are extremely high. Until there are solid pragmatic reasons to think that normative assumptions about the biological reality of race will produce better science and better medicine, those who are inclined to grasp about for biological justifications for the classification of human populations into races ought to proceed with a level of caution that reflects the seriousness of these risks.

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