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Abstract

In June 2012, *Sociological Theory* published “The Genomic Challenge to the Social Construction of Race” by Jiannbin Lee Shiao, Thomas Bode, Amber Beyer, and Daniel Selvig. The article argues that “recent research on the human genome challenges the basic assumption that human races have no biological basis” (p. 68). The authors advance a “bounded nature” account of race to suggest that “biological ancestry” might lead to “different frequencies of personality and cognitive characteristics” by race (p. 83). In this response I investigate three propositions central to Shiao et al.’s argument: (1) the contention that contemporary genetics research has documented a biological basis to race, (2) the assertion that such research warrants inquiries into the way “biological ancestry” might “contribute to average group differences” by race (p. 83), and (3) the claim that there is no “essential characteristic” of their findings that might be complicit with biological racism.

Keywords

race, ethnicity, social construction, racial formation, genomics

“The Genomic Challenge to the Social Construction of Race,” by Jiannbin Lee Shiao, Thomas Bode, Amber Beyer, and Daniel Selvig (hereafter “GC”), argues that “recent research on the human genome challenges the basic assumption that human races have no biological basis” (p. 68). Shiao et al. advance what they describe as a “bounded nature” alternative to social constructionist theories of race that “accepts the existence of genetic clusters consistent with certain racial classifications as well as the validity of the genomic research that has identified the clusters, without diminishing the social character of their context, meaning, production, or consequences” (p. 67). These clusters, they maintain, might help account for “different frequencies of personality and cognitive characteristics” among racialized groups (p. 83).

To place Shiao et al.’s (2012) main argument within a broader scholarly context, it is important to note that the large majority of researchers specializing in the sociology of race,

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as well as an extensive group of geneticists, evolutionary biologists, anthropologists, and other natural scientists, rejects the position that the race concept is based on or derived from group-based biological or genetic variance. GC's argument to this effect also contradicts the respective statements on race of the American Anthropological Association and the American Sociological Association, as well as the federal Office of Budget and Management's Directive 15, which explains that the standard racial and ethnic categories used in the U.S. census "should not be interpreted as being scientific or anthropological in nature" (American Anthropological Association 2003; American Sociological Association 2003; U.S. Census Bureau 1977). Most research and teaching on race within the disciplines of sociology, history, political science, cultural studies, anthropology, geography, and economics examines the social, political, and historic structures that produce (and reproduce) the concept of race rather than the biological or genetic markers alleged to signify group differences (Bernasconi and Lott 2000; Bobo 1999; Bonilla-Silva 1999; Brown et al. 2003; Cox 1948; Dupré 2008; Fields 1990; Gossett 1963; Haney-Lopez 1996; Haslanger 2008; Omi and Winant 1994; Roberts 2011; Royal and Dunston 2004).¹

GC argues, however, that the social constructionist position on race can allow for some bounded or limited biological determination of the race concept without altogether abandoning the claim that race can also have important social and political dimensions. From the authors' perspective, it is unfair to stigmatize and discredit scholarship that simply recognizes a connection between social and biological race. Indeed, Shiao et al. (2012) suggest that social constructionists have become "unnecessarily burdened with a conception of human biological variation that is out of step with recent advances in genetic research" (p. 68). Freed from this burden, they contend, such scholars could more accurately and effectively make the case for constructivist frameworks that incorporate rather than reject basic scientific evidence.

At some moments, Shiao et al. (2012) frame this intervention in minimalist terms, suggesting they are merely calling on constructivists to acknowledge that patterns of human variation described by the concept of "race" *may* have a biological basis. At other moments, they cast their argument much less modestly, as when they instruct their colleagues to reformulate their entire paradigm: "Sociology should set aside the claim of biological nonreality [of race] and adopt an approach more consistent with recent genetics research." They also assert that a "bounded nature" revision to the "pure constructionism" approach could account for the way "biological ancestry" might "contribute to average group differences" by race (p. 83). GC additionally proposes to rehabilitate the concept of "human subspecies" as one way to describe human genetic variation (p. 72), even as the term has long been disfavored by most natural scientists (Templeton 1998). It goes so far as to suggest that the bounded nature framework might offer a biological account of a purported association between West African ancestry and superior sprinting ability (p. 74).

These are not minimalist claims; they require serious debate and scrutiny.²

In this response I investigate three propositions that I understand to be central to Shiao et al.'s (2012) argument: (1) the contention that "recent research on the human genome challenges the basic assumption that human races have no biological basis" (p. 68), (2) the assertion that such research warrants inquiries into the way "biological ancestry" might "contribute to average group differences" by race (p. 83), and (3) the claim that there is no "essential characteristic" of their findings that might be complicit with biological racism and that any such interpretation would be rooted in a mistaken "social interpretation" of these findings (p. 83).³

RACE, POPULATION STRUCTURE, AND GENOMIC ANALYSIS

According to Shiao et al. (2012), quantitative geneticists have "identified an empirical structure within human genetic variation that at a certain scale resembles the continentally based

racial classifications of the U.S. federal government” (p. 68). According to GC’s authors, this new research warrants their assertion that “the vast majority of contemporary persons ‘know,’ that is, self-identify with, their genetic ancestry, that is, whether their ancestors lived in sub-Saharan Africa, western Eurasia, the Pacific Islands, eastern Eurasia, or the Americas 50,000 to 2,000 years ago” (p. 79). In other words, the authors seem to suggest, go to any corner of the globe today and most everyone you encounter will self-identify with the basic racial categories of the current U.S. census.⁴

Shiao et al. (2012) base their assertion about the biological basis of race almost entirely on three published sources: A 2002 article led by geneticist Neil Risch (Risch, Burchard, Ziv, and Tang) and papers published in 2002 and 2005 by computational biologist Noah Rosenberg.⁵ Since one of the premises of GC is that social scientists must seriously engage the substance and findings of this research, it is worth reviewing the findings of these papers in some detail.

Risch, Rosenberg, and other scholars working in the field of population genetics and population biology analyze large genetic data sets to infer population groupings based on the frequencies of particular DNA sequences drawn from individuals imagined to be from discrete populations (Roberts 2011). These researchers use specialized computational genomic software (the most popular is called *Structure*) to examine the frequency of certain combinations of alleles, or gene variants, at many different loci (the location of a gene on a chromosome) in order to statistically estimate population structure and paths of migration (Bolnick 2008; Kalinowski 2011).

GC’s claim that there is a newly discovered “biological basis of race” is derived from an interpretation of Risch and Rosenberg’s findings suggesting that these estimates of population structure do not exist as a series of continuous clinal variations, as some have argued, but instead are patterned as “clinal clusters” or classes that correspond to major continental areas and thus to continentally based racial classifications (e.g., “African,” “European,” “Asian,” Native American”) (pp. 71–72).

Isolated by geography or social custom, the authors explain, these clusters evolved in genetically distinct ways, though an evolutionary genetic mechanism for these divergences is never specified. The authors contend that while these clusters do not suggest any absolute boundaries between population groupings, the variation and distribution of particular gene variants empirically verifies their proposition that “clinal classes provide a biological basis for racial and ethnic categories” (p. 73). In their account, an influential body of research by scholars such as Richard Lewontin (1973), which argued that variance within any “racial” group is greater than variance between such groups, was limited because it could not simultaneously analyze genetic variation at many loci. But the rapid advancement of DNA sequencing technologies in the past 10 years and the unprecedented capacity to compare genetic variance at thousands of loci simultaneously effectively undermines these claims. Shiao et al. present this assertion as largely incontrovertible; they do not discuss or cite any research that disputes it.⁶

The article then develops an abstract model for theorizing the way genetic inputs might interact with environmental conditions to yield particular social outcomes (a process they describe as “genomic individualism”) and applies this model to several published studies on the sociology of race.

Is There a Scientific Consensus about the “Biological” Basis of Race?

The debate about the relationship between population structure, geographic ancestry, and the concept of race spans many hundreds of years. It was questions about this relationship that

led Austrian anthropologist Johan Blumenbach in the late eighteenth century to classify and rank skulls he had collected from around world. In the *Natural Variety of Mankind* (Blumenbach [1795] 2000), he concluded that a prized specimen from the Caucus region represented “the most beautiful form of the skull,” thus coining the “scientific” term *Caucasian* (Blumenbach [1795] 2000:31). Blumenbach utilized the race concept to describe the variation in skull shape and “beauty” he observed, using quasi-geographic referents (“Caucasoid,” “Mongloid,” “Amerindian,” “Negroid”) to organize his taxonomic structure. Scientists who followed Blumenbach focused on other dimensions of human variation—ear shape, skin pigmentation, facial structure, hair texture, posture, skull size—as referents for their classificatory schemes. All of these scientists insisted that they were disinterested and objective observers recording natural group-based biological variation, untainted by any social bias or cultural framework (Ewen and Ewen 2006; Graves 2001; Smedley 1993).

Scientific research on population structure has advanced considerably since Blumenbach’s time. While Risch, Rosenberg, and others have access to far more sophisticated software and computing power today, the basic structure of ancestry relationships and migration patterns that they and others have uncovered has been known to geneticists for years (Bolnick 2008).

Geneticists and evolutionary biologists have discerned these population clusters (or more precisely, the geographic patterns of clinal variation) at many different scales—hemispheric, continental, subcontinental, regional, and so on. Since software like *Structure* requires the user to prespecify the number of groups in which to organize a given sample, that sample can be divided into any number of clusters. As the population geneticist Luigi Luca Cavalli-Sforza and colleagues (1994:19) explain, “at no level can clusters be identified with races, since every level of cluster would determine a different partition and there is no biological reason to prefer a particular one.”

Put another way, if “African” is a “biological” category with explanatory power, then so might be every other grouping inferred in a population structure analysis. Risch et al.’s 2002 paper, for example, reviews the findings of multiple population inference studies, each of which lists different clusters. A sample analyzed by one study discerned 14 different population groups including CAR pygmies, Zaire pygmies, Lisongo, Northern Europeans, Northern Italians, Melanesians, New Guineans, Australians, Surui, and Karitiana (p. 3). Thus, following GC’s logic, “Northern Italian” is as valid a biological category as “African.”⁷ As Cavalli-Sforza et al. (1994:19) maintain, “there are clearly no objective reasons for stopping at any particular level of taxonomic splitting” to pronounce a biological basis of race. The tautological reasoning here is clear: The observer selects the characteristics to be defined as “racial” and then asserts that those characteristics delineate the basis of “racial” difference. The same fatal flaw that has undermined two centuries worth of scientific efforts to establish a biological basis for racial distinctions also discredits the use of population genetics to this end: Ultimately the observer and not the observed declares which differences constitute a racial group and which do not (Lewontin 2006). Shiao et al. are absolutely incorrect to suggest this approach constitutes a “race-neutral” method of letting the data define the groups (p. 72). The researcher must still apply an a priori definition of race to the patterns of genetic variation estimated by population inference analysis.

GC also fails to engage a critical body of research that has long disputed Risch’s assertion that “race” descriptors have any generalizable correspondence to continental land masses or provide any “objective” determination of racial difference. Celeste Condit’s (2007) article “How Culture and Science Make Race ‘Genetic’: Motives and Strategies for Discrete Categorization of the Continuous and Heterogeneous” carefully documents the rhetorical strategies of “shrinking” and “stretching” used in the Risch et al. (2002) study to suggest that the categories of race he employs somehow correspond to continental groupings. They do

not. For example, Risch uses Blumenbach's term *Caucasian* to delineate "those with ancestry in Europe and West Asia: including the Indian Subcontinent and Middle East: North Africans typically are also included in this group." As Condit points out, "this group is neither named for a continent, nor composed of members from a continent, but rather of two subcontinental areas and a third continental area. The term 'continental' is stretched so far it should be virtually unrecognizable in this case." She explains that the "shared associational history, however, derives not from the use of 'Caucasian' as a term for continents, but as a term for races. . . . Despite its flawed logic, the associations it engenders may be effective to an audience steeped in racial vocabulary" (p. 256).

The same is true for Risch's use of *African* (to describe a subcontinental area that excludes North Africa), *Native American* (a designation that Condit explains "folds two continents into a single racial designation"), as well as the geographic referents for the terms *Asian* (which excludes Central Asia) and *Pacific Islanders* (which refers to a small continent—Australia—plus large dispersed islands). In another study, Risch similarly uses the category *Hispanic* as a descriptor of racial cum ancestral origin, even though a majority of self-identified "Hispanics" checked the racial designation "white" on the 2010 U.S. census. Condit (2007 p. 257) concludes: "Indeed, none of the groups claimed to be delineated as 'continental' groupings [by Risch et al.] are actually very closely coterminous with a continent as the term is otherwise understood." It is not surprising then that Kenneth Prewitt, former U.S. Census Bureau Director, describes Risch as a brilliant scientist but "careless in his treatment of demographic data, especially self-reported race in the U.S. census" (Prewitt 2012:13).

As Condit and others make clear, genetics researchers such as Risch operate in the same field of cultural logic, folk wisdom, and common sense that has long shaped popular understandings of race in the United States (Fullwiley 2007; Reardon 2004). Numerous ethnographic and anthropological studies of genetics research affirm Johnny Williams's recent finding that "unexamined and unrecognized racial thinking is an integral part of genetic researchers' interpretations and understandings of genetic variation" (Williams 2011:551). As Ann Morning (2011) documents persuasively, individual anthropologists and biologists vary widely in their understanding and use of the race concept within their research and teaching.

GC similarly fails to acknowledge a large body of literature that is critical of using race and ethnic descriptors to discern population structure and ancestry, even for the purposes of disease risk assessment (Collins 2004; Foster and Sharp 2002; Hamilton 2008; Jorde and Wooding 2004; Keita et al. 2004; Roberts 2011; Royal and Dunston 2004; Serre and Pääbo 2004; Tishkoff and Kidd 2004). These scholars have critiqued the reliance on folk or anthropological categories to generate ethnic and racial descriptors, the imprecise use of those descriptors in lab settings, and the profound limitations of so-called "race based medicine" (Kahn 2013).

Moreover, it is critical to remember that the population clusters inferred by programs like *Structure* are representations of statistical variability; they are not, in themselves, biological entities or natural types with causal powers. The software's algorithms calculate the probability of dividing individuals into a predetermined number of clusters, and different runs of the same data set can produce different results. Even the software's designers caution the program may produce arbitrary results for certain data sets (Bolnick 2008:75). In a 2011 article in *Heredity*, population geneticist Steven Kalinowski (2011:625) argues that *Structure* "does not reliably identify the main genetic clusters within species." When Kalinowski reanalyzed Rosenberg et al.'s 2005 data set, for example, his results suggested a stronger similarity with regards to allele sharing between many sub-Saharan African populations and European populations than Rosenberg found.⁸ Condit (2007) similarly argues that "when

programs such as [*Structure*] tell us that there are distinguishable groups, therefore, it is wrong to read this as indicative of discrete populations. [*Structure*] is just telling us that if you wanted to identify places of greatest difference, these would be places where there is a distinguishable change in the overall pattern of changes in levels of difference” (p. 253). Yet GC, which premises its argument almost entirely on estimations generated by researchers using *Structure*, does not mention or attempt to engage any of these well-established critiques.

And even if one accepts the (contested) finding that self-identified race or ethnicity correlates with population structure, this finding does not justify a conclusion that “race” (or clinal class) has a biological *basis*. At the most quotidian level, the findings suggest that a statistical analysis of genetic ancestry informative markers of a population in the United States that self-identifies as “black” is likely to bear a relationship to an analysis of populations sampled in some region of sub-Saharan Africa. And a population that self-identifies as Chinese is likely to be statistically related with a population in China (Dupré 2008). That a new statistical technique has validated a high probability of such histories of migration is hardly revelatory; it does not establish a biological basis of race. Similarly, even if one remains skeptical of Risch et al.’s (2002:3) decision to treat descriptors like *Caucasian* and *Hispanic* as biological and geographical categories, their paper only argues that such labels are a defensible data point for epidemiologists to consider in assessing risk factors for disease across populations.

Indeed, this body of research as a whole largely affirms the scientific consensus about the origins and patterns of human migration during the past 80,000 years, the associations between genetic variation and migration patterns, and the genetic unity of *homo sapiens* as a whole (Cavalli-Sforza et al. 1994; Keita et al. 2004; Roberts 2011). As Rosenberg et al. (2002:2384) make clear, it is “only in the accumulation of small allele-frequency differences across many loci that population structure [is] identified.”

GC’s authors also inexplicably omit a critical statement from Rosenberg et al.’s 2005 paper emphasizing that their findings “should not be taken as evidence of our support of any particular concept of biological race” (p. 668). Rosenberg et al. continue: “The arguments about the existence or nonexistence of ‘biological races’ in the absence of a specific context are largely orthogonal to the question of scientific utility, and they should not obscure the fact that ultimately, the primary goals for studies of genetic variation in humans are to make inferences about human evolutionary history, human biology, and the genetic causes of disease” (p. 669). Similarly, Risch et al.’s 2002 article cited by GC specifically contends that “although some investigators might quickly jump to a genetic explanation for an ethnic difference, this is rarely the case with epidemiologists, who have a broad view of the complex nature of most human traits” (p. 8).

Rosenberg et al. (2002:2384) further explain that “genetic difference among human populations derive mainly from gradations in allele frequencies rather than from distinctive ‘diagnostic’ genotypes.” Even when such minor allele variations are associated with statistically estimated population clusters, these differences are not necessarily expressed as traits; most of this variation has no observable effect. Genetics research has never demonstrated a relationship between a statistical clustering of allele frequencies based on ancestry inference and any measurable social or psychological behavior. Algorithms to infer population structure are not designed to identify the location of the proverbial “gene for” any particular trait, much less a complex social behavior.

The Risch and Rosenberg papers are engaged in a wider scientific debate about whether self-described racial and ethnic labels might prove useful to biomedical and epidemiologic research (Foster and Sharp 2002; Gibbon, Santos, and Sans 2011; Hamilton 2008; Keita

et al. 2004; Morning 2011; Roberts 2011; Royal and Dunston 2004; Serre and Pääbo 2004; Tishkoff and Kidd 2004). Risch and Rosenberg make clear that their findings apply to these questions alone.

In sum, the clinal patterns and population structures documented by contemporary genetics research affirm long-standing accounts of human migration and evolution. Scientists have long known that these migration patterns are associated with minor genetic variations even as they continue to debate the relevance of these variations (and the labels we use to describe them) to biomedical research and treatment.

GENETICS, RACE, AND “PERSONALITY AND COGNITIVE CHARACTERISTICS”

The main research by Risch and Rosenberg cited by Shiao et al. (2012) is now a decade old—a lifetime in the field of genetics research—and the findings have been thoroughly debated during that time by sociologists of science, geneticists, epidemiologists, and many other researchers. Yet of the many geneticists and social scientists who have reviewed this research and participated in these debates, no one has suggested, as Shiao et al. have, that the statistically discerned allele clusters documented within Risch and Rosenberg’s work should be considered as a “potential input to the social definition of racial and ethnic categories” (p. 73). Given the extraordinary growth in the fields of evolutionary psychology, behavioral genetics, and sociobiology and the immense scholarly and popular interest in seeking genetic explanations for social outcomes, why have no other scholars cited evidence from population genetics research that might explain “average group differences” or the “distribution of personality and cognitive characteristics” by race (pp. 83–84) on the basis of this research?

The answer is simple. There is no genetics research that warrants such claims.

Shiao et al. (2012:77) acknowledge this deficiency directly: “We admit that presently there is an absence of direct evidence for clinal class differences in the distribution of individual outcomes with substantial heritability.” They continue: “It remains an empirical question whether there is ancestral variation within those individual characteristics that are of particular interest to social scientists.”

If a lack of evidence might inhibit other scholars, it does not restrain Shiao et al. They propose that the “potential ancestral effects” they set out to describe “should be regarded as conceptual ‘placeholder[s],’ indicating our lack of understanding of what about [genetic ancestry] is responsible for the unresolved effects.” They grant that while there is no empirical evidence on which to base such speculations, there is “a common component of quantitative genetic research that makes their existence plausible” (p. 77).

This assertion is confounding for two reasons. First, there is no basis to assume that the ancestry informative markers used to estimate ancestry groupings in population structure analyses imply the existence of a “common component” of genetic similarities. To the contrary, these analyses examine a special group of nonfunctional DNA microsatellites selected to distinguish geographic ancestry; no inference about overall genetic variation can be drawn from variation at these loci (Lewontin 2006). Second, it is remarkable that an article premised on urging social scientists to pay close attention to recent genomic research does the exact opposite, elaborating at length on hypothetical “placeholder” scenarios untethered to any empirical body of evidence and based on a deeply biased interpretation of population inference research.

To conjure a world in which there was evidence for its claims, GC reviews the findings of several well-known studies within the sociology of race. The analysis that GC ultimately produces demonstrates precisely why making claims about the social effects of population genetics research in the absence of any underlying evidence is such a flawed enterprise.

For example, Shiao et al. assert that patterns of exclusion, domination, and hierarchy documented by sociologists on the basis of race or ethnicity might at least be partly explained by a genetic predisposition for “ethnocentrism.” Social actors, they reason, genetically conditioned to detect similarities or differences with others based on “visible ancestry,” might be genetically predisposed to act on this perception of ancestry in particular ways. They ask readers to consider the existence of a heritable, genetically determined hostility toward those from a differing “clinal class” (p. 83). They reason that “clinal class differences in the frequency of ethnocentrism” might shape this process (p. 81), as divergent evolutionary histories might determine the distribution of (unnamed) alleles that produce “ethnocentrism” (p. 82).

In one example, GC considers whether the white contempt for Native American treaty rights documented in a book by Lawrence Bobo and Mia Tuan (2006) could have a genetic component: “We suggest the effect in question to be a partially heritable tendency for ethnic nepotism or in-group favoritism centered on a more basic tendency to distrust nonkin and that this tendency could be a cause of both white attitudes about Indians and white attitudes about treaty rights” (p. 80). This appropriates Risch and Rosenberg’s epidemiology research on population structure to establish not only a biological “white race” but also a biological “white kinship” that might partially explain experiences of genocide, colonialism, and treaty abrogation. Shiao et al.’s final assessment that the “distrust of specific groups” documented by Bobo and Tuan “has a qualitatively more social character” that is not fully determined by “clinal class differences in the frequency of ethnocentrism” (p. 81) is a meaningless disclaimer, since there is no empirical evidence to resolve the claim one way or the other. It is akin to developing a theoretical model to explain the effect of wind shears on the flight patterns of unicorns and then determining that they may have no effect.

Similarly, Shiao et al. (2012) urge scholars to consider some role for “biosocial causation” with regard to the “phenomena of discrimination, inequities in neighborhood resources, ethnic solidarity, and group stereotyping” (p. 83). Urban sociologists, for example, might consider the ways in which a partially heritable “tendency for ethnocentrism may moderate how immigrant families respond to their institutional reception and network resources and also how nonblack merchants respond to regular contact with black customers” (p. 83). That is, GC considers whether genetics might partially explain the social, economic, and political hierarchies within housing and labor markets documented and analyzed in these studies.

Again, it is important to remember that the clinal clusters that serve as the basis of this theory are estimations of variability created by an algorithm. They do not represent any molecular entity or biological characteristic. In this theory, however, they are given metaphysical powers to shape complex human behaviors.

An inherited predisposition toward “ethnocentrism” has no grounding in any genetics research cited by Shiao et al. (2012). (It is admittedly, however, a popular folk theory.) Across human history, the vast majority of episodes of political conflict and violence have taken place within populations regarded as “races” by Shiao et al. In addition, if GC’s theory of a heritable basis for ethnocentrism can be applied to the study of racial and ethnic hierarchy within the United States, should scholars similarly seek a “partial” genetic explanation for the transatlantic slave trade? The Holocaust? Anti-miscegenation and Jim Crow laws? How would Shiao et al. distinguish these cases from the ones they examine?

And if Shiao et al. (2012) believe that statistically discerned population clusters serve as a defensible basis for explaining variance in social and psychological outcomes, then an unbiased and “scientific” inquiry would view all potential differences to be equally plausible. One could ask readers to consider, for example, the relationship between documented allele clusters and variations in folk dancing ability or gardening talents or excellent

penmanship. After discerning an empirically verifiable clinal cluster of Northern Italians, one could propose that scholars should investigate the genetic basis for the superior preparation of polenta. In the absence of any actual evidence, variations in these behaviors could also plausibly be linked to variations discerned by population inference analysis. Why would explanations for white racial domination or black subordination (the issues addressed in the studies reviewed by GC) lend themselves to speculative genetic theorization but not these other cases, which could be explained through the same logic?

ON BIOLOGICAL RACISM AND THE ESSENTIAL CHARACTERISTICS OF GC

Shiao et al. (2012) claim there is no “essential characteristic” of their findings that might be complicit with biological racism and that any such interpretation would be rooted in a mistaken “social interpretation” of these findings. Setting aside for the moment the question of whether “social perceptions” and “essential characteristics” are so easily distinguishable and deferential to authorial intent, we can still consider the extent to which the arguments in GC converge with major currents of racial determinism and white supremacy.

Let’s review some of the core claims of the GC article:

1. Current genetics research confirms that the categories invented by eighteenth-century race scientists (e.g., “Caucasian”) to describe human variation are in fact reflective of some innate group-based biological differences or variances (pp. 68–69).
2. These variances may explain differences in social and psychological behavior and the distribution of personality and cognitive characteristics across groups (pp. 80–84).
3. Many decades of scientific research that has discredited the biological concept of race has actually been based on faulty logic and outdated science (pp. 69–74).
4. White racial domination and black exclusion may at least partially be determined by genetic differences or variation (pp. 80–84).
5. Speculation alone (placeholder theories) provides an adequate scientific grounding for making claims about group-based racial difference and domination (p. 77).

As previously discussed, these claims, taken directly from GC, do not come from any body of contemporary genetics research. Indeed, the authors of the studies (Risch and Rosenberg) cited by GC state explicitly that the allele variance and clustering patterns they document do not warrant a biological conceptualization of race, nor do they claim that such variance might shape social behavior.

In a recent interview, Neil Risch states plainly that assertions about genetic explanations for group-based variance in social outcomes without underlying genetic data have no scientific basis. He explains, “in my view, at this point, any comment about the etiology of group differences, for ‘intelligence’ or anything else, in the absence of specific identified genes (or environmental factors, for that matter), is speculation” (Coates 2013).

Tracing the true origins of such speculation sheds important light on evaluating Shiao et al.’s (2012) insistence that their article is in no way shaped by or complicit with currents of biological racism.

The authors of GC derive their hypothesis that estimations of clinal clusters might help to explain social outcomes from two non-geneticists: the philosopher Neven Sesardic and a physicist named Stephen Hsu. And because there is no scientific or evidentiary basis for these claims, the political orientation of their respective work matters deeply. Hsu and

Sesardic's ideological assumptions and goals are critical to understand because they also constitute the framework of the GC article.

GC's claim that clinal clusters prove a biological basis of race is taken directly from Hsu's (2007) blog posting asserting a "scientific basis for race." The interpretation of the Rosenberg and Risch studies, the notion of clinal classes defined by distribution in the frequency of particular gene variants, and the equivalence of clinal clusters to race are all adopted from Hsu's 2007 post and are cited by GC as such in both the footnotes and the acknowledgements.

Hsu has a background in theoretical physics but no formal training or publication record in genetics or the sociology of race. As his extensive blog details though, he has a long-standing interest in exploring the genetic basis of social inequalities, including racial inequalities.⁹ He currently leads a privately funded research investigation searching for the genetic and heritable basis of intelligence, regarded as the holy grail of the early twentieth-century eugenics movement (Graves 2001; Stern 2005).¹⁰ Hsu has written enthusiastically about government-supported genetic selection of human embryos in order to generate "increased economic output" and to "decrease welfare and criminality rates" among the general population.¹¹

And it is Hsu, rather than Risch or Rosenberg, who argues that clinal "clusters (race)" might form the basis for differences in "measurable characteristics, such as cognitive abilities, personality, athletic prowess, etc." Hsu characterizes the social constructivist position on race as "the PC mantra" and "wishful thinking" and argues that the lessons of "animal breeding" affirm the possibility that "differential natural selection" has produced "group differences in deep characteristics." Hsu concludes the 2007 post cited by GC by advising us to avoid the "the scientifically unsupported claim that we are all equal."¹²

In addition to Hsu, GC draws heavily on philosopher Neven Sesardic's (2010) article "Race: A Social Destruction of a Biological Concept." Like Hsu, Sesardic uses the work of Risch and Rosenberg to assert that statistically discerned allele clusters demonstrate the biological basis of race. GC restates Sesardic's argument that scientists who claim to have disproven the biological basis of race, such as evolutionary biologists Richard Lewontin and Stephen Gould, have relied on overly restrictive criteria of racial difference. If scholars would agree to abandon their demands for evidence of absolute categorical distinctions and instead accept that statistically determined allele clusters also constitute racial difference, then the biological concept of race would be self-evident. GC reprints a figure from the Sesardic article to substantiate this claim and approvingly cites Sesardic's use of the term *subspecies* to describe human variation on the basis of "race" (p. 70).

A cursory review of Sesardic's (2010) article makes clear that Sesardic advances this argument in large part to recover and legitimate the work of scholars affiliated with the Pioneer Fund, a group founded by American Nazis and Eugenicians in 1937 that has supported some of the most infamous white supremacist research in the twentieth century: studies by Richard Herrnstein and Charles Murray, Arthur Jensen, William Shockley, Linda Gottfredson, and Phillipe Rushton (Tucker 2002). These theorists have argued across a range of studies that black people, on average, are cognitively inferior to white people. Sesardic states clearly that these claims should be given greater consideration (Tucker 2002; Zeskind 2009). Sesardic concludes his article by contending that scholars must consider the "psychological differences" that might result from biologically differentiated racial groups and specifically urges investigations into group differences in criminality, violence, intelligence, and "economic backwardness" (pp. 158–59). Sesardic develops the "genomic challenge" thesis in order to recover and legitimate intellectual claims for white supremacy.

Thus, the two theorists who have most significantly shaped GC's framework are not geneticists but social theorists who are quite explicit about their use of a biological concept

of race to explain racial hierarchy. Both Hsu and Sesardic deploy population genetics research to explain variance in the same domains long fetishized by white supremacists: intelligence, athletic ability, criminality, and violence. And I would suggest here that Hsu and Sesardic are not asking readers to consider the possibility of the inherent cognitive superiority of African-descended people or a genetic predilection toward violence and genocide on the part of populations descending from Northern Europe. The race concept emerged in the seventeenth century as an effort to link human variation to explanations for hierarchy and inequality (Bernasconi and Lott 2000; Smedley 1993). Of the infinite taxonomies that could be used to describe this variation, the race concept developed explicitly to situate the groups it identified within a colonial worldview. As the cases of Hsu and Sesardic make clear, the invocation of race as a scientific category has always been linked to the production and naturalization of a social hierarchy. The very substance and rationale of their inquiry is only cognizable within this implicit framework of white supremacy. Absent this framework to legitimate the questions they pose and the possible answers they conjure, they are simply trading in junk social science with no defensible methodological basis or socially relevant implications.

Finally, the implicit argument in GC that unnamed evolutionary processes and mechanisms may have resulted in the unequal distribution of personality, cognitive, and other characteristics between racialized groups rehearses many of the same claims made by early to mid-twentieth-century anthropologists of race, such as Carleton Coon—claims that have long been discredited. Coon's body of work, invoked by segregationists in the 1960s to defend Jim Crow segregation, defined races as "breeding populations" and embraced the idea of geographically defined human subspecies differentiated in part "by molecular differences in their regulatory genes" (p. 9). Shiao et al.'s theory of "genetic watersheds" and clinal classes bears important similarities to Coon's conception of "breeding populations." Both imagine geographically isolated populations developing higher frequencies of particular genetic traits that are identifiable by "race." GC's argument that clinal classes might shape racialized outcomes relies on a very similar interpretation of human evolutionary history.

Thus, in many ways GC is better understood as a contribution toward theories of biological racial determinism rather than as a modification of social constructionism. In positing that genetically or biologically determined human subspecies (or other biologically determined "classes") are the basis or foundation for existing social hierarchies (even if those hierarchies are also shaped by social and environmental forces), the article is in dialogue with the theoretical positions of Hsu, Sesardic, Coon, and many of the researchers supported by the Pioneer Fund. Social constructionist accounts of race are premised on more than the proposition that the race concept does not represent naturally occurring categories or classes of human variation. Constructionist theory also argues that race itself is an artifact of power, a historical legacy of colonial expansion, slavery, and mass violence that has shaped much of the past 500 years of world history. In these accounts, race does not form the basis for domination; domination forms the basis for race. As the American Anthropological Association's 1998 statement put it, "present-day inequalities between so-called 'racial' groups are not consequences of their biological inheritance but products of historical and contemporary social, economic, educational, and political circumstances" (American Anthropological Association 2003).

PROSAIC WHITE SUPREMACY AND JUNK SOCIAL SCIENCE

Speculative racial science has been with us for more than 200 years. Its terminology, objects of study, and scientific methods have varied, but at the core, it has always been animated by

the same ambition: to analyze, categorize, and differentiate human bodies in order to legitimate group-based social and political hierarchies (Ewen and Ewen 2006). To be sure, GC's authors employ qualifiers and delimiters that crude racial determinists would not use: ethnic nepotism is *partly* heritable; natural explanations are *bounded*; genetic characteristics are *mediated* by social factors; allele cluster effects are *plausible*. But as Dorothy Roberts (2011) has argued, studies such as GC presume that race is rooted in a biological "reality" that then is acted upon by "constructed" social forces. The logical conclusion of GC's speculations is that group-based differences in social standing and power can be partly explained by differences in the body: it suggests a hereditary explanation for racial inequality.

If the underlying concern did not turn on whether hereditary differences might explain contemporary racial inequalities, then we would be left with a cartoonish inquiry in which social scientists distort and misrepresent findings of biomedical and epidemiological researchers, ignore explicit warnings within those studies not to apply their findings to other domains, ignore a large body of literature critical of their foundational assumptions, and then speculate on all the effects that might be possible if actual evidence existed.

Under what conditions might such an endeavor be considered legitimate social science and theory building? If the "clinal class as one explanatory input" theory were applied to nearly any other area of observed social variation in the absence of any empirical evidence, it could not be taken seriously. Scholarly standards requiring a clear and balanced explication of the relevant literature, a sound explanatory framework, and appropriate uses of empirical findings would render such claims unrecognizable.

But in a context in which an unnamed and often prosaic white supremacy structures the kinds of research questions that can be legitimately asked about human variation and hierarchy, it still can be perceived as acceptable to trade in junk social science in the service of racial speculation. To be sure, a vigorous debate is now underway over the theoretical and methodological role that evolving genetics research will play in explaining outcomes of interest to social scientists. While many scholars remain critical of these approaches (Charney 2008; Charney and English 2012), even the most steadfast advocates of incorporating genetics research into social science paradigms, such as sociologist Guang Guo (Guo 2008; Guo and Adkins 2008) and political scientists Peter Hatemi and Rose McDermott (Hatemi and McDermott 2011, 2012), take care to link their claims to clear interpretations of published genetics and neurobiological research. Articles such as GC, which misrepresent the findings of such research in service of far-fetched claims, ultimately undermine this effort. The rapid pace of genomics research does not require social scientists to abandon common sense and sound scholarly judgment in adjudicating specific claims, especially those that counsel colleagues to revise entire theoretical paradigms in the absence of any empirical evidence. And it certainly does not require us to draw from eighteenth-century theories of race determinism to explain and interpret the complexities of our contemporary social world.

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NOTES

1. As Ann Morning (2011) has recently documented, however, there is considerable variation in the ways the race concept is used in undergraduate biology and anthropology classes, and the popular or folk concept of race often draws on biological or genetic distinctions.

2. The implications for the arguments of “The Genomic Challenge to the Social Construction of Race” (or GC) also extend beyond the academy. Almost immediately after GC’s publication, the article was uploaded to two white supremacist websites. It appeared as “recommended reading” on the Occidentalist, a white supremacist website primarily devoted to race, genetics, and measures of intelligence, and to the official “study library” for Stormfront, one of the largest and most widely followed white supremacist and neo-Nazi websites in the world (official slogan: “White Pride World Wide”). The article appears to have been uploaded on September 12, 2012, by an unidentified poster under the title “Biodiversity” on the website’s stormchan.org “study library” at <http://stormchan.org/study/res/292.html> (accessed August 19, 2014). On contemporary white supremacists movements, see Zeskind (2009). To be sure, we cannot make any claims about the intent of the individuals who reposted the GC article to white supremacist websites, and GC’s authors do not bear culpability for their appearance. The circulation of the GC piece on these websites simply reveals the heightened stakes in debates over the scientific basis of racial difference and hierarchy.
3. See Duster (2003) regarding the notion of contemporary genomics research opening a “backdoor” to deterministic or eugenicist thought.
4. This claim is problematic on multiple grounds. It generalizes the contested findings of a small group of studies to “the vast majority of contemporary persons,” ignores the role of scientists themselves in ordering racial and ethnic taxonomies (Hunt and Megyesi 2008), and presumes that a United States–specific system of racial and ethnic descriptors applies globally (Gibbon, Santos, and Sans 2011).
5. The other three references cited in support of this statement (Abraham 2006; Leroi 2005; Wade 2006) are to newspaper columns published six or more years ago, so this analysis will be limited to the genetics research alone. Elsewhere the paper cites two other studies in support of its claims about the biological basis of race: an unpublished conference paper (Guo et al. 2010) and another paper involving Risch (Tang et al. 2005).
6. Across the entire article, they cite in a single paragraph studies that express concern over a new “biological determinism” in genetics research, which they characterize as “effective response to the ‘less nurture’ critique of the proponents” but which “fail to provide a reformulation of racial constructionism that would be consistent with the new advances” (p. 68).
7. GC’s authors argue that while population clusters may indeed be inferred at various scales, those scales are hierarchically related or nested, meaning that under the category “African” there exist various subpopulations that all empirically “belong” to the master category “African.” They use the analogy of a watershed in which a series of riparian elements all drain into a broader watershed. But no given subpopulation (i.e., Ethiopian) “belongs” exclusively to the master category “African” in the same way that all streams and rivers in the Mississippi Basin exclusively belong to that watershed. In addition, as previously stated, population clusters are not physical entities, they are representations produced by an algorithm. The analogy is false.
8. Bolnick (2008) also notes that Rosenberg’s (2005) paper found multiple population clusters and that clusters based on continental racial classifications were not necessarily the most probable or natural clustering, a finding widely ignored when news media reported the results.
9. Again, Hsu has no publication record in this area, so his arguments for a scientific basis of race and genetic determinants of inequalities are all found on his blog, <http://infoproc.blogspot.com/search/label/genetics> (accessed August 19, 2014).
10. Hsu’s assumptions about the hereditary basis of intelligence converge strikingly with those espoused by eugenics founder Sir Francis Galton in his 1882 work *Hereditary Genius: An Inquiry into Its Laws and Consequences*.
11. This quotation is from a comment authored by Hsu on his blog from an entry dated July 12, 2012 titled “Whole genome sequence from 10 to 20 human cells” at <http://infoproc.blogspot.com/2012/07/whole-genome-sequence-from-10-to-20.html> (accessed August 19, 2014).
12. Hsu does explain that human rights should be respected in spite of these inequalities in abilities and genetics, suggesting that Jefferson’s assertion that “all men are created equal” in the Declaration of Independence deserved some qualification.

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