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A racial classification for medical genetics

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Abstract In the early 2000s, Esteban Burchard and his colleagues defended a controversial route to the view that there's a racial classification of people that's (epistemically) useful in medicine. The route, which I call 'Burchard's route,' is arguing that there's a racial classification of people that's useful in medicine because, roughly, there's a racial classification with medically relevant genetic differentiation (Risch et al. in Genome Biol 1–12, 2002; Burchard et al. in N Engl J Med 348(12):1170–1175, 2003). While almost all scholars engaged in this debate agree that there's a racial classification of people that's useful in medicine in some way, there's tremendous controversy over whether any racial scheme is useful in medicine because there are medically relevant genetic differences among those races (Yudell et al. in Science 351(6273): 564–565, 2016). The goal of this paper will be to show that Burchard's route is basically correct. However, I will use a slightly different argument than Burchard et al.'s in order to provide a firmer foundation for the thesis, both metaphysically and genetically. I begin by reviewing Burchard's route and its critics. Second, I present an original argument for establishing Burchard et al.'s conclusion using a Burchard-like route. I call it 'Spencer's route'. I reply to major objections along the way, and I end with a summary.

Keywords Genetic · Medical · Medicine · Race · Racial

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1 Introduction

In the early 2000s, the medical geneticist Esteban Burchard and his colleagues presented a highly controversial argument for the existence of a racial classification of people that's epistemically useful in medicine, and by 'medicine' I intend to include clinical practice (e.g. diagnosis and treatment) as well as medical research (e.g. genome-wide association studies, drug efficacy studies, etc.) (Risch et al. 2002; Burchard et al. 2003).[1] Suppose we call the debate about whether there's any racial classification that's useful in medicine *the biomedical race debate*.[2] What made Burchard et al.'s argument controversial in the biomedical race debate was not its conclusion. To the contrary, it's difficult to find an interlocutor in the debate that thinks there's *no* racial classification that's useful in medicine. For example, most scholars in the debate at least agree that there's a racial classification that's useful in medicine for tracking the health effects of racism.[3] Rather, what made Burchard et al.'s argument controversial was *the route* (the argument) it took to reach its conclusion. In short, Burchard et al.'s argument contains premises that together imply that there's a racial classification with medically relevant genetic differentiation. This racial classification is the five major races used on the 2000 US census questionnaire, which is also currently the official racial classification of the US government. I'll call Burchard et al.'s argument 'Burchard's route' for convenience.

The major objections to Burchard's route in the literature have been from critics who either reject that there's any racial classification with medically relevant genetic differentiation or who reject that the OMB's racial classification possesses this property. For example, Yudell et al. (2016, 565) have bluntly said that "racial classifications do not make sense in terms of genetics," and Kaplan (2010, 281) has said that "…current folk racial categories—those categories usually used on surveys, recognized by the U.S. Office of Management and Budget (OMB), and used on census forms and by U.S. Federal Drug Administration (FDA)—do not correspond to meaningful biological categories." However, the goal of this paper is to show that Burchard's route is basically correct.

To be precise, I will defend a slightly different argument for Burchard et al.'s conclusion that is on a firmer foundation both metaphysically and genetically. Most importantly, I will defend a relationship of identity between the 1997 OMB races and the human continental populations. But also, I will shed an unnecessary and controversial genetic premise in Burchard et al.'s argument. The result will be an original Burchard-like route to Burchard et al.'s conclusion that I'll call 'Spencer's route'. I will begin by discussing Burchard's route and its critics. Next, I will

[1] From here on, I will drop 'epistemic' and 'people' as modifiers for 'useful' and 'racial classification,' respectively. Instead, I will just assume that the usefulness under consideration is epistemic and the racial classification under consideration is human racial classification. Also, since I'm being careful, I should clarify that by 'human' I mean '*Homo sapiens*'.

[2] The name and characterization of this debate is from Spencer (2014, 41).

[3] For a few examples, see Root (2003), Andreasen (2008), Kaplan (2010), Morris (2011), and Sullivan (2013).

introduce and defend Spencer's route. I will reply to major objections along the way and end with a summary of the paper.

2 Burchard's route and its critics

2.1 Burchard's route

A charitable reconstruction of Burchard's route is below. It's based on two landmark papers by Burchard and his colleagues in the early 2000s.[4]

(1) The set of 1997 OMB races is a racial classification (Burchard et al. 2003, 1171).[5]
(2) Primary membership in any 1997 OMB race is "very highly correlated" with primary membership in a specific human continental population (Burchard et al. 2003, 1172).[6]
(3) The set of human continental populations is the human population subdivision with "the greatest genetic differentiation in the human population" (Burchard et al. 2003, 1171).[7]
(4) There's medically relevant genetic differences among human continental populations (Burchard et al. 2003, 1172–1174).[8]
(5) If (1)–(4) are true, then there's a racial classification that's useful in medicine (Burchard et al. 2003, 1172–1174).[9]
(6) Thus, there's a racial classification that's useful in medicine.[10]

Now, let me clarify what each premise means and why Burchard and his colleagues think that each premise is true. I'll also discuss major objections to each premise and judge whether the premise can survive those objections.

2.2 Clarifying Premise 1

(1) Is a simplification of what Burchard et al. actually say which is that the five major races used on the 2000 US census questionnaire is a racial classification (Risch et al. 2002, 5–6; Burchard et al. 2003, 1171). However, the US Census

[4] However, note that Burchard and his colleagues still adopt this argument today. For evidence, see Bustamante et al. (2011).

[5] Also, see Risch et al. (2002, 5).

[6] Also, see Risch et al. (2002, 6).

[7] Also, see Risch et al. (2002, 3).

[8] Also, see Risch et al. (2002, 6).

[9] Also, see Risch et al. (2002, 11).

[10] It can be shown that this argument is deductively valid when correctly translated into a symbolic logic that's appropriate for doing metaphysics. The one I used was quantified modal free logic with necessary identity and a T interpretation of necessity. See Girle (2009, 14–15, 39, 107–108, 133) for the syntax and semantics of this logic.

Bureau is very clear that this racial classification is the OMB's.[11] The relevant background is that the OMB is an office in the executive branch of the US government whose job it is to manage the federal budget and federal agencies. In 1977, the OMB issued an executive order known as 'Directive No. 15' that requires all federal agencies in the US government (e.g. CDC, NIH, DOJ, FBI, etc.) to report racial data to other federal agencies in the US government in a way that's translatable into the OMB's racial classification. However, most federal agencies simply use the OMB's racial scheme in order to facilitate compliance with this executive order.

The OMB (1997a, b, 58782) issued Directive No. 15 first and foremost "to provide consistent data on race and ethnicity throughout the Federal Government," but also, "to enforce civil rights laws." In 1977, the OMB adopted four races with non-overlapping members and with limited coverage. However, in 1997, the OMB (1997a, b, 58782) radically changed its racial scheme to consist of five races with overlapping members and that's "comprehensive in coverage." The OMB did this in order to address the rise in "immigration" and "interracial marriages" in the USA that occurred since 1977 (OMB 1997a, b, 58782). Here's an example of the change that occurred.

During 1977–1996, the OMB used 'American Indian' in such a way that excluded the indigenous people of Central and South America (e.g. Maya Mexicans and Quechua Peruvians) as well as the indigenous people of the Americas north of the continental USA (e.g. Alaskan Aleuts and Greenlandic Inuits). In addition, before 1997, the OMB did not recognize multiracial people. However, all of that changed in the OMB's 1997 revision. In 1997, the OMB (1997a, b, 58782) expanded its racial classification to consist of five "broad population groups" that are "comprehensive in coverage" (thus not leaving out Maya Mexicans, Alaskan Aleuts, etc.), and they embraced multiracialism. One important footnote is that the OMB has never considered Hispanics to be a race.[12] The OMB (1997a, b, 37; 1997, 58789) has always considered Hispanics to be people of "Spanish culture or origin, regardless of race."[13] Below are the specifics about the OMB's racial scheme.

The OMB (1997a, b, 5879) calls its first race 'American Indian or Alaska Native' (or 'American Indian' for short) and says that this group consists of people "having origins in any of the original peoples of North and South America (including Central America) and who maintains tribal affiliation or community attachment." Interestingly, the OMB doesn't provide any examples of people in this race. However, some Americans who self-reported being in this race on the most recent federal census

[11] For evidence, see Grieco and Cassidy (2001, 2–3).

[12] Even though the OMB uses 'Hispanic' and 'Latino' interchangeably to refer to Hispanics, I will only use 'Hispanic' to refer to Hispanics in this paper. This is not only for concise writing, but also because the Pew Hispanic Center has discovered that 'Hispanic' is the preferred name for Hispanics among Hispanic Americans who care about the issue by more than a two to one margin (Taylor et al. 2012, 3).

[13] With that said, the OMB is currently reviewing its racial classification to decide whether any changes should be made. The major items of review are whether Hispanics should be added as a race, and whether Arabs or (but not both) Middle Easterners and North Africans (MENA) should be added as a race (OMB 2017). Nevertheless, this paper is about the OMB's 1997 racial classification.

were Aleut, Choctaw, Iroquois, Mexican–American, Navajo, Sioux, and Yup'ik (Norris et al. 2012, 18–19). The OMB (1997a, b, 58789) calls its second race 'Asian' and says that this group consists of people "having origins in any of the original peoples of the Far East, Southeast Asia, or the Indian subcontinent." Also, the OMB lists the following people as examples of Asians: Cambodians, Chinese, Indians, Japanese, Koreans, Malaysians, Pakistanis, Filipinos, Thai, and Vietnamese (OMB 1997a, b, 58789).

The OMB (1997a, b, 58789) calls its third race 'Black or African American' (or 'Black' for short) and says that this group consists of people "having origins in any of the black racial groups of Africa."[14] Some examples of Blacks according to the OMB are African Americans, Afro-Brazilians, Cape Verdeans, Ethiopians, Haitians, Jamaicans, Louisiana Creoles, and Nigerians (OMB 1995, 44682; 1997a, b, 58789; 2000, 28). The OMB (1997a, b, 58789) calls its fourth race 'Native Hawaiian or Other Pacific Islander' and says that this group consists of people "having origins in any of the original peoples of Hawaii, Guam, Samoa, or other Pacific Islands." Although Native Hawaiians, Chamorro, and Samoans are explicit examples of Pacific Islanders according to the OMB, it's important to note that thousands of Melanesian Americans racially self-reported as Pacific Islander as well on the last federal census, especially Fijian Americans (Hixson et al. 2012, 14). The OMB (1997a, b, 58789) calls its fifth and last race 'White' and says that this group consists of people "having origins in any of the original peoples of Europe, the Middle East, or North Africa." Of course, this group includes Arabs, Europeans, European Americans, Jews, and Persians. But also, the OMB (1995, 44682) has offered up a few multiracial groups as examples of Whites, such as Cape Verdeans and Louisiana Creoles. In addition, many Hispanic Americans racially self-reported as White on the last federal census—especially Cuban, Puerto Rican, and Mexican Americans (Ennis et al. 2011, 14).

While Burchard et al. consider (1) to be so obvious that they don't defend it, it's worth pointing out that some biologists and philosophers would consider (1) to be at least misleading.[15] There is a long tradition in the life sciences of using 'race' as a synonym for 'subspecies,' and from that linguistic context, it's not clear at all that any human subdivision is a *racial* classification given the high standards in systematic biology for what counts as a *subspecies*.[16] However, Burchard and his colleagues have an easy reply here. The subspecies objection to (1) involves an equivocation on 'racial' that results in the objection itself being non-threatening. So,

[14] The OMB is notoriously ambiguous about what they mean by 'racial groups.' Sometimes the OMB uses 'racial groups' interchangeably with 'races' and sometimes they use the term interchangeably with 'ethnic groups.' For evidence, see OMB (1997a, 36886, 36894, 36924). However, when the OMB talks about Black racial groups, they use 'racial groups' interchangeably with 'ethnic groups.' For that reason, I'll interpret the use of 'racial groups' in the OMB's "definition" of 'Black' as interchangeable with 'ethnic groups'. Also, note that the OMB intends to pick out a skin color, not a race, with its use of 'black' in its "definition" of 'Black.' Otherwise, the "definition" would be viciously circular.

[15] Some examples of biologists and philosophers of biology who would likely consider (1) to be misleading—though not literally false—are Rotimi (2004), Hochman (2013) and Templeton (2013).

[16] For a detailed and critical discussion of what counts as a subspecies among contemporary systematic biologists, see Spencer (2018b).

for clarity, Burchard and his colleagues are not saying that the 1997 OMB races are subspecies. They're just saying that these groups form a racial classification in a weaker (non-subspecies) meaning of 'racial.'

2.3 Premise 2 and its critics

As for (2), 'human continental population' is a term of convenience for talking about any one of five biological populations in humans that population geneticists have recently discovered to be a subdivision of biological populations (a population subdivision) in our species.[17] Burchard and his colleagues talk about these five groups using various aliases, such as "the five continental groups," "continentally separated groups," and "continentally defined groups" (Risch et al. 2002, 3; Burchard et al. 2003, 1171). While the names used for each human continental population varies among biologists, I'll use the names 'African', 'Caucasian', 'East Asian', 'Native American', and 'Oceanian'.[18]

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. In a landmark study, Rosenberg et al. (2002, 2381) used a novel genetic clustering computer program known as *structure* to divide the human species into a series of hierarchical levels of "genetic clusters" based on observed genomic similarity among individual people. 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 $K = 6$. At each level, the clusters identified were fuzzy, and by 'fuzzy' I mean that the clusters were permitted to have overlapping members subject to two constraints. The first was that any person's membership grade in a cluster was a value in the unit interval. The second was that the sum of all membership grades any person has across all clusters at a level equals 1.[19] 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). However, for reasons that I will delve into later, Rosenberg et al.'s $K = 5$ clusters have been widely accepted among population geneticists as a real human population subdivision.

One interesting fact about the human continental populations is that they are, essentially, genealogical groups whose current members are people with genomic

[17] I'm borrowing the term 'continental populations' from Richard Cooper et al. (2003, 1167). Also, a *biological population* in the population-genetic literature is typically understood to be a breeding population (e.g. a panmictic group of organisms) or a genealogical population (e.g. a haplogroup) (Gannett 2003, 997). For clarity, a *haplogroup* is a group consisting of the first organism to possess a specific nucleotide sequence in its genome and all of its descendants that also possess that genomic sequence. An example is mitochondrial haplogroup M in humans.

[18] Except for 'Oceanian,' these are the names that Burchard and his colleagues use (Risch et al. 2002, 3). 'Oceanian' is the preferred name among population geneticists for the fifth group (Tishkoff et al. 2009, 1037).

[19] For a more detailed and precise discussion of the fuzzy set-theoretic assumptions embedded in this research, see Spencer (2016, 793–794).

ancestry from that population. Also, a person has *genomic ancestry* in a population *p* just in case one or more of the alleles in her diploid genome—hereafter just *genome*—was inherited from a member of *p*.[20] For this reason, some population geneticists call these populations "ancestry groups" (Feldman 2010, 157). In any case, here's a short introduction to each human continental population.

The African population mostly exists in Sub-Saharan Africa. Also, some examples of people with strong membership in the African population are African Americans (0.81), Maasai Kenyans (0.70), Mbuti Congolese (0.99), San Namibians (0.98), and Yoruba Nigerians (0.98) (Rosenberg et al. 2002, Table S2; Halder et al. 2009, Table 2; Wall et al. 2013, 206).[21] The East Asian population mostly exists in Northeast and Southeast Asia. Some examples of people with strong membership in this population are Han Chinese (0.98), Khmer Cambodians (0.94), and Yakut Siberians (0.87) (Rosenberg et al. 2002, Table S2; Xing et al. 2010, Table S1). The Caucasian population mostly exists in Europe, North Africa, Central Asia, South Asia, and West Asia. Some examples of people with strong membership in this population are the French (0.97), Kalash Pakistanis (0.99), Mozabite Algerians (0.76), Palestinians (0.95), and Turkmen (0.73) (Rosenberg et al. 2002, Table S2; Martínez-Cruz et al. 2011, 222).

Next, the Native American population exists mostly in North and South America. Some examples of people with strong membership in this population are Greenlandic Inuits (0.73), Karitiana Brazilians (0.99), Mexican Americans (0.48), and Pima Mexicans (0.91) (Rosenberg et al. 2002, table S2; Manichaikul et al. 2012, Table 1; Pereira et al. 2015, table S9). Finally, the Oceanian population exists mostly in Australia, Melanesia, Micronesia, and Polynesia. Some examples of people with strong membership in this population are Aboriginal Australians from the Riverina (0.64), Nasioi Bougainville Islanders (0.97), Māori New Zealanders (0.87), and Palauans (0.73) (Rosenberg et al. 2002, table S2; Friedlaender et al. 2008, table S6; McEvoy et al. 2010, 300).

Now, the reason why Burchard and his colleagues originally judged (2) to be true was because of a *structure* analysis done on a sample of 354 people by James Wilson et al. (2001, 266) that showed that primary membership in four human continental populations "broadly corresponds" to primary membership in four 1997 OMB races. For example, from scrutinizing Wilson et al.'s results, Burchard and his

[20] Unfortunately, geneticists are not careful when talking about a person's genome. Sometimes, geneticists talk as if every non-reproductive cell of a person has its own genome. However, at other times, geneticists talk as if there is a single set of DNA that represents an individual's genome. However, in order to be clear, I will operationally define a person's *genome* as her inherited DNA from the nucleus in a randomly selected non-reproductive cell in her body together with her inherited DNA from a randomly selected mitochondrion from that same cell. Nuclear DNA in humans is typically divided into a pair of sex chromosomes (one from each parent) and 22 pairs of other chromosomes (the autosome). While geneticists usually only sample alleles from autosomes in human genetic clustering studies, that's not a huge problem because the autosome usually comprises 94.0% of a person's genome (as measured in nucleotide base pairs). This count comes from the Ensembl genome database project, and specifically, page http://useast.ensembl.org/Homo_sapiens/Location/Genome, which was accessed on January 26, 2018. One last point is that an *allele* in this context is just a sequence of nucleotides (even as small as one nucleotide) at a locus in a genome.

[21] Average membership grades are in parentheses.

colleagues discovered that 95% of the sampled Pacific Islanders had primary membership in the Oceanian population, 94% of the sampled Whites had primary membership in the Caucasian population, and 84% of the sampled Asians had primary membership in the East Asian population (Wilson et al. 2001, 267). However, since 2001, (2) has received much stronger support. For example, using a sample of 3224 American and Taiwanese adults, Tang et al. (2005, 271) showed that 100% of sampled Asians had primary membership in the East Asian population, 99.8% of sampled Blacks had primary membership in the African population, and 99.9% of sampled Whites had primary membership in the Caucasian population. This is an average of 99.9% predictive accuracy (across races)! Also, using a sample of 1773 US college students, Guo et al. (2014, 153) were able to predict the self-reported race (Asian, Black, or White) of their subjects with an average of 98.8% accuracy (across races) using primary human continental population membership. With statistics like that, it's hard to disagree with (2). However, (2) turns out to be the most controversial premise in Burchard's route.

On one hand, many race scholars have rejected the claim that there is a very high correlation between primary racial membership understood in any folk way and primary human continental population membership (Glasgow 2009, 94–97; Kaplan 2010, 281; Roberts 2011, 51–52). On the other hand, some biologists and philosophers of biology have rejected the reality of the human continental populations due to concerns about *structure* and other *structure-like* programs, or the genomic data sets that are typically used (Bolnick 2008; Weiss and Long 2009; Kalinowski 2011; Winther et al. 2015).[22] I'll start with the race scholars.

The objection from race scholars to this premise is that the correlation between primary 1997 OMB racial membership (or any folk racial membership) and primary human continental population membership is not "very high" because folk race terms pick out significantly different extensions than human continental population terms.[23] One example of this objection comes from Dorothy Roberts who claims that the African population does not overlap the Black race well at all, at least given how 'Black' is currently defined in the USA. This is because, according to the folk American conception of Blacks, people with "any amount of African ancestry" are 100% Black (Roberts 2011, 51). However, only people with $> 50\%$ or else a plurality of African genomic ancestry are primarily African. What this implies is that racial self-reports can be very misleading about who's actually Black, and, furthermore, once we identify the actual Blacks in any of these studies, we'll see that the overlap between Blacks and Africans is not that high.

As an example, I took the liberty of reevaluating Guo et al.'s (2014) results assuming that any subgroup of subjects with, on average, $\geq 1\%$ African genomic ancestry consists entirely and exclusively of Black people. Given that assumption, there were 590 Black people in this study (Guo et al. 2014, 155). However, Guo et al. (2014, 153) only identified 353 people with primarily African genomic

[22] The term "*structure*-like programs" is from Weiss and Long (2009, 704).

[23] Here, the term 'extension' is intended to be used in Quine's (1951, 21) sense, which is that of "all entities of which a general term is true."

ancestry. So, according to Roberts, the actual accuracy that Guo and his colleagues had in predicting who's Black with genomic data was 59.8%, as opposed to the 99.3% that they reported (Guo et al. 2014, 153).

While it's important to question whether racial self-reports are reliable indicators of primary racial membership in the relevant sense, there's a fatal flaw in Roberts' critique. Namely, what matters for determining 1997 OMB racial membership isn't what the folk US concept of race says, if there is such a thing. Rather, it's what the OMB intends racial membership to be in its racial scheme. Furthermore, the OMB is clear that it rejects the idea that anyone with ancestry from the black ethnic groups of Africa is 100% Black. For example, the OMB (1995, 44682) acknowledges that Cape Verdeans and Louisiana Creoles are, on average, both Black and multiracial people. The deeper point is that the OMB is perfectly fine with multiracialism, but Roberts (2011, 51) views folk races in the USA as, essentially, "discrete." So, while Roberts' critique might work for some folk racial schemes, it doesn't work for the OMB's.

However, a stronger version of the *mismatch objection* (as it's called in the literature) is that the studies that supposedly show a very high correlation between 1997 OMB race term extensions and the extensions of human continental population terms are actually just an artifact of sampling bias.[24] For instance, Joshua Glasgow (2009, 95–97) makes this claim, and so does Jonathan Kaplan (2010, 281). Here's an example of how this version of the mismatch objection unfolds.

Again, if we look at Guo et al.'s (2014, 153) study, we can calculate that they were highly successful in predicting 'Asian' racial self-reports from East Asian genomic ancestry (97.7% accuracy) only because they deliberately excluded the 'Asian' self-reports from their South Asian subjects! If they had included them, one can calculate that their accuracy of predicting self-reported Asians would have dropped to 66.1%. Also, people of South Asian descent are not wrong to self-report as 'Asian' in the OMB's racial scheme because the OMB's (1997a, b, 58789) "definition" for 'Asian' includes people with "origins" from "the Indian subcontinent." Nevertheless, the mismatch arose in this case because these South Asians' primary genomic ancestry was Caucasian (0.684), which is normal for South Asian people (Guo et al. 2014, 155). So, there seems to be a mismatch between who's primarily Asian in the OMB's racial scheme and who's primarily East Asian.

While this version of the *mismatch objection* has been persuasive to many in the literature, it rests on the assumption that the extensions of OMB race terms are different from the extensions of human continental population terms. To be fair, Burchard and his colleagues make this assumption as well. Otherwise, it'd be strange for them to talk about the two sets of terms being "correlated" in the first place. Nevertheless, I will argue later on when defending Spencer's route that this idea of extensional difference is a confusion that stems from misidentifying what OMB racial terms actually mean. So, I will return to the mismatch objection later.

[24] I'm borrowing the term 'mismatch objection' from Joshua Glasgow (2009, 94).

However, right now, it's worth addressing the concern of some philosophers of biology and biologists that Rosenberg and his colleagues are reifying a human division that's obtainable with *structure-like* clustering programs, but that, in truth, doesn't actually exist.[25] Suppose we call this *the reification objection.*[26] To be perfectly honest, this is a strong objection against Burchard's route. There has been much understandable skepticism about which human population subdivisions can be justifiably inferred as actually existing using genomic data sets like the one used in Rosenberg et al. (2002)—which was the HGDP-CEPH cell line panel—and *structure-like* clustering programs.[27]

Specifically, with respect to the data sets, many have objected that the samples of people in the typical genomic data sets used for human genetic clustering analyses are skewed to favor finding genetic clusters (Serre and Pääbo 2004; Bolnick 2008, 78; Templeton 2013, 268; Hochman 2013, 346). For example, Rosenberg et al.'s (2002) sample was stacked with unmixed and geographically isolated people (e.g. Mbuti Congolese, Kalash Pakistanis, She Chinese, Nasioi Papuans, Suruí Brazilians, etc.) and light on cosmopolitan or heavily mixed people (e.g. African Americans, Mestizos, Polynesians, South African Coloureds, etc.). While this objection is understandable and while the HGDP sample is certainly not perfect, this sampling bias claim is testable, and so far, Rosenberg et al.'s original $K = 5$ result has been replicated using the largest and most diverse sample of people ever assembled in a human genetic clustering study.

In the early 2010s, Trevor Pemberton and his colleagues combined the compatible genomic data (645 loci) from all of the human genetic clustering studies that have used the largest and most diverse samples of people—such as Wang et al.'s (2007) study of human genomic diversity in the Americas, Friedlaender et al.'s (2008) study of human genomic diversity in Oceania, and Tishkoff et al.'s (2009) study of human genomic diversity in Africa (Pemberton et al. 2013, 893). The result was obtaining a sample of 5795 people from 267 ethnic groups. The study included, among other highly mixed people, African Americans, Mestizos, South African Coloureds, and Polynesians. Next, Pemberton et al. (2013, 902) performed a genetic clustering analysis on the genomic data and replicated Rosenberg et al.'s $K = 5$ result.[28]

Another version of the reification objection stems from the observation that geneticists using different genomic data sets have obtained "inconsistent" results at $K = 5$ (Barbujani et al. 2013, 157; Hochman 2013, 348). For example, some

[25] By 'reifying' I mean 'attributing an actual or concrete existence to something that doesn't exist or only exists abstractly.'

[26] I'm using the jargon of 'reification' because this is how these critics actually talk. For examples, see Winther et al. (2015, 17) and Maglo et al. (2016, 3).

[27] 'HGDP-CEPH' stands for the Human Genome Diversity Project of le Centre d'Etude du Polymorphisme Humain. It contains 1063 cell lines from 1056 people from 52 ethnic groups (Cavalli-Sforza 2005, 337–338).

[28] However, it's worth noting that Pemberton and his colleagues did not use a *structure-like* clustering method. They used a non-fuzzy method called 'multidimensional scaling.' For a large and diverse human genetic clustering study (300 people from 142 ethnic groups) that confirms Rosenberg et al.'s $K = 5$ result using a *structure-like* clustering program (*admixture*), see Mallick et al. (2016).

geneticists have found three African clusters at K = 5 and others have found two Oceanic clusters at K = 5 (Friedlaender et al. 2008, 178; Tishkoff et al. 2009, 1038). While this objection is worthwhile, there are two facts that should assuage the critic's concern here. First, and as previously mentioned, the largest and most diverse genomic data set ever used in a human genetic clustering study has replicated Rosenberg et al.'s K = 5 result. Second, it turns out that Rosenberg et al.'s K = 5 result has a $\sim 70\%$ replication frequency across human genetic clustering studies that have been in a position to test the result, and this is despite the use of different genomic data sets and different genetic clustering methods (Spencer 2015, 48).

Yet another version of the reification objection is that the set of human continental populations possesses no *biological reality* if it's not very important in biology in some way. For example, Bolnick (2008, 76–77) requires that a set of *structure* clusters obtains at the K level with the highest posterior probability (in the Bayesian sense) given the genomic data (Pr{K|G}) in order to be "biologically significant." However, in Rosenberg et al.'s own Pr{K|G} analysis, they were not able to identify K = 5 as having the highest Pr{K|G} value (Bolnick 2008, 75).[29]

In addition, Maglo et al. (2016, 2) require that a set of infraspecific genetic clusters be either a division of clades or a genetic division with taxonomic significance in order for it to have "biological reality."[30] While this version of the reification objection is alluring, Spencer (2015, 52) has already shown that these are inappropriately high standards for genetic clusters being biologically real because there are other genetic clusters that are considered to be uncontroversially real by biologists and that do not satisfy these standards. For example, *local populations* are widely regarded as biologically real among population geneticists, and despite the fact that local populations do not always occur as genetic clusters at the K level in their respective species with the highest posterior probability given the genomic data, they are not always clades, and they do not always satisfy any widely accepted standards for taxonomic significance (e.g. $F_{st} > 0.25$).[31]

A final version of the reification objection is 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 (Weiss and Long 2009; Winther et al. 2015). For instance, Kenneth Weiss and Jeffrey Long (2009, 706) point out that *structure-like* clustering programs that assign graded cluster memberships at a level of clustering *K* presuppose that at some point in the past, the species being studied was divided into *K* number of "isolated and independent ancestral populations." However, according to Weiss and Long (2009, 706–707), it's far from clear that such a time has ever existed in the human species. Weiss and Long (2009, 704) also point out that the inferred genetic clusters

[29] At K = 6 in Rosenberg et al.'s (2002, 2382) study, the Kalash separated from Caucasians to form their own cluster.

[30] A *clade* is a group consisting of an ancestor and all of its descendants.

[31] In addition, note that Kalinowski's (2011) famous critique of the reliability of *structure* at low K values is non-threatening to (2) as well because his computer simulations assume that the accurate genetic clusters are clades, which is an unreasonably high standard for biological reality in this context.

of *structure-like* programs are usually "assumed to be randomly mating with Hardy–Weinberg equilibrium genotype proportions." But the latter assumption entails that each inferred cluster was, at some point in the past, both infinitely sized and randomly mating (Gannett 2003, 991).[32]

While this is by far the strongest version of the reification objection, it's not the fatal objection that some scholars think it is. For one, scientists routinely employ false model assumptions when making inferences about concrete (space–time) reality. However, that alone doesn't imply, or even make it likely, that the objects that are inferred to exist in concrete reality do not exist in concrete reality. Here's an example that illustrates my point.

When the astronomer Urbain Le Verrier predicted the existence of a new planet in 1846 in order to explain perturbations in Uranus's orbit (a planet we now call 'Neptune'), he intentionally used several model assumptions he knew to be false in order to simplify his mathematical calculations. Some examples are that all planets in our solar system are spherical and have uniform masses. However, Le Verrier's false assumptions didn't prevent Johann Galle from observing Le Verrier's planet in the sky a few days later within 1° of the location that Le Verrier predicted![33] So, an appropriate way to assess the reliability of an inference to objects existing in concrete reality from a model is not to assess whether all of the model's assumptions are accurate. This is rarely true in scientific modeling. Rather, an appropriate way to assess the reliability of such an inference would involve checking how accurate the model is at the inference in question under the circumstances in which it's actually being used—for example, by using computer simulations or real-world experiments. In fact, even if one learns that the model is not reliable in the desired way given how it's being used, it's usually possible to learn how to use the model to make more reliable inferences using these accuracy studies.

In our case, *structure* and *structure-like* programs have been studied extensively for how accurate they are at identifying known population structure despite the populations in question not being infinitely sized, randomly mating, and so forth. Furthermore, so far, the results have been encouraging. For instance, Rosenberg (2001, 710) discovered that *structure's* accuracy is a function of the number of sampled loci, the quality of sampled loci, and the number of sampled organisms; and they used known chicken breeds to show that *structure* can reach up to 99% accuracy in identifying population structure and assigning organisms to populations given the right sampling strategy. But what's more relevant to our situation is that Latch et al. (2006, 295) conducted accuracy studies on *structure* and other *structure-like* programs assuming low levels of genetic variance among genetic clusters and low K values and found that *structure* "worked extremely well" under these conditions given the right sampling strategy.[34]

[32] Winther et al. (2015) essentially have the same reification concerns as Weiss and Long (2009).

[33] The details of this story are from Smart (1946).

[34] For replications of this result for *structure* or other *structure-like* programs, see Shringarpure and Xing (2014) and Gilbert (2016).

With that said, I do not want to suggest that inferences from models to actually existing concrete objects are reliable if those models have been verified to have high accuracy under the conditions that they're used. There's also semantic and metaphysical criteria that must be met before such an inference is truly reliable (Spencer 2013, 116). For example, Neptune must satisfy the current astronomical meaning of 'planet' before it'd be true (in our current scientific lexicon) that Le Verrier predicted the existence of a new *planet* in 1846. For instance, the reader probably knows that Pluto does not satisfy the current astronomical meaning of 'planet' and thus Clyde Tombaugh's discovery of Pluto in 1930 was not the discovery of a new planet. Furthermore, in order for it to be true that Le Verrier discovered a *real* planet in 1846, it needs to be true that Neptune satisfies sufficient criteria for being physically real, such as being a *natural kind* according to an empirically successful theory of natural kinds.

In our case, it turns out that it is possible to defend the results of population geneticists' accuracy tests of *structure-like* programs as tests of whether these programs identify real biological populations, at least in certain cases. For one, population geneticists typically consider a *biological population* to be a group of organisms that are capable of being a modified descendant or producing modified descendants via evolutionary forces (e.g. mutation, selection, drift, etc.).[35] So, for example, if we have evidence that one genetic cluster gave rise to another via, say, a bottleneck and genetic drift, then we have evidence that the genetic clusters in question are biological populations.

Next, while there are several accounts of what makes something biologically real among philosophers of biology, Spencer's (2012) account works nicely for capturing the reality of biological entities with modest reality (e.g. cryptic biological populations) as opposed to merely focusing on biological entities with robust reality (e.g. biological species). Spencer (2012, 197–198) also shows that this feature of his theory makes it empirically successful in preserving paradigm cases of real biological objects (e.g. clade, enzyme, gene, etc.) and ruling out paradigm cases of objects that aren't biologically real (e.g. baramin, gemmule, destructiveness organ, etc.).

In Spencer's (2012, 193) theory, one sufficient condition for an entity e being *biologically real* is that e is epistemically useful for generating a theory T in a scientific research program in biology P, using e to generate T is warranted according to the epistemic values of P to explain or predict an observational law in P, and P is well-ordered (e.g. it has coherent and well-motivated aims, competitive predictive power, and routine and rigorous cross-checks). So, given that population genetics is a well-ordered scientific research program in biology, one way to support an inferred genetic cluster of *structure-like* programs as a real biological population is by offering up evidence that it not only satisfies the criteria for being a biological population, but also, that it's epistemically useful for generating a theory that explains or predicts a population-genetic observational law in a way that exemplifies

[35] This is a pretty common interpretation of what population geneticists mean by 'biological population' according to philosophers of biology. For evidence, see Millstein (2009), Stegenga (2016), and Spencer (2016).

population-genetic epistemic values. For example, if we have evidence that a level of genetic structure is best explained (in a population-genetic sense of 'best') by underlying biological population structure, then that itself is evidence that the biological populations in question are biologically real. Interestingly, the human continental populations clear both of these hurdles.

For one, human continental populations are biological populations in the aforementioned sense. For example, it's widely accepted in population genetics that Native Americans are modified descendants of Northeast Asians due to evolutionary forces like drift and mutation (Wang et al. 2007, 2059; Reich et al. 2012, 2). But also, the proposition that *the human continental populations form a human population subdivision* is a theory that explains why humans have a $K = 5$ level of genetic structure, why this genetic structure tracks "continental" barriers to human interbreeding (e.g. the Sahara, the Himalayas, etc.), why an isolation-by-distance explanation leaves 1.53% of the genetic variance at this level unexplained, and why this genetic clustering pattern is $\sim$ 70% robust across replicability tests (Spencer 2014, 1033–1036). Furthermore, this theory accomplishes these feats in a simple, predictively powerful, and quantitatively precise way, which are important epistemic values among population geneticists.

However, the one lingering concern is Weiss and Long's worry that *structure-like* programs assume that the species being studied has had at some point in the past "isolated and independent ancestral populations." This concern cannot be assuaged with the approach I've used above. This is because this assumption needs to hold exactly just in order to make sense of what a mixed organism is in a genetic cluster. A mixed organism in a genetic cluster is an organism that has inherited at least two different alleles in her genome from at least two different unmixed ancestors in at least two different clusters (Pritchard et al. 2000, 948). So, in order for this concept of genomic admixture (as it's called) to make sense for humans and at a fivefold level, there must have been some time in the past when the human species was partitioned into five groups of unmixed people.

Suppose 't_5^x' is a general term for any time in human history when humans were partitioned into five groups of unmixed people. Furthermore, what *structure-like* programs actually assume when they're calculating human genomic admixtures is that the alleles in a mixed person were inherited from ancestors at the *last* time in the t_5^x sequence. Suppose we call this time 't_5^ℓ.' Since we know there was interbreeding among Europeans and indigenous Americans in the fifteenth century, and we know that people did not occupy the Americas until $\sim$ 15 kya, we know that t_5^l is roughly between 0.5 and 15 kya if it exists at all (Bryc et al. 2010, 8954; Reich et al. 2012, 2).[36]

While some biologists and philosophers are extremely skeptical that t_5^ℓ exists, this is almost always because they think its existence is incompatible with frequent and reoccurring gene flow among people across continental boundaries throughout human history.[37] But it's not. In order for the calculations of human genomic

[36] 1 kya is equivalent to 1000 years ago.

[37] For examples, see Weiss and Long (2009, 706–707) and Templeton (2013, 269).

admixtures to make sense in *structure-like* programs, it needn't be the case that once all human continental populations were born, they were isolated until $t_5^{\prime}$. This is sometimes called the "candelabra model" of human evolutionary history (Templeton 1998, 635). Rather, what *structure-like* programs require with respect to calculating human genomic admixtures is that t_5^{ℓ} exists, which is compatible with there having been lots of gene flow among human continental populations before t_5^{ℓ}.

Furthermore, it can be shown that obtaining an entire population of unmixed organisms after gene flow into the population can occur relatively quickly (e.g. a few generations) depending upon the effective population size, the relative fitnesses of mixed organisms, the extent of the gene flow, and other relevant population parameters. So, it's far from clear that t_5^{ℓ} doesn't exist, although more research is needed to confirm its actual existence.

2.4 Premise 3 and its problems

As for (3), unfortunately, it's currently unknown whether (3) is true. Now, one may believe that (3) is true because of the analysis of molecular variance (AMOVA) that Rosenberg and his colleagues reported in 2002.[38] To be specific, Rosenberg et al. (2002, 2382) found that $K = 5$ was the level of human genetic structure with the highest genetic variance among genetic clusters (4.3%). In fact, $K = 5$ human genetic clusters were shown to have more genetic variance among them than the sample of local populations (2.5%). While Rosenberg et al.'s result is worth taking seriously, there have been other AMOVAs that show a different level where the genetic variance among genetic clusters possesses a higher share of human genetic variation than 4.3%. For example, Bastos-Rodriguez et al. (2006 661) and Jun Li et al. (2008, 1102) both did AMOVAs at $K = 7$ (where Caucasians split into Europeans, Central & South Asians, and Middle Easterners & North Africans) and calculated genetic variance components of 12.1 and 9.0%, respectively, among genetic clusters. So perhaps $K = 7$, as opposed to $K = 5$, is where genetic differentiation is greatest among human populations.

To be fair, it's unclear whether Bastos-Rodrigues et al.'s and Li et al.'s $K = 7$ AMOVA results are higher than Rosenberg et al.'s $K = 5$ AMOVA results merely due to a difference in the type of alleles used in the analyses.[39] However, at the very least, what these additional data tell us is that it's not clear whether the set of human continental populations is actually where genetic differentiation is greatest among human populations.

[38] AMOVA is a technique that separates the total genetic variance in a group of organisms into three components by proportion of the total: genetic variance within local populations, genetic variance among local populations, and genetic variance among genetic clusters.

[39] Bastos-Rodrigues et al. used short indels (insertions or deletions that are just a few nucleotides in length) and Li et al. used SNPs (single-nucleotide polymorphisms), while Rosenberg et al. used microsatellites (short nucleotide sequences that are repeated in a genome). For nice a discussion about how allele type choice can affect an AMOVA, see Rosenberg et al. (2003). Also, a *polymorphism* (in the genetic context) is an allele that has greater than 0% but less than 100% frequency at its locus in a population (Hartl and Clark 2007, 321).

2.5 Premise 4 and its Critics

As for (4), Burchard et al. (2003, 1172–1173) offer lots of examples of genetic differences (esp. allele frequency differences) among human continental populations that are medically relevant, and there are plenty more that can easily be found in the literature. However, for the sake of time, I'll just present one good example. This example is the difference in frequencies of lactase persistence (LP) alleles (alleles that allow people to digest lactose after weaning). According to the Global Lactase Persistence Association Database (GLAD)—which is the largest and most diverse database of data related to LP—LP alleles have an average frequency of 26% among Caucasian populations, 16% among African populations, 2% among East Asian populations, and 0% among Oceanian populations.[40] Also, while GLAD does not have data on Native Americans, the frequency of LP alleles among Native Americans is known to be less than 5% (Swallow 2003, 202).

Of course, LP alleles are medically relevant alleles because, first, lactase persistence is a trait that is primarily genetically controlled by two genes in humans (the LCT gene and the MCM6 gene on chromosome 2), and, second, lacking the lactase persistence trait can lead to health problems in certain contexts. For example, in countries where the majority of residents have the LP trait (e.g. Canada, USA, and the UK), non-lactose-containing food sources of calcium and vitamin D are hard to find, which tends to lead to deficiencies in these nutrients for people without the LP trait (e.g. many African, Asian, and Mexican Americans) (Swallow 2003, 202).

A careful critic may point out that there is considerable heterogeneity among people within each human continental population with respect to having LP alleles, and so much so that it may be more appropriate to view this pattern as merely "accidental" (Haslanger 2012, 259).[41] For example, 61% of Maasai Kenyans have an LP allele, while 0% of Wolof Senegalese have an LP allele. Also, 82% of Scots have an LP allele, while 5% of Southern Italians have an LP allele.[42] However, despite the intrapopulational variation, the frequency differences in LP alleles across human continental populations are genuine genetic differences as opposed to mere accidents. This is because we know that these frequencies are a result of a threefold biological cause.

First, LP alleles arose as mutations thousands of years ago in the MCM6 region of chromosome 2 in multiple different people from multiple different dairy-farming populations in the old world (e.g. northern European populations, north Indian populations, pastoralist African populations, etc.). Second, LP alleles spread among people within the continental populations where these alleles arose (Africans and Caucasians) from a combination of natural selection and gene flow. However, they spread most widely in Europe due to extreme selection pressure. Finally, LP alleles

[40] These data were retrieved from https://www.ucl.ac.uk/mace-lab/resources/glad on January 24, 2018.

[41] Actually, Haslanger (2012, 259) calls the link between "HbS carriers" and "relatively recent Sub-Saharan African ancestry" 'accidental,' but her concern applies here as well.

[42] Both of these data are from GLAD's website, accessed on January 24, 2018.

have not spread too much outside their continental populations of origin due to the same interbreeding barriers that sustain $K = 5$ population structure (Gerbault et al. 2011, 864–865). So, intrapopulational heterogeneity doesn't automatically undermine a genuine genetic difference among populations, and it doesn't undermine the LP frequency differences among human continental populations.

2.6 Premise 5 and its critics

Last, but not least, Burchard and his colleagues defended (5) using the following line of reasoning. First, they understood 'useful in medicine' as including, at least, useful in diagnosing, researching, or treating genetic disorders (Burchard et al. 2003, 1174). Next, they explain how the set of human continental populations are useful in all three respects. According to Burchard et al. (2003, 1174), a person's membership grades in the human continental populations can be used to improve her risk assessments for developing a genetic disease and giving birth to a child with a genetic disorder. Burchard and his colleagues also claim that these membership grades can be used to improve a person's treatment for a genetic disease (Burchard et al. 2003, 1174). For example, it's standard practice in American pediatrics to provide an extra round of chemotherapy to children with acute lymphoblastic leukemia if they have at least 10% Native American ancestry (Bustamante et al. 2011, 164). This is because, for some reason, these children do not respond to the first round of treatment.

Next, Burchard and his colleagues claim that the human continental populations are useful for improving our sampling in medical research where it's important to have a representative sample of human genetic diversity (Burchard et al. 2003, 1174). For instance, if a medical researcher wants to do a genome-wide association study (GWAS)—which is an exploration of human genomes to find links between alleles and traits—then she doesn't want to just look at Caucasian genomes because that's not going to be representative of human genetic diversity. However, due to the fact that most GWASs are done in countries where the majority of people are of primarily European descent (e.g. USA, UK, Australia, etc.), it has actually turned out to be the case that 96% of GWASs have been done on people of primarily European descent (Bustamante et al. 2011, 164)!

The final piece of the rationale for Burchard and his colleagues is that the OMB's racial classification is useful for all three of the activities above because there is a high correlation between primary OMB racial membership (as judged by self-reports) and "primary continent of origin" (Risch et al. 2002, 3). For example, if you're a medical researcher in the USA and you're trying to get more genomes of primarily African descent in your GWAS, it would (presumably) be useful for you to include more self-reported Black Americans in your study since 99.3–99.8% of self-reported Black Americans have primarily African genomes (Tang et al. 2005, 271; Guo et al. 2014, 153).

While few interlocutors in the biomedical race debate disagree with Burchard and his colleagues that the human continental populations are useful for diagnosing, treating, or researching genetic disorders, there are plenty who disagree with Burchard and his colleagues that the correlation between primary OMB racial

membership and primary continental ancestry is high enough to be useful in using the former as a proxy for the latter. For instance, the critics who have advanced the mismatch objection disagree that the correlation is high (Glasgow 2009; Kaplan 2010). But also, there are critics who agree that the correlation is high, but disagree that the correlation is stable enough through time to be useful in the proposed way. In short, these critics think it's merely a historical accident that this correlation exists given the radically different essences of folk races (e.g. being political constructs) compared to the continental populations (e.g. being genealogical groups) (Root 2003; Yudell et al. 2016). And as such, the extensional link that exists today can easily disappear tomorrow given the right social event (e.g. the Trump administration radically revising OMB race term extensions), which makes for an unstable and unreliable correlation.

Like the mismatch objection, this last objection—which I'll call *the diachronic mismatch objection*—is metaphysical. Burchard and his colleagues indirectly addressed the diachronic mismatch objection when they addressed the objection that folk races have "no biological basis" (Risch et al. 2002, 4). However, their reply was simply to restate the very high correlation between the current extensions of OMB race terms and the current extensions of human continental population terms, which, of course, misses the point of the *diachronic* mismatch objection.

Last, but not least, there is one final objection to (5) that I should bring up. It's the objection that the human continental populations aren't useful for diagnosing, treating, or researching genetic disorders because there are more informative human subdivisions available for use (Cooper et al. 2003, 1167). For example, while using OMB races as proxies for continental populations will get you a better genomic sample of people for a GWAS than sampling US residents randomly (since 63.7% of US residents are non-Hispanic White Americans), using ethnic groups as proxies for local populations (e.g. African American, Haitian American, Sudanese American, etc.) will get you an even better genomic sample of people (Morris 2011, 1265–1269; Hixson et al. 2011, 3).

While the observation made in the last objection is true, it doesn't undermine the usefulness of human continental populations that Burchard and his colleagues have proposed. In short, the fact that there is a more useful tool for a task doesn't imply that the tool being used isn't useful. In fact, this objection misunderstands the whole point of classifying at a higher level. Scientists tend to do this only when classifying at a lower level is impractical (e.g. financially prohibitive), unnecessary for the amount of desired precision, or counterproductive (e.g. if the point is to get a broad summary). And in our case, it certainly is impractical to stratify the human species by ethnic group in GWASs since there's at least 7105 ethnic groups in our species (Spencer 2014, 1029).

Now that I've discussed Burchard's route in depth, I'm inclined to agree that the mismatch objection and the diachronic mismatch objection are serious problems for the argument. It's not clear that (2) is true due to the mismatch objection; and even if it is true, it's not clear that (5) is true due to the diachronic mismatch objection. In addition, (3) is a controversial claim and no one really knows whether it's true yet. So, if there were a way of getting Burchard et al.'s conclusion using something like Burchard's route, but without adopting (2) and (3) and with a strong response to the

diachronic mismatch objection, that would make for a compelling argument for Burchard et al.'s conclusion. Here's one such argument.

3 Spencer's route

The argument that I've been calling *Spencer's route* is just (1) and (4) as premises, (6) as its conclusion, and the following two new premises:

(2′) The set of 1997 OMB races is identical with the set of human continental populations.
(5′) If (1), (2′), and (4) are true, then there's a racial classification that's useful in medicine.

Notice that neither (3) nor a replacement for (3) occurs in Spencer's route. This is because I think that (3) is an unnecessary distraction from the goal. The quantity of genetic differentiation among human continental populations is irrelevant to whether the genetic differentiation is important to medicine. Furthermore, if (4) is true, then the genetic differentiation is important to medicine. Couple that with the fact that we really don't know whether (3) is true yet, and we have ample reason for giving up (3) and any (3)-like substitute.

As for (5′), of course I had to create a (5) substitute given that I'm dropping (2) and (3). But also, the truth of (5′) should be easy to see given my adoption of (2′). For if the OMB races just *are* the human continental populations, and these populations actually exist, and they're useful in medicine for, at least, stratifying samples of people to better represent human genetic diversity in GWASs and other observational studies in medical genetics, then, according to Burchard et al.'s (2003, 1174) interpretation of 'useful in medicine,' which is uncontroversial, it follows that there's a racial classification that's useful in medicine.

As for (2′), I should clarify that what I mean here is that these two sets of objects are identical insofar as Asians are identical to East Asians, Blacks are identical to Africans, and so forth. So, if (2′) is true, we will have a compelling response to the mismatch and diachronic mismatch objections. This is because there are no mismatches among the current extensions of OMB race terms and human continental population terms if these two sets of extensions are identical. Also, there *can be no* mismatches throughout time among these two sets of extensions if these two sets of extensions are identical. Now, all that remains is to justify why (2′) is in fact true.

I will not try to reinvent the wheel here. Instead, I will engage in a bit a philosophical engineering and merely apply a perfectly good theory from Spencer (2014, 2015, 2018c) to justify this premise. According to Spencer (2014, 1027), the correct way to understand the meanings of OMB race terms are as the referents of those terms. Furthermore, Spencer (2014, 1031) also claims that the referent of each OMB race term is a unique human continental population (e.g. 'Asian' means East Asian, 'Black' means African, etc.). The evidence for Spencer's referential theory of OMB race term meanings is both hypothetico-probabilistic and abductive. Some of the evidence is hypothetico-probabilistic insofar as Spencer (2014, 1031) shows

that assuming his hypothesis is true makes it likely that each of OMB's "definitions" for its race terms is an approximately true description of a unique human continental population.

For instance, Spencer (2014, 1032) explains how the OMB's "definition" for 'Pacific Islander' as people "having origins in any of the original peoples of Hawaii, Guam, Samoa, or other Pacific Islands" is true for almost all Oceanians due to how Oceanians originated and diversified. Oceanians originated $\sim 50kya$ as the indigenous people of Sahul (an ancient continent consisting of present-day Australia, New Guinea, and Tasmania). Next, ocean levels rose a few thousand years ago to create the present-day continent of Australia and the islands of New Guinea and Tasmania. Third, all of the indigenous people to the remaining Pacific islands (Polynesia, Micronesia, and the rest of Melanesia) were migrants from New Guinea or hybrids of Taiwanese aborigines and Papuans. So, all Oceanians today are either descendants of the indigenous people of New Guinea (a Pacific island), or descendants of the indigenous people of Australia (or Tasmania) but not the indigenous people of New Guinea (a.k.a. Aboriginal Australians). Furthermore, new calculations from Spencer (2015) show that Aboriginal Australians compose just 3.84% of all current Oceanians, which implies that the OMB's "definition" of 'Pacific Islander' applies to 96.2% of all current Oceanians, which is a pretty accurate description.[43]

In addition to his hypothetico-probabilistic evidence, Spencer provides considerable abductive evidence for his hypothesis. For instance, he considers multiple serious rival meanings for OMB race terms, but finds none of them as good as his hypothesis for explaining the relevant phenomena. For example, Spencer (2015, 50) points out that Glasgow's theory that folk races in the USA are, by definition, visibly distinguishable from one another by skin color, hair texture, and facial features to a significantly disproportionate extent, fails to distinguish Blacks from Pacific Islanders in the OMB's racial scheme.[44] This is because Pacific Islanders are overwhelmingly Melanesians (75.1%) and Melanesians are a subgroup of Sub-Saharan Africans in terms of racial traits (e.g. they tend to have dark skin, curly black hair, wide noses, etc.) (Spencer 2015, 50). Also, Spencer shows that the OMB's own "definitions" for its race terms are inadequate as meanings for those terms. For example, according to Spencer (2018c, 578), the OMB intends its racial scheme to not contain "redundant" races. However, the OMB's "definition" for 'White' as people "having origins in any of the original peoples of Europe, the Middle East, or North Africa" makes the American Indian, Asian, and Pacific Islander races redundant, since, according to the Out-of-Africa model of human migration, every single American Indian, Asian, and Pacific Islander descends from the indigenous people of the Middle East (Spencer 2018c, 578).

Of course, Spencer's hypothesis has its critics. For instance, Michael Hardimon (2017, 43, 93–94) agrees with Spencer that the current referents of the OMB's race

[43] This calculation is from page 7 of the supplementary material from Spencer (2015).

[44] Spencer (2015, 50; 2018a, 5–6) also points out that this shortcoming also applies to US race theories from Linda Alcoff, Lawrence Blum, Paul Taylor, Naomi Zack, and Michael Hardimon.

terms are biologically real ancestry groups, but rejects that the *meanings* of these terms are the human continental populations or any other referents. This is a worthy objection, but it can be adequately addressed by clarifying what Spencer means by 'meaning' in his hypothesis and by giving some additional semantic evidence for his hypothesis. First, Spencer's use of 'meaning' is borrowed from John Perry (2001). According to Perry (2001, 18, 32), a meaning of a term *t*(in an ordinary sense) is simply the contribution (esp. its referent or identifying conditions) that *t* makes to the truth-conditions of the propositions in which *t* occurs. So, a good test of what a term means in this sense is a comparison of predicted versus intended truth-values for propositions in which the term occurs. In our case, the intended truth-values must come from the OMB because these are their race terms. Nevertheless, after we conduct such propositional truth-value tests, we will see that Spencer's hypothesis is indeed well supported by the test results. For example, consider the following proposition:

(7) The division of people into American Indians, Asians, Blacks, Pacific Islanders, and Whites is comprehensive in coverage.

As previously discussed, the OMB intends (7) to be true because they want their racial scheme to have a race for any potential US immigrant and any potential child from an interracial mating. Of course, (7) is true if we take each race term to mean a unique human continental population. Because of what a population subdivision is and because the set of human continental populations is a population subdivision, there isn't a single living person that's not a member of at least one human continental population. Here's another one. Consider the proposition below:

(8) Pacific Islander is not too heterogeneous for health research.

The OMB considered adding many new candidate races to its racial scheme during the revision process in 1993–1996, and one candidate the OMB considered adding was the union of American Indians and Native Hawaiians. The proposed race was called "Native Americans" (OMB 1995, 44685). However, the OMB (1995, 44685) did not add this group to its racial scheme due to the group being seen as "too heterogeneous for health research."[45] So, the OMB intends (8) to be true as well. Of course, (8) is true if 'Pacific Islander' means Oceanian and the rest of Spencer's route is sound. Also, we have plenty of evidence by now that these two claims are true. In fact, one recent health study that illustrates the value of the Pacific Islander race in health research is from Forester and Merz (2003). In this fascinating study, Forester and Merz (2003, 627) show that, due to some unknown cause, Pacific Islander women, on average, do not give birth to Down syndrome children at $\geq$ 40 years of age at a higher rate than they do at 35–39 years of age, which is stunning and contradicts the observed pattern for women of all other OMB

[45] Interestingly, the OMB (1995, 44687, 44688) also rejected "multiracial" and "Hispanic" as races because they were "too heterogeneous" "for health researchers."

races.[46] Also, this pattern is robust across Polynesian and Micronesian women, which strongly suggests that the Pacific Islander race is not too heterogeneous to be useful in health research (Forester and Merz 2003, 626).

4 Summary

The purpose of this essay was not to defend a novel thesis in the biomedical race debate, but rather, to engage in a bit of philosophical engineering by weaving together a new argument that preserves the spirit of Esteban Burchard et al.'s argument for the thesis that there's a racial classification that's useful in medicine, which is an argument that I've called 'Burchard's route.' I began by clarifying Burchard's route and presenting Burchard et al.'s defense of each premise in the argument. While I was able to fend off several strong objections to Burchard's route (e.g. the reification objection to (2)), ultimately, I judged two premises in Burchard's route to be serious liabilities, namely, (2) and (3). In response, I dropped (2) for the new premise (2′), I dropped (3) without any replacement, I replaced (5) for (5′), and I combined (2′) and (5′) with premises (1) and (4) in Burchard's route to create a new and stronger set of premises that support (6), which is Burchard et al.'s thesis. I called this new argument 'Spencer's route'. Finally, I defended (2′) and (5′) in Spencer's route and addressed some salient objections to them. The result is that we now have a stronger argument for Burchard et al.'s thesis that significantly preserves Burchard et al.'s unique path to that thesis. I'll close with a disclaimer and a dilemma.

Even though Spencer's route implies that there's a racial classification with medically useful genetic differentiation (the OMB's racial classification), none of that 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. Also, it really is a dilemma whether we should use any racial classification in a genetic way in medicine. For instance, 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 (Donovan 2014, 462, 472). However, on the pro side, organizing observational data in racial terms may allow medical researchers to more quickly find the genetic causes of and treatments for genetic disorders. I don't have any solution to this ethical dilemma, but I do know that there's a racial classification with medically useful genetic differentiation that's available for use if medical scientists want to use it.

[46] Down syndrome is a genetic disorder caused by an extra whole chromosome 21 or a translocated segment of chromosome 21 in all or some of a person's non-reproductive cells.

References

Andreasen, R. O. (2008). The concept of race in medicine. In M. Ruse (Ed.), *The Oxford handbook of philosophy of biology* (pp. 478–503). Oxford: Oxford University Press.

Barbujani, G., Ghirotto, S., & Tassi, F. (2013). Nine things to remember about human genome diversity. *Tissue Antigens, 82,* 155–164.

Bastos-Rodriguez, L., Pimenta, J. R., & Pena, S. D. J. (2006). The genetic structure of human populations studied through short insertion-deletion. *Annals of Human Genetics, 70,* 658–665.

Bolnick, D. (2008). Individual ancestry inference and the reification of race as a biological phenomenon. In B. Koenig, S. Lee, & S. Richardson (Eds.), *Revisiting race in a genomic age* (pp. 70–85). New Brunswick: Rutgers University Press.

Bryc, K., Velez, C., & Ostrer, H. (2010). Genome-wide patterns of population structure and admixture among Hispanic/Latino populations. *Proceedings of the National Academies of Sciences, 107,* 8954–8961.

Burchard, E., et al. (2003). The importance of race and ethnic background in biomedical research and clinical practice. *The New England Journal of Medicine, 348*(12), 1170–1175.

Bustamante, C. D., Burchard, E. G., & De La Vega, F. M. (2011). Genomics for the world. *Nature, 475*(7355), 163–165.

Cavalli-Sforza, L. L. (2005). The human genome diversity project: past, present, and future. *Nature Genetics, 6,* 333–340.

Cooper, R. S., Kaufman, J. S., & Ward, R. (2003). Race and genomics. *The New England Journal of Medicine, 348*(12), 1166–1170.

Donovan, B. M. (2014). Playing with fire? The impact of the hidden curriculum in school genetics on essentialist conceptions of race. *Journal of Research in Science Teaching, 51*(4), 462–496.

Ennis, S. R., Ríos-Vargas, M., & Albert, N. G. (2011). *The Hispanic population. 2010 Census Brief*. Washington, DC: US Census Bureau.

Feldman, M. (2010). The biology of ancestry: DNA, genomic variation, and race. In H. R. Markus & P. M. L. Moya (Eds.), *Doing race: 21 essays for the 21st century* (pp. 136–159). New York: W.W. Norton & Co., Inc.

Forester, M. B., & Merz, R. D. (2003). Maternal age-specific down syndrome rates by maternal race/ethnicity, Hawaii, 1986–2000. *Birth Defects Research (Part A): Clinical and Molecular Teratology, 67,* 625–629.

Friedlaender, J. S., Friedlaender, F. R., & Weber, J. L. (2008). The genetic structure of Pacific Islanders. *PLoS Genetics, 4*(1), 173–190.

Gannett, Lisa. (2003). Making populations: Bounding genes in space and time. *Philosophy of Science, 70*(5), 989–1001.

Gerbault, P., Liebert, A., Itan, Y., & Thomas, M. G. (2011). Evolution of lactase persistence: An example of human niche construction. *Philosophical Transactions of the Royal Society B, 366,* 863–877.

Gilbert, K. J. (2016). Identifying the number of population clusters with structure: Problems and solutions. *Molecular Ecology Resources, 16,* 601–603.

Girle, Rod. (2009). *Modal logics and philosophy* (2nd ed.). Montreal: McGill-Queen's University Press.

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

Grieco, E. M., & Cassidy, R. C. (2001). *Overview of race and Hispanic Origin. Census 2000 Brief*. Washington, DC: U.S. Census Bureau.

Guo, G., Fu, Y., Lee, H., Cai, T., Harris, K. M., & Li, Y. (2014). Genetic bio-ancestry and social construction of racial classification in social surveys in the contemporary United States. *Demography, 51*(1), 141–172.

Halder, I., Yang, B., Kranzler, H. R., Stein, M. B., Shriver, M. D., & Gelernter, J. (2009). Measurement of admixture proportions and description of admixture structure in different US populations. *Human Mutation, 30*(9), 1299–1309.

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

Hartl, D. L., & Clark, A. G. (2007). *Principles of population genetics* (4th ed.). Sunderland: Sinauer Associates.

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

Hixson, L., Hepler, B. B., & Kim, M. O. (2011). *The White Population. 2010 Census Brief*. Washington, DC: US Census Bureau.

Hixson, L., Hepler, B. B., & Kim, M. O. (2012). *The Native Hawaiian and Other Pacific Islander Population. 2010 Census Brief*. Washington, DC: US Census Bureau.
Hochman, A. (2013). Against the new racial naturalism. *The Journal of Philosophy CX, 6,* 331–351.
Kalinowski, S. T. (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.
Kaplan, Jonathan. (2010). When socially determined categories make biological realities: Understanding Black/White Health Disparities in the U.S. *The Monist, 93*(2), 281–297.
Latch, E. K., Dharmarajan, G., Glaubitz, J. C., & Rhodes, O. E. (2006). Relative performance of Bayesian clustering software for inferring population substructure and individual assignment at low levels of population differentiation. *Conservation Genetics, 7,* 295–302.
Li, J. Z., Absher, D. M., & Myers, R. M. (2008). Worldwide human relationships inferred from genome-wide patterns of variation. *Science, 319,* 1100–1104.
Maglo, K. N., Mersha, T. B., & Martin, L. J. (2016). Population genomics and the statistical values of race: An interdisciplinary perspective on the biological classification of human populations and implications for clinical genetic epidemiological research. *Frontiers in Genetics, 7,* 1–13.
Mallick, S., Li, H., Lipson, M., & Reich, D. (2016). The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. *Nature, 538*(7624), 201–206.
Manichaikul, A., et al. (2012). Population structure of hispanics in the United States: The multi-ethnic study of atherosclerosis. *PLoS Genetics, 8*(4), e1002640.
Martínez-Cruz, B., et al. (2011). In the heartland of Eurasia: The multilocus genetic landscape of Central Asian populations. *European Journal of Human Genetics, 19,* 216–223.
McEvoy, B. P., Lind, J. M. et al. (2010). Whole-genome genetic diversity in a sample of Australians with deep aboriginal ancestry. *The American Journal of Human Genetics*, *87*, 297–305.
Millstein, Roberta. (2009). Populations as individuals. *Biological Theory, 4*(3), 267–273.
Morris, S. G. (2011). Preserving the concept of race: A medical expedient, a sociaological necessity. *Philosophy of Science, 78*(5), 1260–1271.
Norris, T., Vines, P. L., & Hoeffel, E. M. (2012). *The American Indian and Alaska Native Population. 2010 Census Brief*. Washington, DC: US Census Bureau.
OMB. (1995). Standards for the classification of federal data on race and ethnicity. *Federal Register: The Daily Journal of the United States Government, 60*(166), 44674–44693.
OMB. (1997a). Recommendations from the interagency committee for the review of the racial and ethnic standards to the office of management and budget concerning changes to the standards for the classification of federal data on race and ethnicity. *Federal Register: The Daily Journal of the United States Government, 62*(131), 36874–36946.
OMB. (1997b). Revisions to the standards for the classification of federal data on race and ethnicity. *Federal Register: The Daily Journal of the United States Government, 62*(210), 58782–58790.
OMB. (2000). *Provisional guidance on the implementation of the 1997 standards for Federal Data on race and ethnicity*. Washington, DC: Office of Management and Budget.
Pemberton, T. J., DeGiorgio, M., & Rosenberg, N. A. (2013). Population structure in a comprehensive genomic data set on human microsatellite variation. *G3: Genes, Genomes Genetics, 3*(5), 891–907.
Pereira, V., et al. (2015). The peopling of Greenland: Further insights from the analysis of genetic diversity using autosomal and X-chromosomal markers. *European Journal of Human Genetics, 23,* 245–251.
Perry, John. (2001). *Reference and reflexivity*. Stanford: CSLI Publications.
Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics, 155,* 945–959.
Quine, W. V. (1951). Two dogmas of empiricism. *The Philosophical Review, 60*(1), 20–43.
Reich, D., et al. (2012). Reconstructing Native American population history. *Nature, 488*(7411), 370–374.
Risch, N., Burchard, E., Ziv, E., & Tang, H. (2002) Categorization of humans in biomedical research: Genes, race and disease. *Genome Biology* 1–12.
Roberts, Dorothy. (2011). *Fatal invention: How science, politics, and big business re-create race in the twenty-first century*. New York: The New Press.
Root, Michael. (2003). The use of race in medicine as a proxy for genetic differences. *Philosophy of Science, 70*(5), 1173–1183.
Rosenberg, N. A. (2001). Empirical evaluation of genetic clustering methods using multilocus genotypes from 20 chicken breeds. *Genetics, 159,* 699–713.

Rosenberg, N. A., Pritchard, J. K., Cann, J. L., Weber, H. M., Kidd, K. K., Zhivotovsky, L. A., et al. (2003). Response to comment on "Genetic Structure of Human Populations". *Science, 300,* 1877c.
Rosenberg, N., Pritchard, J., & Feldman, M. (2002). Genetic structure of human populations. *Science, 298*(5602), 2381–2385.
Rotimi, C. N. (2004). Are medical and nonmedical uses of large-scale genomic markers conflating genetics and 'race'? *Nature Genetics, 36*(11), S43–S47.
Serre, D., & Pääbo, S. (2004). Evidence for gradients of human genetic diversity within and among continents. *Genome Research, 14,* 1679–1685.
Shringarpure, S., & Xing, E. (2014). Effects of sample selection bias on the accuracy of population structure and ancestry inference. *G3: Genes, Genomes Genetics, 4*(5), 901–911.
Smart, W. M. (1946). John Couch Adams and the discovery of neptune. *Nature, 158,* 648–652.
Spencer, Q. (2012). What 'Biological Racial Realism' should mean. *Philosophical Studies, 159*(2), 181–204.
Spencer, Q. (2013). Biological theory and the metaphysics of race: A reply to Kaplan and Winther. *Biological Theory, 8*(1), 114–120.
Spencer, Q. (2014). The unnatural racial naturalism. *Studies in History and Philosophy of Biological and Biomedical Sciences, 46,* 38–43.
Spencer, Q. (2015). Philosophy of race meets population genetics. *Studies in History and Philosophy of Biological and Biomedical Sciences, 52,* 46–55.
Spencer, Q. (2016). Do humans have continental populations? *Philosophy of Science, 83*(5), 791–802.
Spencer, Q. (2018a). Are Folk Races Like Dingoes, Dimes, or Dodos? In G. Rosen, A. Byrne, J. Cohen, E. Harman, & S. Shiffrin (Eds.), *The Norton introduction to philosophy* (pp. 571–581). New York: W.W. Norton & Company Inc.
Spencer, Q. (2018b). Racial realism I: Are biological races real. *Philosophy Compass, 13*(1), e12468.
Spencer, Q. (2018c). Racial realism II: Are folk races real? *Philosophy Compass, 13*(1), e12467.
Sullivan, S. (2013). Inheriting racist disparities in health: Epigenetics and the transgenerational effects of white racism. *Critical Philosophy of Race, 1*(2), 190–218.
Swallow, D. M. (2003). Genetics of lactase persistence and lactose intolerance. *Annual Review of Genetics, 37,* 197–219.
Tang, H., Quertermous, T., & Risch, N. J. (2005). Genetic structure, self-identified race/ethnicity, and confounding in case-control association studies. *American Journal of Human Genetics, 76*(2), 268–275.
Taylor, P., Lopez, M. H., Martínez, J. H., & Velasco, G. (2012). *When labels don't fit: Hispanics and their views of identity*. Washington, DC: The Pew Hispanic Center.
Templeton, Alan 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., & Williams, S. M. (2009). The genetic structure and history of Africans and African Americans. *Science, 324,* 1035–1044.
Wall, J. D., et al. (2013). Higher Levels of Neanderthal Ancestry in East Asians than in Europeans. *Genetics, 194,* 199–209.
Wang, S., et al. (2007). Genetic variation and population structure in native Americans. *PLoS Genetics, 3*(11), e185.
Weiss, K. M., & Long, J. C. (2009). Non-Darwinian estimation: My ancestors, my genes' ancestors. *Genome Research, 19,* 703–710.
Wilson, J. F., Weale, M. E., Smith, A. C., & Goldstein, D. B. (2001). Population genetic structure of variable drug response. *Nature Genetics, 29,* 265–269.
Winther, R. G., Giordano, R., Edge, M. D., & Nielsen, R. (2015). The Mind, the Lab, and the Field: Three Kinds of Populations in Scientific Practice. *Studies in History and Philosophy of Biological and Biomedical Sciences, 52,* 12–21.
Xing, J., et al. (2010). Toward a more Uniform Sampling of Human Genetic Diversity: A Survey of Worldwide Populations by High-density Genotyping. *Genomics, 96*(4), 199–210.
Yudell, M., Roberts, D., DeSalle, R., & Tishkoff, S. (2016). Taking race out of human genetics. *Science, 351*(6273), 564–565.