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They Say It's in the Genes: Decoding Racial Ideology in Genomics

Johnny E. Williams[1]

Abstract

Science is delving into genetics more deeply and thoroughly than ever before, and in the process, scientists are uncovering new layers of "truth" about the essence of humanity and human disease. But in a social world colored by inequalities and value judgments that place some members of humanity above others, to what degree is genome science codifying ideology in our very genes? Thirty secondary interviews with genome researchers from various subfields are analyzed to determine the extent to which the ideology of "race" enters their discourse on genome variation. Findings suggest that unexamined and unrecognized racial thinking is an integral part of genetic researchers' interpretations and understandings of genetic variation.

Keywords

genetics, race, culture

Science is delving into genetics more deeply and thoroughly than ever before, and in the process, scientists are uncovering new layers of "truth" about the essence of humanity and human disease. But in a social world colored by inequalities and value judgments that place some members of humanity above others, to what degree is genome[1] science codifying racial ideology in our

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very genes? Reinscribing racial ideology as group biological differences will have severe repercussions for healthcare and sociopolitical relations. Given these potential outcomes, I investigate how racial thought informs genome researchers' understanding of human genetic variation.

Although social science researchers are recognizing increasingly that scientific activity is interwoven with meanings, beliefs, and power, critical inquiry into the implicit expectations, assumptions, and values informing science is only now consistently starting to emerge (Duster 2003; Fullwiley 2008; Reardon 2005). However, this new emphasis on studying how social, cultural, and historical processes stylize science's descriptions of reality tends to focus on how science shapes the social realm without investigating the effect of sociocultural conditioning on science (Restivo 1994, 21). There are a few exceptions. Fullwiley (2007b, 2008) examines how commonsense racial ways of knowing interpenetrate genome scientific practices to perpetuate ideas about racial genetic homogeneity and intergroup distinction. Montoya's (2007) work examining how sociohistorical meanings about genetic purity and hybridity inform scientists' thinking regarding the genetic etiology of diabetes among Mexicans provides insight about how social conditioning shapes genome researchers' interpretations of genetic information. Moreover, Nelson's (2008) research demonstrating how users of genetic genealogy tests alter the uncertainty of genetic data to fit their socially constructed conception of reality also denote the importance of culture in configuring researchers' understanding of genetics. I seek to contribute to this emerging literature by examining how researchers' understanding of genome variation intersects with society and culture.

In the social sciences, "race"[2] is commonly defined as an ideology composed of beliefs, ideas, and assumptions held on faith alone and generally unrelated to empirical facts about human differences (Smedley 2007, 18). For social scientists, the "race" concept usually corresponds to ideological and social values within cultures about human differences. These values justify social privileges and are predicated upon the assumed inherent biological superiority of one group over another. While the natural sciences recognize the existence of physical differences between groups, the concept of "race" is rarely used to describe this differentiation, but when it is, it is employed generally as a synonym for subspecies (Templeton 2002, 34). The traditional meaning of a subspecies is that of a sharply genetically differentiated geographical group within a species (Templeton 1999, 632). As Templeton (1999) notes, this definition is problematic in that many traits and their underlying variation reveal diverse patterns of geographical differences within and between human groups. Thus, the idea that human subspecies exist as sharply genetic

differentiated geographical groups is implausible given the tremendous variation and relatedness between social groups (Templeton 2002, 34). Most contemporary evolutionary biologists and population geneticists (Gould 1981; Jorde and Wooding 2004; Templeton 1999) contend human "races" have no biological validity under the definition of subspecies (Long and Kittles 2003, 795). Despite this fact, efforts to establish the genetic basis of "race" persist in genome science.

For the purposes of my analysis, *racialized culture* refers to both content (shared racial meanings, beliefs, values, symbols, habits, and customs) and the interpretive process that transforms content into understandings of social groups on the basis of skin color and other physical characteristics. My use of the *racialized culture* concept attempts to convey how raced cultures' norms, symbols, and practices are used to construct biological differences between groups, revealing how changing sociohistorical circumstances shape the construction of "race." Similar to Bourdieu's (1977) *habitus*, which maintains that we interpret the world using preexisting social meanings or scripts, I maintain that racialized culture serves as a conceptual reservoir from which genome researchers draw to construct creative meanings about biological differences. As Marx observed, "men make their own history, but they do not make it just as they please; they do not make it under circumstances chosen by themselves, but under circumstances directly found, given, and transmitted from the past (Tucker 1978, 595).

In what follows, I provide a brief overview of various promising theories about how racial processes intersect with genome variation research. I then examine how genome researchers' embeddedness in racial contexts shapes their interpretations and understandings of human genetic variation. I conclude with a brief summary of the mediating effects of racialized culture on researchers' understandings of human genetic variation.

Theorizing Culture in Genome Science

Research exploring interactions between genome science and cultural processes generally use the theory of social constructionism and its two variants: feminist standpoint theory and coproductionism. Rooted in the work of Mead (1934) and, more recently, the writings of scholars like Berger and Luckman (1967) and Pinch and Bijker (1984), social constructionism holds that the creation of knowledge is relational in the sense that we cannot examine reality—objectively and scientifically—without interpreting it through our own prefabricated, culturally inherited, ubiquitous frames of reference (Burr 2003; Franklin 2006). The fact that biological science is not independent of social

processes is apparent in the wide-ranging debate among human genetic variation researchers about the proper meaning and use of "race" in their work (Burchard et al. 2003; Cooper, Kaufman, and Ward 2003; Long and Kittles 2003; Risch et al. 2002). This scholarly debate suggests there are multiple ways to define "race" and its meanings scientifically, and that these meanings are formulated using a variety of social scripts about group differences. These conceptual processes are evident even though genome researchers who use "race" as a proxy to infer genetic variation (Burchard et al. 2003; Risch et al. 2002; Wilson et al. 2001) acknowledge "race" is a sociohistorical construct transmuted into biology. Their use of "race" within racialized social contexts to infer genetic variation unavoidably perpetuates the myth that "genetic diseases" are racially distinct, instead of clarifying why genetic risk for diseases varies unevenly among and within various groups (Lancaster 2005). Given this deleterious outcome, why do some genome researchers continue to use the "race" concept as a proxy for biodiversity among social groups? Social constructionists contend the answer lies partly in their failure to recognize that their means for conceptualizing genetic diversity is a result of their interaction with it. In other words their embeddedness in specific racial histories and cultural experiences influences how they constitute genome knowledge (Franklin 2006, 169).

Problems arising from unexamined racial assumptions in genomics are obvious in recent drug metabolism research by Evans and Relling (1999) and Xie and his colleagues (2001). Despite the fact that previous research (Brace 1995; Livingstone 1962) overwhelmingly suggests that "race" is a social creation as opposed to a biological result, Evans and Relling (1999) and Xie et al. (2001) argue that biological racial distinctions contribute to interindividual variability in drug metabolism. Their preoccupation with empirically substantiating genetic racial differences reflects the fact that racial thought influenced how they collected and interpreted data relating to drug metabolism variation (Graves and Rose 2006, 484). This is exactly what Duana Fullwiley (2007b) documents in her research exposing how taken-for-granted laboratory practices (e.g., recruiting, organizing, storing, and racial categorization of human DNA) among scientists investigating drug response differences preserve ideas about racial homogeneity and intergroup distinction. According to Fullwiley (2007b, 22), scientists engage in commonsensical racialized laboratory practices without considering how these procedures shape their thinking about genetics. Because these racialized laboratory practices often go unexamined and unrecognized, genome research is often structured in ways to suggest that disease and drug toxicity variations are the result of genetic racial differences (Fullwiley 2007b). By not problematizing racial ideology in their thinking

and practices, many genome scientists do not consider how their research comes to reflect racial biases and priorities. Social constructionism offers an important theoretical means for unpacking how racialized ways of knowing intermix with genome knowledge.

Although social constructionism is useful in understanding the dynamic between racialized culture and genome knowledge production, some critics charge its premise that knowledge is fluid, relative, and dependent on sociohistorical forces is problematic because social influences are evident only in the framing of scientific questions, not in the answers and the "contents" of science. However, social constructionists such as Ernst von Glasersfeld (1996) insist that though human genetic diversity objectively *exists*, how genetic differences are interpreted *is mediated* through a socially created discourse that tends to substitute itself for the facts it is supposed to merely describe or reflect (van Rinsum, Henk, and Tangwa 2004, 1038). Like social constructionists, I uncover the ways in which human subjectivity (i.e., racialized social contexts, ideas, vocabularies, and distinctions) imposed on genome variation reality become objective fact.

Feminist standpoint theory, which developed out of social constructionism, contends that since our social relations with others shape our conception of reality, knowledge is not universal. Instead, it is partial and situationally constructed by our various social structural locations (i.e., racial, ethnic, class, gender, etc.). Because different social structural locations vary by power and yield a variety of perspectives about biological reality, standpoint theorists maintain that although all genome knowledge is structurally situated, not all social positions are equally good locations from which to observe and explain how human genetic processes work. In other words, members of racially defined groups with power have more interests in excluding questions about genetic diversity that might challenge their privileged positions than do members of subordinate groups. This predilection is evident among "white" feminist critiques of science that tend to routinely overlook science's role in making "race" (Collins 1999). To counter the dominant racial group's hierarchical interests, proponents of standpoint theory make certain that "the class, race, culture and gender assumptions, beliefs and behavior of the researcher [are] placed within the frame of [biological reality] s/he attempts to paint. . . . Thus the researcher appears . . . not as an invisible, anonymous voice of authority, but as a real, historical individual in concrete, specific desires and interests" (Harding 1987, 9).

Although standpoint theorizing can potentially illuminate how genome researchers' structural locations predispose them to generate distinct understandings of human genetic diversity that are more or less congruent with

society's racial conceptions of biological differences, much like social constructionism, scholars are concerned it conflates "facts" with values. Standpoint theorists (Collins 1999; Haraway 1988) take umbrage with this criticism because, as they practice it, standpoint theory does not reject "objective science" but rather seeks to expose how "objective science" is informed by social meanings (Collins 1999). Criticism, albeit not pertaining to relativism, is also levied by proponents such as Patricia Hill Collins (1999), who insists standpoint theory poorly addresses how marginalized groups' sites of counterdiscourse are themselves contested terrain where power differences between and among these groups influence how reality is perceived and interpreted. Standpoint theory's concern with dialogical relations between and among people in different social positions (i.e., class, "race," gender, sexuality, etc.) also incline it not to consider how subordinate groups' internalization of prevailing values and ways of knowing influence their thinking about reality. Such considerations in analyses of genome science may illuminate why many researchers, no matter their group membership, are oblivious to racial thinking in their interpretations of biological differences. Despite this shortcoming, standpoint theory is analytically useful for grasping how genome researchers' racial prejudices shape their genetic language and conceptual apparatus.

The coproductionism variant of social constructionism views genome science as neither a simple reflection of nature nor an epiphenomenon of social and political interests. Rather, coproduction theorists focus on understanding how knowledge about genome variation informs the social, and how the social in turn shapes understandings of genome reality. In short, rather than approaching genome knowledge production as being beyond social influences, coproductionists view it as a product of socialized interpreters and decoders whose understandings of genetics are culturally mediated.

Like its constructivist predecessors, critics see coproduction theory as a promoter of scientific relativism because of its notion that factual statements are fashioned by the social milieu individuals and groups inhabit. Coproduction theory proponents counter that their theorizing is not relative in the sense that social reality is not ontologically prior to natural reality, nor do social factors alone determine the workings of reality (Jasanoff 2004, 19). Rather coproductionism attempts to make science practitioners aware of the depth and complexity of the dynamic between science and culture. Consequently, coproduction proponents argue that their theorizing in no way implies the social world determines the "objective" knowledge of genome variation or vice versa; instead their theorizing highlights the importance of understanding genetic knowledge and society not as independent, free-standing phenomena but as interacting named constructs, each underwriting the other's existence (Jasanoff

2004, 17). Because coproduction theory maintains that our understanding of biological reality is sociohistorically constituted and predicated on established cultural and power considerations, it can help clarify the hierarchical social processes through which genome science acquires racial form and meaning.

An adequate examination of the interrelatedness of racialized culture and genetic variation knowledge requires we view genome scientists as socialized individuals possessing internalized racial notions about various social groups. Similar to constructionism and its variants, I argue it is impossible to comprehend the persistence of racial thinking in genome research without considering how socially constructed definitions and engagements mediate genome scientists' understandings of objective genetic difference.

Method

Social science generally uses two different techniques when examining the production of science: (1) reviewing journal articles, research protocols, or journals' policies about the collection and presentation of research and (2) analyzing how producers of scientific data—scientists themselves—comprehend reality (Ellison and Goodman 2006; Fullwiley 2007a, 2007b; McCann-Mortimer, Augoustinos, and LeCouteur 2004; Pinch and Bijker 1984). I use the latter technique to investigate the social dynamics at the intersection of genome variation knowledge and racialized culture drawing from interviews with genome researchers in monographs, journals (*Science*, *Nature Genetics*, *Nature, PLoS Genetics*, etc.), organizational archives (The Naked Scientists, Genetics and Public Policy Center, Post Genetics, Rediscovering Biology, Cold Springs Harbor Laboratories, and Gene Expression), and newspapers from 1996 to 2008. Within these secondary sources, I identified and collected 80 interviews with genome researchers from various genetic subfields (e.g., molecular biology, evolutionary biology, genetic epidemiology, pharmacogenetics, and neurogenetics). I was able to secure interviews with genome researchers from these secondary sources because they were published primarily as expert interviews, profile pieces, featured stories and articles announcing some genome variation finding. Since my analysis is driven by the need to evaluate genome researchers' understanding of genetic relatedness and "race," I identified 30 interviews within the 80 as dealing with this issue. These interviews are the data set because in some cases and in the context of discussing human genome variation, researchers' talk explicitly involved racial differences and/or obliquely referred to genetic differences as a synonym for "race." For this reason, I selected interviews in the data set not to ensure representativeness but for their rich discussion of the genetic basis of "race."

The interview data set includes one genetic epidemiologist, eight evolutionary biologists, eight pharmacogeneticists, three neurogeneticists, and ten molecular biologists. The interview respondents hailed primarily from North America (four Canadians and twenty-three Americans) and Europe (three English and one Swede). The interviews were conducted by medical anthropologists, medical doctors, geneticists, sociologists, and science and medical journalists who asked a wide range of open-ended questions regarding genetic differences among social groups. These include, What is the social impact of your work? Can you comment on a group of scientists to which you belong that regularly discuss human evolution? What can your research tell us about ideas of racial difference? How closely are modern humans genetically related? How genetically different are humans from each other? Why the obsession with difference? Do environmental and lifestyle choices influence gene expression? Do you worry about scientists racializing their data and conclusions? Interviews were conducted at respondents' laboratories or professional conferences.

While I did not personally conduct the interviews, the books, journals, newspapers, and organizational material from which they were gathered offer an accessible and efficient means to determine, in a preliminary way, how racialized culture influences some genome researchers' discourse and understanding of human genetic variation. While conducting my analysis I was mindful how my social position as a middle-aged African American, male social scientist might influence my examination of the data. For this reason, I attempted to bracket my biases during my analysis of racialized culture effect on genome variation researchers thinking to ensure I carefully and consistently reflected on how my location within the grid of racial power relations may affect my interpretation of the data. In this way, I sought to be thoughtful and forthright regarding any tensions that surface while collecting and analyzing the data.

Since my study is ethnographic in the sense that it investigates how racial "webs of meaning" inform genome researchers' definition of genetic reality, I use ethnographic content analysis to examine the interviews and verify theoretical relationships. Because ethnographic content analysis stresses the importance of reflexivity and interaction among the investigator, concepts, data collection and interpretation, I assume genome researchers' racial meanings regarding human genetic variation are reproduced in various modes of interview contexts, formats, and other nuanced social settings (Altheide 1987, 68). Ethnographic content analyses require reflexive movement between concept development, sampling, data collection, data coding, data analysis, and interpretation in order to uncover the patterned categories and theories emerging from genome scientists' talk regarding human genetic variation. Specifically, I examined interview data by looking at one feature of the interview in the context of what is understood

about other aspects of the dialogue, providing me the constant comparison necessary to perform an extensive grounded theoretical analysis.

I used grounded theory to systematize ethnographic content analyses via comparison with interview data and other meaningful information so I could discern and categorize the pattern meanings emerging from respondents' explanations of the biological basis of "race" (Glaser 2001; Strauss and Corbin 1998; Suddaby 2006). After reading and coding all the interviews, I compared the various categories and notes with those identified within and between interview data. This process enabled me to identify a list of core themes or categories emerging from the interviews. In this way, grounded theory helped to reveal the interrelationships among multifaceted dimensions of interviewees' interactions and provided me with a rich means for observing how racial meanings meld into their interpretations of biological reality.

I also examined interview data using discourse analysis to probe beneath the surface meanings of respondents' spoken words. Discourse analysis enabled me to observe respondents' "talk" about biological reality as a social activity. More precisely, discourse analysis enhanced my ability to evaluate respondents not as passive recipients of fixed racial meanings but as individuals who are ontologically and epistemologically preequipped with fluctuating meanings about human biological differences that are more or less congruent with society's racial conceptions of reality. In other words, although racial meanings influence how respondents describe and conceive human genetic variation, some interviewees possess the wherewithal to consider how their specific racial histories and cultural experiences shape their sense making. I used discourse analysis as a means to analyze respondents' talk about the biological basis of "race" in order to examine their conscious and unconscious racial assumptions regarding human genetic variation. Through constant comparison and coding of respondents' language, discourse analysis helped expose the underlying structures of belief and perception from which their genome variation knowledge emerges. In sum, applying ethnographic content analysis, grounded theory, and discourse analysis helped me render transparent how respondents' socialized racial ways of knowing seamlessly blend into their conceptualizations of human genome variation. Knowing exactly how this social process works, as Geertz (1973) argued, is crucial because it is through the flow of human interaction that cultural forms like genome science find articulation.

Human Genome Diversity in a Racialized Culture

The centrality of racial ideology in culture as a fundamental organizing principle and way of knowing ensures its deep infusion in knowledge systems like

genome science where folk assumptions about "race" regularly blend into the biological discourse of researchers like Nobel laureate geneticist James Watson. Watson made this observation during a London *Sunday Times Magazine* interview: "All our social policies are based on the fact that [Africans'] intelligence is the same as ours—whereas all the testing says not really. . . . [This] 'hot potato' [is going to be difficult to address] . . . but people who have to deal with black employees find [equality] is not true" (Hunt-Grubbe 2007, 24). Watson made a similar assertion in his book *Avoid Boring People*, in which he writes:

> The relative extent to which genetic factors determine human intellectual abilities will . . . soon become much better known. . . . As we find the human genes whose malfunctioning gives rise to . . . devastating developmental failures, we may well discover that sequence differences within many of them also lead to much of the observable variation in human IQs. A priori, there is no firm reason to anticipate that the intellectual capacities of people's geographically separated in evolution should prove to have evolved identically. (Watson 2007, 326)

Because "races" as subspecies do not exist, it is disingenuous for Watson to suggest there are racial differences in any specific gene, including traits for intelligence (Templeton 2002, 49). Despite this fact, some geneticists, like Watson, talk about their findings in terms of the genetics of *racial differences* rather than the genetics of *difference* [emphasis mine] (Fujimura, Duster, and Rajagopalan 2008). This discourse persists in genome research, particularly in studies suggesting people in geographical regions are genetically similar in a manner that corresponds roughly with "race." This respondent, like a number of scientists examining human geographical genetic differences, argues that though

> there are difficulties in where you put boundaries on the globe, . . . we know there are enough genetic differences between people from different parts of the world that you can classify people in groups that correspond to popular notions of race. (Wade 2007, F3)

Racialized thinking of this kind ignores research showing human hereditary features are not necessarily products of geographical isolation but independently inherited adaptations to local conditions or genetic intermixing via exogamy practices (Graves 2001, 2004, 147-48; Jorde and Wooding 2004). For instance, the higher lung capacities and red blood cell counts of continentally

separated Kenyans and Peruvians are physical trait adjustments to their living at a high altitude (Graves 2004, 17). Because human genome structures are complex products of exogamy and environment, our genetic composition is essentially alike. A point buttressed by this genome researcher who reportedly asserted in the *Globe and Mail*, genetic mutations or differences exist in all human groups. Therefore, "almost all the [genetic] differences you see in people in North America are differences you see in Africa, are differences you see in Asia. It's very rare to have something you see in [one place] but not someplace else" (Abraham 2005, F1). Although some genome researchers persist on arguing that continent-based groups possess drastically different genetic structures contributing to or detracting from intelligence, these claims are, in fact, scientifically inconclusive (Gould 1981; Graves 2004; Lewontin 1991; Marks 2005; Templeton 2002).

While interviewees understood that genetic distinction claims are scientifically suspect, many, such as this individual, maintained:

> Overall, we (as scientists) feel that there are tremendous benefits from studying "race-based medicine." We shouldn't be afraid of studying the medical implications of race or genetics. The information gathered from these types of studies may help further medicine in the long-run . . . [because it] is clear that there are significant biologic differences between racial groups. For example, there is a very well known risk factor for Alzheimer's Disease, the ApoE4 gene. Many people agree that if you carry this gene your chances of developing early-onset Alzheimer's is significantly increased. What is less discussed is that there is a racial modifier for Alzheimer's disease. (Johmar 2006, para 4, 10)

The implicit claim that genetic difference indicates a distinct "race" makes little sense in light of the well-known fact that having a gene for Alzheimer's disease does not necessarily mean a person will contract it, and having no ApoE4 marker does not mean a person is protected (Kolata 2006, A1). Only a few respondents expressed this understanding, such as the following interviewee who stated:

> There is only one race; the human race. There are [genetic] variants, and the variants we pay more attention to are visible to us. But in fact the variants that probably matter much more than whether your skin is black or your skin is white are variants that predispose you to . . . Alzheimer's disease. And these variants do not track by race [given the fact that the ApoE4 gene exist in all human groups]. (O'Brien 2000, para 21)

Since nuanced remarks of this sort were the exception rather than the rule, what explains the persistence of racial thinking among responding genome researchers? To address this question, it is necessary to examine respondents' talk and genetic conceptual frames as social creations that guide and delimit their genome thought.

The Central Dogma and Racial Thinking

Interview data suggest that heuristic strategies (i.e., educated guesses, intuitive judgments and commonsense) of the central dogma of molecular biology can stimulate racial thinking among some genome researchers. As an artificial schemata, the central dogma is both a representation of genetic knowledge and information-processing mechanism using taken-for-granted typification (mental structures) and cognitive shortcuts that promote efficiency at the expense of synoptic accuracy. In the schematic reasoning of the central dogma are the mechanisms by which racial culture shapes and bias human genome variation thought. Scientists rarely depict all the particular details when describing a mechanism schema like this central dogma diagram DNA → RNA → Protein. In this respect, the central dogma heuristic is a truncated abstract description of genetic sequencing that can be instantiated by filling it in with a more specific and complex description of sequencing. The central dogma, as a form of preliminary analysis, defines the benchmarks around which genetic variation and differences is understood using heuristic strategies that can encourage genome researchers to acquire and process information through their own likes, dislikes, and experiences (Berger and Luckman 1967; Bourdieu 1990). Although it is possible to overcome the bias the central dogma heuristic strategies facilitate through awareness and reflexivity, more often than not genome researchers ignore how racialized culture shapes their analyses. Hence, when genome researchers employing the central dogma in a more reflexive and critical way reveal that gene reproduction and phenotypes emerge from complex interacting causal processes (i.e., genes, environment, gene and environment, covariance of genes on environment, and chance), unreflexive users are inclined to minimize the fact that phenotypical (e.g., disease susceptibility and drug metabolism) differences are irreducibly complex phenomena. This inclination is discernible in the interviewee's remarks below:

> I'm still learning so much about population genetics and how variation differs between groups—but I feel as though there are ethnic specific SNPs.[3] Because it seems as though people—when people do these large scale genome screens, they see these frequencies in the groups. One SNP

> will only pop up in one group, and another SNP will pop up only in another group. So I think that there's some genetic basis for ethnicity or race. In terms of defining race based on SNPs or genetic variation, I don't think we know enough yet to do that. But from what I've seen, I do think that there are genetic differences. (Fullwiley 2007b, 18)

Another genome researcher proffered a similar response in a conversation with the *New York Times*:

> We may believe that most differences between races are superficial, but the differences are there, and they are informative about the origins and migrations of our species. To do my work, I have to get genetic data from different parts of the world, and look at differences within groups and between groups, so it helps to have labels for groups. (Angier 2000, D1)

The researcher's explanation suggests he is unaware that labels are overlaid with social meaning that shapes his understanding of human genetic variation and dismissive of evidence suggesting genetic variation is continuous in that there are uninterrupted gradients in allele frequency among groups. The respondent's belief that biological "races" correlate to continents leads him to falsely assume that racially sampling human genetic variation at widely separate points along a geographical continuum adequately represents the spectrum of human diversity (Graves and Rose 2006, 488). Because racial labels are not objective but infused with racial understanding, the respondent downplays the significance of other intuitive central dogma analytical and conceptual avenues for exploring trait variation while highlighting explanations suggesting phenotypical difference signifies racial genetic distinction.

Because many respondents are unreflective about how commonsense racialized notions pervade central dogma schemata, they interpret the 0.5% difference between human genomes to argue that "race" is a biological concept. Respondents maintained, like this individual, "that people do differ by that remaining 0.1% [*now believed to be .5%*] and people do cluster according to their ancestry" (Gitschier 2005, 5). Consequently, this respondent, like several others, declared: "The problem is not that we're so similar. The problem is that we're so different. Our genomes are about 3 billion DNA building blocks long. If we are even only 1% different, that's 30 million nucleotides. That's a huge number of differences" (The Naked Scientists 2004, para 10). The notion that a small percentage of difference indicates intergroup genetic distinction results largely from searching for differences and unexamined racial assumptions embedded in heuristic strategies of the central dogma.

This belief in and search for difference fuels racial thinking among some researchers, as social constructionism and its variants argue, because taken-for-granted racial ways of knowing shape how they perceive and understand genome variation.

Because respondents disregard how their social conceptions of "race" inform the central dogma's heuristic mechanism, most, like this researcher, insist that

> the recognition of race may improve medical care. Different races are prone to different diseases. . . . [G]eneticists have started searching for racial differences in the frequencies of genetic variants that cause diseases. They seem to be finding them. (Leroi 2005, 12)

Respondents "find" genetic differences among social groups as anthropologist Margaret Lock observed because "to assign someone to a 'race' based on skin color or other specific anatomical features attributes primary importance to those features, and forces all other variation into the background" (2001, 76). This proclivity is observable in the interview data, particularly among prostate cancer experts whose work is predicated upon finding genetic distinction among African Americans to explain their greater predisposition to developing the disease. Although there are numerous prostate cancer studies that include "race" as a variable or category in their analyses but find no genetic differences, these investigations are usually not reported in journals whereas those that do find differences are published and hyped (McDowell, Coleman, and Ferner 2006). As a result, the public and researchers reading these published works come to accept genetic differences between "races" as conventional wisdom even though the majority of research finds no group differences. Focusing on finding biological rather than external causations for genetic variation among social groups encourages genome cancer respondents like this one to downplay the significance of social determinants. Reuters reported him saying:

> We *believe* there is a genetic basis [for prostate cancer]. Of course, it is not all genetic. There are also going to be lifestyle and environmental factors as well. But our findings . . . suggest that *a large fraction* of the disparity between African Americans and other populations *[is] due to genetic variation in this region*. (Dunham 2007, para 12-13, emphasis mine)

This scientist's focus on "finding" what he insists are distinct genetic differences among groups serves to deemphasize how "it is not that different

biological processes underlie disease formation in different groups, but that different life experience activates physiological processes common to all, but less provoked in some" (Fausto-Sterling 2004, 26). The link between illness and social factors is also confirmed in a study by David and Collins Jr. (2007) in the *American Journal of Public Health*. Their study unambiguously found that the high preterm births and infant mortality rates among African American women are not the result of a "pre-term birth gene" but rather the stress of racism, poverty, and other social pressures impinging on African American females' bodies throughout their life cycle. Given this, "the consistent emphasis given to the genetic elements of racial contrasts distracts [respondents] from the more relevant issue of defining and intervening to prevent [the onset of diseases], which are likely to have a similar impact regardless of ethnic and racial background" (Cooper et al. 2005, 6). Because many interviewees' racialized genetic frames imply the environment plays only a negligible role in genetic variation, they tend to preserve the authority of essentialist/typological notions of "race" when using the central dogma heuristic. For example, a *Times* of London news story on metabolism differences reported that one scientist it interviewed for the article asserted:

> Some people are so-called fast acetylators and some slow acetylators—this becomes important in the breakdown of alcohol and explains why, for example, Japanese people feel the effects of alcohol more quickly. Medical treatment is not to do with skin color per se but with genetics. The reason race makes an impact in genetics, and what your liver, kidney and blood cells are doing to the drugs, and nothing to do with skin color. . . . However, to close one's eyes to color is tantamount to a neglect of clinical duties, [especially] if there is real evidence that because of your genetic inheritance you should be offered a certain drug. (Ahuja 2004, para 20)

This scientist's maladroit iteration regarding racial categorizing and skin color (a visible feature of "race") is also problematic in that he uses racial ideology to argue that members of social groups are physiologically similar yet different from one another, contradicting solid biological evidence (Fausto-Sterling 2004; Hunter 2005; Long and Kittles 2003) indicating that genetic variation is more common within groups than between them. Moreover, skin color is a range not a single color. For example, how well African Americans fare in the United States depends in part on the shade of their skin (Pager 2003). For this reason, many thousands of light-skinned African Americans choose to—and are able—to pass as European Americans. Is their genetic material

African American or European American? Is their disease potential the same? Based on the researcher's logic, similar disease potential is highly unlikely since his analysis of genetic material centers on the donor's appearance.

Because the heuristic strategies of the central dogma provide a means for socialized racial notions to insinuate themselves into reasoning about biological differences, some researchers, like this individual, contend that denying the biological basis of "race" "flies in the face of clinical reality, . . . physical appearance, including skin color, is now the only way to distinguish populations for study. You'd have to use a blindfold to keep physicians from paying attention to the obvious [racial] differences that may influence diagnosis and treatment" (Satel 2001, 50, 2002). Since respondents think and perceive genetic differences between racially defined groups as biologically racial and "obvious," it is common to find drug metabolism studies like Wood's (2001) *New Journal of Medicine* article arguing that *enalapril*, an angiotensin-converting enzyme (ACE) inhibitor used primarily to treat hypertension and congestive hearts, is ineffective in Africans and African Americans because their biological profiles contain high frequencies of the cytochrome P gene (CYP2D6), a poor drug metabolizing genetic marker. Wood's (2001) contention that enalapril is less effective in Africans and African Americans than in Europeans and European Americans because of their genetic uniqueness unraveled after Dries and associates (2002) published research in the *Journal of the American College of Cardiology* demonstrating enalapril's efficacy in both groups. The fact that differences in responses to medication do not map well to "race" is also apparent in Tate and Goldstein's (2004) examination of 22 drugs that purportly show racial differentiation in medical outcome, including the ACE inhibitors. Despite their deliberate attempt to find genetic racial differences in drug effects, only one weak association was found, thus suggesting that differences in drug response vary widely between and within socially defined groups (Graves and Rose 2006, 491). While many interviewees consistently observe such findings in the literature and their own research, their immersion in racialized ways of thinking lead them to misperceive groups and individuals from particular geographic regions as genetically distinct (Tate and Goldstein 2004; Wilson et al. 2001). According to one very observant respondent, some genome researchers' commitment to the geneticization of "race" is problematic because

> "Race" is of course a very loaded word. Biologists like to talk about "subspecies," and if they can, they like to give them special names. If you have a species of bird that comes in different varieties—if they're clear cut and distinct varieties—then you might want to give them different subspecies' names. Human races are distinct. There is no doubt about it. There is a

> huge amount of variation within each race, and distinct morphological differences between races. . . . Are these differences linked to big genetic differences? The answer is no. The majority of the genetic variation found in the human species is found within racial groups. Very little of that variation—.5% or less—is found between racial groups, and that variation is not such that blacks have one gene and whites have another gene, or something like that. Now what happens is you've got genes that appear at different frequencies in different racial groups. They may be at 20% frequency in one racial group; 60% frequency in another racial group—same genes, different frequency. So the differences then between racial groups have to do primarily with a rather small number of genes that are involved in skin color, hair color, and shape, some morphological differences perhaps facial differences. . . . The enormous majority of genes are essentially the same among different humans. So when we look, then, at these differences and say, oh, wow, you know, this person is one race or another race and then all our prejudices come to bear on this, and so on, we're being fooled by morphological differences that really have very little genetic basis. (Rediscovering Biology 2002, para 77-81)

Preoccupation with finding genetic racial rather than environmental or social determinants diverted interviewees' attention away from investigating what one respondent considered the primary question of genomics: "How did [a gene] come to be like *this* in [this human group] while it is like *that* in some other group, and yet this is basically the same gene or the same molecule found in all groups" (National Academy of Achievement 2001, para 44)? By disregarding the symmetry between elements of the central dogma and racialized social reality, social space is opened in genomics to construct essentialist elaborations (such as "race"-specific therapies) that come to reinforce each other and create the impression of evidence when in fact there is little or none (Kaufman 2006). In this sense, discounting research like Wilson and colleagues' (2001) demonstrating that genetic variation in disease susceptibility and drug response is better determined without knowledge of "race" or geographic origins is directly related to the degree respondents' racialized notions regarding genetic variation bond with heuristic strategies of the central dogma.

Objectivity and Racial Thinking

Interview data suggest that the idea of scientific *objectivity*, which specifies that it is possible to know nature independently of the observer's biases using the scientific method, can also promote racial thinking among researchers.

Many interviewees operated as if proclaiming objectivity shielded their genome investigations from the effects of social influences. Specifically, respondents like this scientist believed that although their research is value-free, "in today's political and ideological climate, science has taken a backseat to ideas, events, and priorities that threaten our way of life and the way we perform science" (Becker 2006, 14). Although most respondents acknowledged their work is susceptible to societal influences, they operated as if history and ideology are not intrinsic parts of their research process. This view is evident in this interviewee's response to questions regarding critics of his research:

> I would ask my critics to do two things. First, when considering scientific results to set questions of history, ideology and social justice aside. And second, to learn some genetics. Of course given my critics are overwhelmingly social scientists and historians, I hold no hope that these modest requests will be fulfilled. (Khan 2005, para 10)

The respondent continued:

> To understand how the [genetic] systems works, I have to step away and look at it dispassionately. I cannot look at it from right or wrong, moral perspective. . . . That does [not mean I am] no longer sensitive to all those important values, the values of equality and compassion. . . . The brain has an emotional center and it has a rational center. Pursuing science, at least at the execution part, has to do with the rational center, but what I do, which includes pursuing science, and what I like and don't like come from the emotional center. We don't know how that works, but it doesn't mean it ceases to have an important function. (Post Genetic 2007, para 44)

Similar reasoning is expressed in the United Kingdom's House of Lords 2000 *Science and Society* report which insists that "though science in itself is neutral, the application of science is not" (MacKellar 2007, para 5). Since many respondents believe the practice of science is beyond sociopolitical influence, they rarely considered how their racialized social situatedness informs their analysis of the genome.

Because structurally situated genome researchers are highly likely to confirm or see whatever their racialized social structures designate as reality in their work, they are disposed to naturalizing racial notions in their search for fundamental biological differences among human groups. This is readily apparent in commonly accepted evidence many respondents cited to advance

their view that genetic racial differences exist. A cursory examination of these sources' designs and analyses reveals that racial cognitive structures more so than evidence of distinct genetic variation informed how investigators designed their studies and interpreted genetic differences between groups (Van Rinsum, Henk, and Tangwa 2004). For example, Graves and Rose's (2006) analysis of Tang and colleagues' (2005) work suggesting that "race" correlates with genetic distinction among human groups revealed that "race" as a social construction and social fact[4] ensured their study found a relationship between the two. Specifically, Graves and Rose (2006) found that by taking representative samples from geographically distant groups (e.g., from one town in East Asia, Europe, and sub-Saharan Africa), Tang and colleagues (2005) guaranteed the genetic differences among the groups clustered along perceived racial divides. In contrast, Serre and Pääbo's (2004) study of global genetic variation accounted for their tendency to implicitly think and organize human groups racially by sampling from the entire range of groups within a geographical region. Their approach revealed that the best way to understand genetic variation in human groups is not by analyzing their distance from one another but their geographical nearness to each other. Groups closer to each other geographically are more likely to share the same genes while those further apart are more likely to share fewer genes. As this respondent explained, these racial biases

> are still far too much in the pattern of looking at diversity of different groups and the boundaries between them because of how we have sampled and how we have looked at things. I think, in a way, it is sad that people interested in population history have gone out and sampled according to preconceived ideas of what groups are there, be those linguistic groups or racial groups, and of course if you sample like that you come up with some differences between groups, and say yes, they are there. (Gitschier 2008, 3)

Despite this view, many respondents are averse to admitting there is no objectivity because such an admission requires them to acknowledge that

> [objective reality] acquires meaning only through human definition and engagement that include a variety of possible mediations and individual perceptions. Ideas, concepts, the theoretical enterprise itself, are all part of a historically-evolving socio-political process and, as such, resist simple determinist models. Methods and techniques of analysis can serve little function independent of their historical content and purpose. (Boggs 1976, 31)

Thus rather than concede that scientific objectivity is an illusion, some interviewees used the pretense of reasoned "objective investigation" to contend:

> Our society, given its sordid history on race related issues, is very confused about how to deal with racially and ethnically sensitive topics. *As a result, science and politics get mixed up when they relate to these topics. I personally feel, like many other scientists, that science should be separate from politics*. In particular, science should meet the same burden of proof regardless of what political implications it might have. But this may be too idealistic if not naïve. (Khan 2006b, para 6, emphasis mine)

In a subsequent interview, the respondent candidly stated that some scientists "start with a political agenda and fit the evidence to that." This political bias, he continued, "takes credibility away from an antiracist program I agree with. . . . If someday we discover that there are genetic differences in cognitive abilities, would that mean that racism is now justified"? (Balter 2006, 1873). These remarks suggest that respondents' objectivity claims allow them to convince themselves that their understandings of genetic processes exist apart from society, so it is not necessary to interrogate how racialized social processes mediate their genetic representations and explanations.

Scientists attempting to make colleagues aware of how objectivity claims obscures their ability to recognize social biases in their performance of science are often dismissed as "politically correct" pseudo-scientists whose own work is void of scientific rigor (Fausto-Sterling 2004, 10; Graves 2001, 2, 161). The labeling of critical reflective scientists as ideologues often occurs very subtly, as illustrated in this interviewee's explication of the debate between A.W.F. Edwards and Richard Lewontin on interpopulational genetic differences:

> Edwards and Lewontin are both right. Lewontin said that between populations, a fraction of the variance is very small in humans, and this is true, as it should be on the basis of present knowledge from archaeology and genetics alike, that the human species is very young. . . . Lewontin probably hoped, for political reasons, that it is TRIVIALLY small. . . . In essence, Edwards has objected that it is NOT trivially small, because it is enough for reconstructing the tree of human evolution, as we did, and he is obviously right. (Khan 2006a, para 16)

By framing Lewontin as "political," the interviewee implies that his genetic variation work is subjectively tainted while Edwards's research reflected the work of an unbiased, objective, truth-seeking scientist. This construction is

devious considering that interviewees' declarations of objectivity are in themselves political acts that imply their unwillingness to struggle with facts that do not fit into their preconceptions.

Professing objectivity, then, provides opportune support for a social dynamic among interviewees that discourages reflexive critique, and allows them to view themselves and their work as nonracists or even antiracist (Gannett 2004). This outlook is apparent in the following interviewee's exhortation regarding science and racism: "I don't think racism is a good thing. I think it's a very bad thing. That is my moral position. I don't see any justification in evolution either for or against racism. The study of evolution is not in the business of providing justification for anything" (Miele 2003, para 52). But interview data suggest genome science is doing exactly that which the interviewee claims it is not. Rather than searching for "objective truth," interviewees' conceptions of objectivity inclines them to "misrecognize" how racialized social relations regularly shape their interpretations of genetic differences (Bourdieu 2004).

Genetic Euphemisms for "Race" and Racial Thinking

While interviewees acknowledge "race" is a crude proxy for inferring genetic difference, their use of genetic terms like "population," "continental groups," "geography," "ancestry," and "admixture," whose meanings correspond to everyday conceptions of "race," can function to racialize understandings of genetic variance. The use of population as a pseudonym for "race" is apparent in this interviewee's reply to questions regarding his research objective:

> I hope that somewhere down the line in the future that we would be able to have a bank of drugs, each of which can be specifically targeted towards *particular population groups*. I think patients from *minority ethnic groups* would welcome wider representation of minorities across both biomedical research, clinical research, and therefore I think they would welcome a wider recognition on the basis of race, ethnicity. (Malik 2005, para 34, emphasis mine)

The respondent's equation of population to "race" is not inadvertent given biology's definition of population conceives of "race" as a distinct genetic breeding group (Gannett 2004). In other words, the population concept frames "races" as variable traits that describe group rather than individual genetic differences because it is used to examine the genetics of particular traits that pass between generations within a particular social group (Gannett 2004, 327).

Given this situation, interviewees using the population concept assume a person is *probably/likely/maybe* genetically a certain way because *most/many/some* individuals belonging to his or her group are that way (Gannett 2001, S490). This logic is observable in the following individual's remarks:

> Like many people, I reach for my inhaler in smoggy conditions. Genetics contributes to this susceptibility and researchers have focused on certain family enzymes that help detoxify everything from carcinogens to pharmaceuticals. There is a gene that is associated with the ability to degrade environmental toxins; however, nearly half of the Caucasian population lacks the gene. . . . [S]o perhaps that is why I am more susceptible to environmental toxins. (Venter 2007)

The juxtapositioning of terms like *Caucasian* and *population* suggest the speaker assumes social suppositions about "race" correspond to distinct biological differences. This practice encourages respondents to view genetic mutations as "belonging" exclusively to some socially defined racial groups and not others (Sankar and Cho 2002).

Language like "Asian genes," "African mutations," "African or European alleles," or "ancestral allele" also perpetuate thinking among interviewees intimating that *distinct types* of genetic racial differences exist. This is apparent in this individual's conversation regarding the genetic differences for skin color:

> Only one variation in SLC24A5 changes amino acid. To our delight, we noted that that variation is associated with extreme frequency difference between African and European populations. In the European HapMap population the ancestral allele has a frequency of zero, whereas both the African and two East Asian populations showed an ancestral allele frequency 97%-98%. (Glaser 2006, 1)

Like the previous respondent, this interviewee's use of "African and European" invokes biological accounts of racial differences in skin color that imply a small amount of genetic divergence indicates there are natural distinctions between socially defined racial groups. Because many interviewees were unreflective about how racial thinking shapes and constrains their genome knowledge, they were less likely to critically assess why "race" is an inadequate descriptor for genetic variation. As a result, most respondents, despite their claims to the contrary, thought racially when conceptualizing genetic variation between groups, as illustrated in the following quote:

> As scientists, we can . . . clarify that race is a complicated term that includes genetic components such as color and physical features (shapes of noses, mouths, and eyes, for example), nongenetic components such as nationality, language, clothes, and customs, and components that are both genetic and environmental components, such as diabetes in Pima Indians. It is clear that Pima Indians have a genetic predisposition to develop diabetes, but only developed the disease in response to a change in their diet. Rather than denying genetic differences, we as scientists can guide conversations about race so that they first presume tolerance, and then are more scientifically precise. (Glaser 2006, 3)

While the respondent acknowledged the importance of the gene–environment dynamics as a factor, he implicitly emphasizes the importance of genetic racial differences in explaining the Pimas' susceptibility to diabetes. This inference, as we have seen, is attributable to racial ideological assumptions embedded in molecular thinking suggesting that individuals are more likely to be susceptible to a disease if many members of their socially defined racial groups carry a similar *determinative* genetic trait.

As Bourdieu's (1977) habitus concept suggests, genome researchers' words are politicized even if they not aware of it because their words and interpretation of biological reality reflect the interest of their immediate social and historical environment. Because they are situated in racialized sociohistorical contexts, interviewees draw heavily from existing racial meanings to drive their interpretations of genetic data, no matter what categories they develop and use to avoid the "race" controversy (Hunt and Megyesi 2008). Although some respondents readily admit racial meanings are subsumed in genetic concepts like "population," they were less likely to consider how such terms racially simplify and exaggerate their interpretation of genetic variation.

Interview data revealed that admixture is another concept used to imply preceding genetic uniformity among socially defined racial groups (Jackson 2000, 160). The genetic admixture concept is generally used in genomics to measure the proportion of African, European, and Amerindian ancestral genetic makeup of individuals and its relationship to disease susceptibility. The genetic admixture approach has three underlying assumptions: first, genetic variation in groups differ markedly from one another due primarily to geographical barriers; second, that when individuals of genetically distinct groups engage in significant intergroup mating, differences are diminished; and third, that the "percent admixture" is medically important if individuals' inherited genes are known to play a role in particular medical conditions and if those genes are known to differ in socially defined racial groups (Fausto-Sterling 2004, 11-12).

In short, the genetic admixture concept suggests that ancestral biological determinants explain racial differences in disease expression. Although respondents using the genetic admixture approach argue it represents the genetic contribution of "race" and socioeconomic status, they tend to concentrate on the former in their research rather than the latter. Given this and the admixture concept's premise that socially defined racial groups are genetically *pure* even after generations of intergroup mating, several respondents, such as this one, maintained:

> I do know Mexico is trying to get a better understanding of how race and racial admixture influence disease expression. My group has proposed a study of this topic to the Mexican government and they have expressed some interest in pursuing it. This is because Latinos are a mixed population of Europeans, Native peoples and Africans. This study will help us gather important information about how disease is expressed in populations with diverse ancestries. My group has published a number of papers showing that disease risk varies depending on a person's racial background. For example, the more Native American you are, the milder the asthma. However, the more European you are, the more severe. (Johmar 2006, para 27)

Hence, rather than examine how group exposure differences to pollution and chemicals contribute to the severity of social groups' asthmatic responses, admixture discourse encouraged the respondent to recreate biological "races" through the naturalization of reaction differences.

Although most interviewees concede that received racial categories, concepts, and constructs are not useful starting points in genetic analyses, their ways of knowing are racialized and a part of common sense. Because of this, medical legal scholar Patricia King maintains that "in a racist society that incorporates beliefs about the inherent inferiority of [socially defined racial others] in contrast with the superior status of 'whites,' any attention to the question of differences that may exist is likely to be pursued in a manner that burdens rather than benefits [these groups]" (1992, 35).

Conclusion

Because very little scholarship exists exploring how racialized culture and genome knowledge interpenetrate, this paper investigated this dynamic through an explication of racial thought in genome researchers' understandings of human genetic variation. Although some scholarship (Duster 2003, 2005; Fullwiley 2007b, 2008; Reardon 2005) examines how racial meanings, beliefs, and values seep into genome diversity investigations, these works, unlike my

study, do not extensively consider how racialized social location and cultural experience socialize some genome researchers into particular ways of thinking about and conceptualizing human genetic variation. Even though "race" as a large, discrete natural division of the human species does not exist. What does exist is the cultural process of creating difference between people who are not really different from one another and making people who are similar different (Marks 2005, 16). This cultural process appears in the interview discourse of scientists evaluated in this study.

Contrary to the pervasive and persistent contention that genome science is above and beyond cultural influences, the evidence reviewed suggests that unexamined and unrecognized racial ways of knowing play an *integral* role in how responding genome scientists interpreted and understood human genetic variation. Specifically, my study suggests the larger racialized social context in which respondents are situated bears on their genome variation conceptual and discursive practices that govern how they think, act, and speak about biological reality. Moreover, my investigation found that elements of the central dogma of molecular biology heuristic, scientific objectivity, and genetic euphemisms for "race" are the primary means through which racial ways of knowing effortlessly blend into researchers' thinking about genetic variation thinking.

While my study suggests it is important for genome scientists to value reflexivity in order to confront racial biases in their research, self-awareness is not enough. Problematizing racial thinking in genome science can only be truly accomplished when it is embodied in the discipline so that it is practiced as a reflex (Bourdieu 2004). For it is only by unmasking the racial ideology encoded in genome variation research that the field can move forward with its efforts to understand the complex biosocial correlates of disease.

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1. Every organism, including humans, has a genome that contains all of the biological information needed to build and maintain a living example of that organism. The

biological information contained in a genome is encoded in its deoxyribonucleic acid (DNA) and is divided into discrete units called genes. Genes code for proteins that attach to the genome at the appropriate positions and switch on a series of reactions called gene expression.

2. "Race" is encased in quotations because it is a problematic cultural invention of arbitrary meanings applied to what appears as natural divisions within the human species. Its meaning has social/ideological value but little intrinsic relationship to biological diversity itself (Smedley 2007, 23).
3. Single nucleotide polymorphisms or SNPs (pronounced "snips") are DNA sequence variations that occur when a single nucleotide (A, T, C, or G) is altered. Many SNPs have no known effect on cell function, but some are believed to predispose people to disease or influence their response to a drug.
4. Social facts are manners of acting, thinking, and feeling external to the individual which are invested with a coercive power through which they exercise control over people. In other words, social facts are collective creations that use coercion to ensure individuals adhere to the standards and conventions of the group (Durkheim 1982).

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Bio

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