

A Radical Solution to the Race Problem

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It has become customary among philosophers and biologists to claim that folk racial classification has no biological basis. This paper attempts to debunk that view. In this paper I show that ‘race’, as used in current US race talk, picks out a biologically real entity. I do this by first showing that ‘race’, in this use, is not a kind term, but a proper name for a set of human population groups. Next, using recent human genetic clustering results, I show that this set of human population groups is a partition of human populations that I call ‘the Blumenbach partition’.

1. Introduction. Philosophers and biologists alike repeatedly assert that folk racial classification has no biological basis. A few representative quotes are below, but many more can be generated with ease:

- “There are no biological races, only man-made races” (Root 2000, 32).
- “The human species does not contain biological races now nor has it at any time in the past 250,000 years” (Graves 2004, 20).
- “We know enough about race to be quite confident that races will not turn out to be significant biological kinds” (Dupré 2008, 52).

However, the goal of this paper is to debunk this common view.

Particularly, I show that ‘race’, in its current US meaning, is a rigidly designating proper name for a biologically real entity, specifically for the

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†I would like to thank the following people for helpful comments on earlier drafts of this paper: Brian Donovan, Michael Ghiselin, Joshua Glasgow, Michael Hardimon, David Hills, Adam Hochman, Christopher Hom, Michael Hunter, Chike Jeffers, Helen Longino, Koffi Maglo, Roberta Millstein, Noah Rosenberg, Kenneth Taylor, Clinton Tolley, Neil van Leeuwen, Manuel Vargas, and Ward Watt. This research was funded by a Ford Foundation Post-doctoral Fellowship and supplementary funding from the University of San Francisco. This research was completed while the author was a Visiting Scholar at Stanford University.

Philosophy of Science, 81 (December 2014) pp. 1025–1038. 0031-8248/2014/8105-0026\$10.00
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partition at the $K = 5$ level of human population structure. Since that partition is roughly coextensive with J. F. Blumenbach's anthropological division of humankind, I call the partition 'the Blumenbach partition' in honor of Blumenbach. I defend my view in three steps. First, I conduct an investigation of the US meaning of 'race'. Here I uncover quite a few interesting things. One is that 'race' directly refers. Another is that 'race' is a proper name for a particular set of human population groups. Second, using recent human genetic clustering results, I show that the US meaning of 'race' is just the set of populations at the $K = 5$ level of human population structure. Hence, 'race', in its US meaning, picks out a biologically real entity. Third, I respond to a series of objections from critics. I end by offering concluding remarks.

2. The US Meaning of 'Race'. Before I begin, I would like to make a few methodological assumptions. First, I assume that a circumstance in which it is valid to model a term's meaning as just its referent is as follows:

1. If, by using appropriate evidential methods (e.g., controlled experiments), one finds that a term t has a logically inconsistent set of identifying conditions but a robust extension, then it is appropriate to identify the meaning of t as just its referent.

Thus, I do not assume that referentialism is a superior theory of meaning compared to descriptivism, but only that it is valid to model the meaning of a term that satisfies assumption 1 as just its referent.

Second, I assume that the US meaning of 'race' is the national meaning of 'race' in the United States. Let me distinguish between an 'official', 'national', 'regional', and 'ethnic' meaning of a term as the federal legal meaning in a nation, the widest-used meaning in a nation that is also used by a majority of its citizens, a meaning prevalent in a certain geographic region in a nation, and a meaning prevalent among a subpopulation in a nation, respectively. The distinction is analogous to official, national, regional, and ethnic languages.

For example, the official language of Belize is English, owing to Belize being a former British colony. The national language of Belize is also English (with 54% fluency).¹ However, the ethnic language of Creole Belizeans is Belize Kriol, which is a language that was invented by African slaves in Belize. Finally, the regional language of the Corozal District is Spanish (with 80% fluency). Hence, I acknowledge upfront that there are several ways that Americans use 'race'. The task, however, is to identify the national meaning of 'race' in the United States.

1. The statistics that I have presented come from table B3 in the document "Population Census 2000: Major Findings," produced by Belize's Central Statistical Office.

This brings me to the last assumption. To avoid circularity, I operationally define ‘racial discourse’ (or ‘race talk’) as discourse involving the use of ‘race’ to classify humans into subgroups, and a ‘race term’ as a name for a subgroup in racial discourse.

Given these assumptions, it is pretty clear that the US meaning of ‘race’ is just its referent, specifically the referent of US census racial discourse. Here is why. First, the national meaning of ‘race’ in the United States is clearly tied to US census race talk. No racial discourse in the United States is more widely used than census racial discourse. Americans are familiar with the census racial groups not only from filling out the federal census but because the census racial scheme permeates just about every important facet of American life. It is used on college applications, scholarship and fellowship applications, job applications, mortgage loan applications, birth certificates, and so forth. Furthermore, Americans know how to pigeonhole themselves into census races.

For instance, out of 299.7 million respondents to the 2010 US census, 93.8% self-identified as either white, black, Asian, American Indian, or Pacific Islander, while just 6.2% identified as “some other race” (Humes, Jones, and Ramirez 2011, 4).² But Americans know how to pigeonhole not only themselves but also others into census races.

For example, over the years, social scientists have been able to show that Americans can predict other Americans’ self-identified census race at rates well above chance using phonetic cues alone (e.g., African American Vernacular English), surnames alone (e.g., “Chen”), first names alone (e.g., “Lakisha”), and visual cues alone (e.g., a person’s face) (Purnell, Idsari, and Baugh 1999; Bertrand and Mullainathan 2004; Fiscella and Fremont 2006; Hourihan, Benjamin, and Liu 2012).

Therefore, census racial discourse is national racial discourse. Furthermore, since ‘race’ in census racial discourse has the extension blacks, whites, Asians, American Indians, and Pacific Islanders, so too does ‘race’ in its US meaning. Be that as it may, Americans do not agree on a logically consistent set of identifying conditions for defining census races.

For example, in Glasgow, Shulman, and Covarrubias’s (2009, 28) experimental study of 449 US adults, they studied Americans’ criteria for how to classify people into black and white races. They found 45.7% rejection (and 54.3% acceptance) of ancestry as a relevant criterion, 52% rejection (and 48% acceptance) of visible phenotype as a relevant criterion, and 51.1% rejection (and 48.9% acceptance) of social relations as relevant. Glasgow et al. (2009) find similar results for other identifying conditions race theorists commonly place in the US meaning of ‘race’, such as the one-

2. See <http://www.census.gov/population/race/about/> for the “definitions” of each US census race term.

drop rule and racialism. Furthermore, Ann Morning (2011) has found similar results.

Thus, Americans adopt census racial discourse as national racial discourse, and there is a robust extension associated with census racial discourse, but there is no single, logically consistent set of identifying conditions that Americans associate with ‘race’ in census racial discourse. According to assumption 1, this suggests that the US meaning of ‘race’ is just its referent in census racial discourse. However, at this point it might be useful to point out that the US Census Bureau does not control its own race talk. By law, the Census Bureau must defer to the Office of Management and Budget (OMB) to define ‘race’.

It is an interesting sociolinguistic fact that the United States has no official language but has official racial discourse. The OMB started regulating racial discourse for the federal government in 1977 when it passed Directive no. 15. In 1997, the OMB revised its race talk to the five racial groups Americans use today. Hence, interestingly, US racial discourse is controlled by a linguistic division of labor, as Hilary Putnam would put it, because when Americans engage in national racial discourse, they are semantically deferring to the OMB as the experts on race. What this means is that ‘race’, in US racial discourse, means whatever the OMB intends to pick out with ‘race’.³ So, what does the OMB intend to pick out with ‘race’? Surprisingly, a set!

In document 97-28653 of the federal register, which declares the 1997 revisions to official racial discourse, the OMB never calls race a ‘kind’ or a ‘category’.⁴ Rather, the OMB refers to race as a ‘set’. Specifically, the OMB refers to race as a “set of categories” six times in 97-28653. Furthermore, the OMB considers race to have exactly five members. While it is true that the OMB says that “the standards provide a *minimum* set of categories for data on race,” the OMB also says that it will “permit the collection of more detailed information of population groups provided that any additional categories can be aggregated into the minimum standard set of categories.” Moreover, the OMB considers its set of racial groups to be “comprehensive.” These statements lead me to believe that, according to the OMB, race is just {black, white, Asian, American Indian, Pacific Islander}.

The result above is undoubtedly a bit startling. Even though ‘race’ looks like a kind term, its current use in US racial discourse is that of a proper name. It is a term that rigidly designates a particular set of “population

3. I say “intends” because I am adopting Kripke’s approach to figuring out the referent of a directly referring term. In 1980, Kripke (1980, 163) gave up his “causal-historical” method of determining reference for a “present intensions” method as a result of the Madagascar problem.

4. Document 97-28653 is available at <https://www.federalregister.gov/>.

groups.” This means that race is a particular, not a kind. It is also interesting to note that this is a relatively recent use of ‘race’ in the United States, dating back no farther than 1997. The question now becomes whether race, as understood in US racial discourse, is an arbitrary set of population groups, a purely socially constructed set of population groups, or, perhaps, a biologically real set of population groups. I think it is the last one. And to see why, I now turn to recent human genetic clustering results from population genetics.

3. Race as a Human Population Partition. One lively area of research in current population genetics is that of identifying infraspecific population structure. A species has *population structure* just in case it has one or more partitions of populations. When a species has more than one partition of populations, it has a hierarchy of levels of populations. The lowest level always consists of local populations, but the highest level can consist of metapopulations.⁵ The gold standard for identifying population structure is the use of what we can call ‘worldwide genetic clustering analysis’, since nonrandom mating is likely to leave behind a genetic trail.

The first step in worldwide genetic clustering analysis is to make an educated guess about the local populations in the target species. Population geneticists typically use ethnic groups (and, more specifically, linguistic groups) to estimate local population structure in humans. The current estimate for humans is 7,105 ethnic groups, half of which are in Africa and New Guinea.⁶ The next step is to sample that species’ estimated local populations across all major geographic regions that the species inhabits. Ideally, one would want a sample that is representative in terms of geographic distribution, genetic variation, genetic admixture, and so on. The third step is to sample appropriate DNA sequences from each individual in the sample. These sequences are usually from noncoding (and, ideally, nonfunctional) regions of the species’ genome, for two reasons. First, since the goal is to identify population structure (not ecotype structure), the sequences should not be under selection pressure. Second, noncoding and nonfunctional sequences will have more variation and so will be more informative for inferring population structure, especially in young species such as humans.

The fourth step is to attempt to partition the sample into $N - 1$ levels of partitions such that the partition at each level is the unique partition that min-

5. For the purposes of this paper, I adopt Roberta Millstein’s (2010) causal-interactionist definitions of ‘local population’ and ‘metapopulation’, but with three emendations. First, I restrict population cohesion relations to successful reproductive interactions and ancestor-descendant relations. Second, I understand populations as perduring objects where temporal parts are connected via population cohesion relations. Third, I consider temporal parts of populations to be fuzzy sets instead of crisp sets.

6. This estimate comes from <http://ethnologue.com/statistics>.

imizes genetic difference in parts and maximizes genetic difference among parts, where N is the number of objects being partitioned. However, no partition may be found if the sampled individuals are too closely related, have too much admixture, or form a panmictic unit. Computer programs are usually used at this stage owing to the computational difficulty involved. There are two methods of partitioning: crisp and fuzzy.

In crisp partitioning, such as principal component analysis (PCA), objects are sorted into crisp partitions. In fuzzy partitioning (e.g., *structure* analysis), objects are sorted into fuzzy partitions. The parts in each partition are called ‘genetic clusters’, and each partition is called a level of ‘genetic structure’. Also, it is customary to name each level in a genetic structure hierarchy a ‘ K level’, where K corresponds to the number of parts in the partition.

For over a decade, population geneticists have been conducting worldwide genetic clustering analyses on humans using the HGDP-CEPH Human Genome Diversity Cell Line Panel (or, ‘the HGDP sample’ for short)—which is a free repository of human genetic data—and a certain result has been robust. Namely, the $K = 5$ level of human genetic structure corresponds to black Africans, Caucasians, East Asians, Amerindians, and Oceanians.⁷ Given the sort of genetic data used in human genetic clustering, this result indicates that the $K = 5$ partition of human genetic clusters is a partition of human populations.

Suppose we call the particular partition population geneticists have identified at $K = 5$ in humans ‘the Blumenbach partition’ in honor of J. F. Blumenbach, who, in 1795, became the first person to (roughly) discover this partition of human populations.⁸ It should be emphasized that the results do not support the idea that Blumenbachian populations, as we can call them, are extremely genetically different. In fact, just the opposite is true!

The equation below represents the relationship that holds between total genetic variation (σ^2), genetic variation among individuals (σ_c^2), genetic variation among populations in parts (σ_b^2), and genetic variation among parts (σ_a^2) at any particular level of genetic clustering:

$$\sigma^2 = \sigma_c^2 + \sigma_b^2 + \sigma_a^2. \quad (1)$$

7. This result is found in Rosenberg et al. (2002, 2005), Li et al. (2008), McEvoy et al. (2010), and Pemberton, DeGiorgio, and Rosenberg (2013), among others. Also, the terms ‘black African’ and ‘Caucasian’ are mine. Population geneticists usually use ‘African’ and ‘Eurasian’ instead. But this convention can be confusing since North Africans turn out to be more Eurasian than African.

8. The one difference is that Blumenbach divided humans into Malays instead of Oceanians.

In the case of the Blumenbach partition, Rosenberg et al. (2002, 2382) calculate that the equation is as follows:

$$1 = 0.932 + 0.025 + 0.043. \quad (2)$$

This means that only 4.3% of total human genetic variation is found among Blumenbachian populations. Nevertheless, it is enough genetic variation to signal that we have a partition of populations at $K = 5$.

Of course, the most fascinating fact about these results is that the Blumenbach partition is just the US meaning of ‘race’. The case can be made by showing that the set Americans call ‘race’ is identical to the Blumenbach partition, which can be done by showing that each race term in US racial discourse is just an alias for a unique Blumenbachian population, similarly to how ‘Snoop Dogg’ is an alias for Calvin Broadus Jr. There are at least three reasons for believing that Americans are really just talking about Blumenbachian populations.

For one, the extensional overlap between current extensions of US race terms and Blumenbachian population terms is statistically significant and high. Specifically, using the Jaccard coefficient, one can calculate that the overlap between ‘black’ and ‘black African’, ‘American Indian’ and ‘Amerindian’, and ‘Pacific Islander’ and ‘Oceanian’ is 1.0, 1.0, and 1.0, respectively.⁹ Also, the overlap between ‘Asian’ and ‘East Asian’ and between ‘white’ and ‘Caucasian’ is 0.692 and 0.571, respectively.¹⁰ The lower overlaps in the last two cases are due to the OMB lumping South Asians with Asians and not with whites. Nevertheless, the extensional overlap here is non-trivial and highly indicative of Americans and population geneticists talking about the same objects.

A second source of evidence is that the definite descriptions Americans use to pick out US races also pick out unique Blumenbachian populations; furthermore, why those descriptions work as well as they do to pick out US races can be explained by the historical essences of Blumenbachian populations along with a few facts about human evolutionary history. For instance, the OMB uses “having origins in any of the original peoples of Hawaii, Guam, Samoa, or other Pacific Islands” as a definite description for Pacific Island-

9. The Jaccard coefficient (J_C) is a statistic used in ecology to measure the extensional similarity between two sets if all one cares about is cardinality and identity of elements. If a and b are two sets, $J_C = |a \cap b| / |a \cup b|$. Note that $0 \leq J_C \leq 1$ for any a and b .

10. This calculation is based on the ethnic group classifications found on the HGDP-CEPH and US Census Bureau websites, which are available at http://www.cephb.ft/en/hgdp_panel.php and <http://www.census.gov>, respectively. Also, crisp cardinality was used to do the counts instead of fuzzy cardinality for ease of calculation.

ers. But, of course, that description also picks out Oceanians. Furthermore, if Pacific Islanders just are Oceanians, we can explain why that definite description works so well to identify Pacific Islanders.

For instance, suppose we define Oceanians as the most inclusive human population born from East Asians in Oceania (Sahul and the Pacific Islands) and from the original human inhabitants of Oceania. Since Sahul was a single landmass composed of present-day Australia, New Guinea, and Tasmania 50,000–60,000 years ago, when humans first inhabited it, and since we know that the original human inhabitants of Oceania interbred to create modern Oceanians, and since temporal parts of populations are genealogically connected, it should be the case that most Oceanians have genealogical connections to the original peoples of some Pacific island. The only Oceanians who will not will be individuals who became Oceanian from interbreeding alone and Oceanians descended from indigenous peoples of Sahul but not indigenous peoples of a Pacific island (e.g., Aboriginal Australians).¹¹ The final source of evidence comes from counterfactual cases.

It is not hard to generate accessible possible worlds that support the claim that US race terms are just aliases for Blumenbachian populations. For example, imagine a possible world τ where human history unfolded exactly how it did in our world except that every Caucasian in τ was killed by an infectious disease in the year 2013. Presumably, we have access to τ , since it violates no logical, metaphysical, or scientific principles. Then, given that we use ‘white’ in its national American meaning in our world, and given that we use ‘Caucasian’ in its Blumenbachian meaning in our world, it is fair to say that both ‘Caucasian’ and ‘white’ are empty terms in τ in 2014—which makes perfect sense if ‘white’ is just an alias for Caucasians. It is counterfactual evidence like this that strongly suggests that the US meaning of ‘race’ is just the Blumenbach partition.

4. Objections and Replies. However, there are detractors to any attempt to tie folk racial classification to a biological source. The objections can be lumped into three groups: semantic, methodological, and metaphysical. Perhaps the most popular semantic objection is that races must satisfy certain ordinary criteria in order to be races (e.g., be “visible,” be “discrete,” be “isolated,” or differ in “cognitive” traits), but Blumenbachian populations do not satisfy all of those criteria noncontingently.¹² However, my answer to this

11. The genetic evidence for the common origin of Aboriginal Australians and New Guineans from indigenous inhabitants of Sahul can be found in McEvoy et al. (2010).

12. For a critic who argues that races must be “visible,” see Glasgow (2009). For a critic who assumes that races must be “discrete” or “isolated,” see Graves (2004, 116). For critics who assume that races must differ in “cognitive” traits, see Feldman and Lewontin (2008, 96).

objection is that while these criteria seem to be part of the US meaning of ‘race’, they are not, since the US meaning of ‘race’ is just its referent.

Yet another concern is what Joshua Glasgow (2009, 94) has called “the mismatch objection.” In short, Glasgow (2009, 96) contends that human genetic clusters do not reasonably overlap ordinary US racial groups, especially if one asks “open-ended” questions about race. In particular, Glasgow (2009, 96) questions whether Arab Americans would really identify as white and whether Hispanics would identify with any census race. While thoughtful, this objection falls flat.

For one, the overlap in question is high (57.1%–100%) and statistically meaningful. Moreover, the relevant question is not whether Arabs, Hispanics, or other “problem” groups would identify with a census race if asked what their race is. The relevant question is whether they would identify with a census race in the context of national racial discourse. In other words, Arab Americans identifying as Arab among friends and family is compatible with identifying as white when applying for college or filling out a job application. Furthermore, this is exactly what happens. On the federal census, 97% of Arab Americans identify as white, and 63% of Hispanics identify with a census race (de la Cruz and Brittingham 2003, 8; Ennis, Ríos-Vargas, and Albert 2011, 14). But perhaps the strongest objections are methodological.

Some critics, such as Kittles and Weiss (2003), argue that $K = 5$ human genetic clustering results are an illusion generated from isolation-by-distance (IBD) and biased geographic sampling. In short, the genetic clustering observed at $K = 5$ is arguably due to selective geographic sampling. Moreover, if we were to sample our species continuously across geography, we would find that human genetic variation is a function of geographic distance only.

There is no doubt that the HGDP sample is not random with respect to geography.¹³ If it were, half of the sample would come from Africa and New Guinea. However, even though the HGDP sample is not perfect, it does not follow that human genetic variation is only clinal. Rather, the HGDP sample could be good enough to pick up on human genetic structure despite its flaws. Thus, the IBD hypothesis is testable. For instance, if the IBD hypothesis were true, any ethnic group in a specific genetic cluster (call it p_1) and another ethnic group from that cluster (call it q_1) separated by a geographic distance d should have the same F_{st} genetic distance (D) as p_1 and a third ethnic group (call it r_2) that is not in the same genetic cluster as p_1 but is at d from p_1 , which is formalized as follows:

$$D(p_1, q_1, d) = D(p_1, r_2, d). \quad (3)$$

13. For simplicity, I talk as if the HGDP sample is the only sample used to generate the Blumenbach partition result.

However, Rosenberg et al. (2005) test equation (3) and find it to be false. Instead, Rosenberg et al. (2005, 668) find that 1.53% of human genetic variation at $K = 5$ is unaccounted for by “geographic distance alone.”

Yet another methodological objection is that the HGDP sample of human ethnic groups is biased with respect to human genetic admixture. For example, Koffi Maglo (2011, 371–73) argues that “continental genetic groupings are mere sampling artifacts” because human genetic clustering studies mostly sample “isolated groups” as opposed to “admixed” groups. Furthermore, if more admixed groups were sampled (e.g., African Americans, Mestizos, Ethiopians), so-called continental populations would dissolve into “genetic clines” (Maglo 2011, 372).

Again, I do not wish to dispute the facts. The fact is that the HGDP sample is not the best with respect to representing human genetic admixture. Most ethnic groups in the sample are indigenous and not heavily admixed (e.g., Mbuti, Adygei, Tujia, Papuan, and Surui peoples). However, just like the last objection, it is testable whether adding admixed ethnic groups will dissolve Blumenbachian population structure. So far the answer is no. For instance, Pemberton et al. (2013, 902) were able to obtain the Blumenbach partition despite adding hundreds of African Americans, Mestizos, Coloured South Africans, Polynesians, and other admixed groups to the sample.

This brings us to a third, related objection. Some critics, such as Adam Hochman (2013, 348), doubt that the Blumenbach partition is a human population partition because “continent-based clusters . . . disappear when more genotypes are added.” In other words, perhaps the HGDP sample of human ethnic groups is just too small. Specifically, Hochman points out that when Tishkoff et al. (2009) added 134 ethnic groups to the 52 found in the HGDP sample, they discovered that the $K = 5$ partition of human populations consists of Caucasians, Mongloids, and three distinct clusters of black Africans!¹⁴

This is a good objection. However, Tishkoff et al.’s results do not conflict with the standard result that the Blumenbach partition is a human population partition. This is because Tishkoff et al. (2009) dramatically oversample African ethnic groups. African ethnic groups make up 65.1% of Tishkoff et al.’s sample, even though they make up 30.2% of human ethnic groups.¹⁵ Combined with the known fact that most $K = 5$ human genetic variation lies within parts, not among them (see eq. [3]), it is unsurprising that a study that greatly oversamples one major geographic region will find that its ethnic groups split into different genetic clusters at $K = 5$. In fact, Tishkoff et al.’s result is not unique.

14. By ‘Mongloids’ I mean ‘East Asians, Amerindians, and Oceanians’.

15. This estimate is from <http://ethnologue.com/statistics>.

Friedlaender et al. (2008) add 20 additional ethnic groups to the HGDP sample, but in such a way that Oceanian ethnic groups make up 48.6% of the sample, even though they make up 18.5% of human ethnic groups.¹⁶ At $K = 5$, Friedlaender et al. (2008, 178) find that the partition consists of Caucasians, non-Oceanian Mongloids, black Africans, and two distinct clusters of Oceanians! However, neither Tishkoff et al.'s nor Friedlaender et al.'s results conflict with the standard result because their samples of human ethnic groups are not appropriate for identifying worldwide human population structure. Rather, these samples are appropriate for studying African population structure and Oceanian population structure, respectively.

Although the population-genetic research that Blumenbachian race theory rests on is sound, some critics may still have metaphysical concerns. Particularly, both Maglo (2011) and Hochman (2013) have objected that the Blumenbach partition is not important enough to deem it biologically real. Maglo (2011, 361, 370) argues that race must be a “fundamental and primitive category” in order to be “biologically real.” Furthermore, Hochman (2013, 347) argues that races need to be “subspecies” or at least have “a large jump in genetic difference between clusters” in order to be “meaningful biological units.” However, Blumenbachian populations are not fundamental to population genetics, are not subspecies, and are not very genetically different. While this concern is thoughtful, I reject that an entity needs to be very important to science in order to be scientifically real.

For example, consider element 117. It is not a very important kind in modern chemistry. For one, it is not fundamental in any field of modern chemistry, unlike, say, carbon in organic chemistry. Furthermore, there is not much chemists can do with 117 owing to its nuclear instability. Nevertheless, 117 is a real chemical element because, among other things, nuclear chemists need two of its isotopes to best causally explain two nuclear decay chains that arise from fusing ^{48}Ca and ^{249}Bk (Hofmann 2010). The situation is similar with US race. The Blumenbach partition is not a very important entity in population genetics. However, population geneticists need to posit the Blumenbach partition in order to best causally explain the 1.53% of among-part human genetic variation that arises at $K = 5$ that is not accounted for by geographic distance alone.

At this point the critic could retort that chemists acknowledge the reality of element 117 because it is objectively real, and it is an entity's objective reality that grants it status as a real scientific entity. For example, Naomi Zack (2002, 5) defines “real entities” in science as ones that occupy “a world that exists independently of thought, sensation, perception, language, and other

16. This estimate is also from <http://ethnologue.com/statistics>.

symbolic representation.” Furthermore, Zack (2002, 4) explicitly says that “human group differences” are “biologically real” only if they “are not culturally constructed.” However, I am going to have to disagree here as well.

While objective reality might be an appropriate way to understand the reality of entities in chemistry and physics, it is entirely inappropriate for biology. One reason is that cultural evolution is often a relevant factor in the origin and persistence of biological entities. Consider the Blumenbach partition. It is a human population partition, but its existence cannot be explained entirely by mind-independent factors. For example, why is it that African Americans, Afro-Caribbeans, and Afro-Latinos cluster with Sub-Saharan Africans instead of Amerindians? Geography cannot explain this, but social factors can.

Specifically, social isolation mechanisms (e.g., racial segregation) make mating nonrandom in the Americas, and social cohesion mechanisms (e.g., black solidarity) make mating assortative in the Americas. Hence, a more appropriate standard for an entity being biologically real is not whether it is objective, but whether it is epistemically useful and justified in a well-ordered research program in biology (Spencer 2012). Furthermore, since the Blumenbach partition is useful for explaining a portion of human genetic variation, and since our evidence for this comes from well-executed human genetic clustering studies in population genetics, it is hard to deny that US race is biologically real, even if it has also been socially constructed.¹⁷

5. Concluding Remarks. In summary, I have attempted to show four things. First, the US meaning of ‘race’ is just its referent. Second, the referent of ‘race’, in its US meaning, is a particular set of human population groups, not a kind. Third, US race is just the Blumenbach partition of human populations: {black Africans, Caucasians, East Asians, Amerindians, Oceanians}. Fourth, US race is both biologically real and socially constructed.

I close by making one important disclaimer. Nothing in Blumenbachian race theory entails that socially important differences exist among US races. This means that the theory does not entail that there are aesthetic, intellectual, or moral differences among US races. Nor does it entail that US races differ in drug metabolizing enzymes or genetic disorders. This is not political correctness either. Rather, the genetic evidence that supports the theory comes from noncoding DNA sequences. Thus, if individuals wish to make claims about one race being superior to another in some respect, they will have to look elsewhere for that evidence.

17. See Outlaw (1990) for the first argument that ‘race’, in the United States, picks out a biosocial entity.

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