

# The Molecular Reinscription of Race: A Comment on “Genetic Bio-Ancestry and Social Construction of Racial Classification in Social Surveys in the Contemporary United States”

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**Abstract** In an article in the February 2014 issue of *Demography*, Guo et al. claimed that their research “establishes geographic genetic bio-ancestry as a component of racial classification” (p. 141). In doing so, they argued that their work has “a larger theoretical significance on identity studies” (p. 169) by providing racial classification categories with a concrete, “measurable,” and “logical” basis against which social construction should be analyzed. Instead, I argue that their main accomplishment is the “molecular reinscription of race” (Duster 2011:104). In this article, I review the existing critiques of this type of work.

**Keywords** Race · Bio-ancestry · Racial classification · Genetics · Social construction

## Introduction

In a recent article titled “Genetic Bio-Ancestry and Social Construction of Racial Classification in Social Surveys in the Contemporary United States,” Guo et al. (2014:142) aimed to “seek fresh insights into the understanding of racial classification in the contemporary United States by combining a social science perspective with recent advances in human molecular genetics.” Unfortunately, in combining these two “perspectives,” their work falls prey to many of the same problems plaguing recent attempts to incorporate developments from the new genetic enterprise into the study of race/ethnicity (Wailoo et al. 2012).

The authors began by countering past work that views race and ethnicity as categories “without an objective basis beyond self-report” (Guo et al. 2014:142). Instead, they argued that “a socially influenced definition of race need not preclude any logical basis for race/ethnic classifications” (Guo et al. 2014:142). For them, the

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“logical” basis comes in the form of genetic data collected in two different surveys of young adults (ROOM and AddHealth).

The authors used a panel of 186 autosomal markers (called ancestral informative markers (AIMs) selected from the HapMap project against which they compared the respondent samples to estimate each individual’s “biogeographical ancestry” (p. 150). Making the assumption that the individuals in the analysis originated from three ancestral populations, they found that individuals who self-classified as white, black, or non–South Asian were largely assigned by cluster analysis of their genetic data into “white,” “black,” and “non–South Asian” categories, respectively. The close matches led them to conclude that “the correspondence between bio-ancestry and self-reports for the three main racial groups is estimated with precision” (Guo et al. 2014:153). They then performed another cluster analysis to estimate the extent of genetic admixture (still making the assumption of three ancestral populations) and, taken together, concluded that their analysis “establishes geographic genetic bio-ancestry as a component of racial classification” (Guo et al. 2014:141).

As the authors themselves acknowledged, this is not new. Claims that an individual’s ancestry can be estimated from predetermined genetic markers and that these estimates of ancestral origins roughly correspond to existing racial groups have been made since the release of the HapMap data and related spin-offs (e.g. Human Genome Diversity Project (HGDP)) nearly a decade ago (Hamilton 2008; Rosenberg et al. 2002; Tang et al. 2005). More recently, efforts to quantify ancestral origins have increasingly become the purview of direct-to-consumer personal genomics companies that estimate ancestry for genealogical purposes or calculate individual risk profiles for a range of diseases and traits (Lee et al. 2009; Royal et al. 2010). However, the science and business of genetic ancestry testing has not been without its detractors (Bolnick et al. 2008). The main critiques center on the probabilistic nature of the results, which is often ignored and obscures the fact that human variation is not categorically distributed at the population level (Bolnick et al. 2008; Gabriel 2012). As a result, genetic ancestry testing is ultimately a statistical exercise, and “the emphasis of admixture estimation on differences over similarities can be misleading about the overall genetic structure of the human species” (Royal et al. 2010:667).

Guo et al. briefly acknowledged the existing critiques (citing Duster 2005 and Rotimi 2003, 2004) but then dismissed them by stating that their “replication using the same set of AIMs across four independent data sets addresses the sample representativeness and the potential problem of predetermined results” (p. 147). What they did not address, however, is the incomplete representation of human genetic diversity in existing databases (including the HGDP), which creates systematic bias that is difficult to quantify statistically (Braun and Hammonds 2012; Royal et al. 2010). Nor did the authors address the problematic assumption that contemporary groups are reliable substitutes for ancestral populations: doing so ignores the diffuse and changing nature of the populations sampled, instead converting them into fixed and unchanging databases (Duster 2011). Their replication also failed to address the problems with an underlying model that stipulates the existence of three discrete genetically distinct parental populations for which there is little evidence at any point in the evolutionary history of our species (Bolnick et al. 2007, 2008).

This leads us to the most problematic aspect of the article: the repeated use of the “biogeographical ancestry” estimates as stand-ins for the biological/genetic component

of race against which racial self-identities are assessed. Critics of ancestry testing have repeatedly charged that ancestry estimates have led to a “molecular reinscription of race,” and the Guo et al. article illustrates how that happens (Duster 2011; Fullwiley 2011). After estimating the “amount” of each of the three ancestral groups reflected in the survey respondents’ DNA samples (e.g. individuals who identify as South Asian are found to be, on average, 39.6 % European, 1.8 % African, and 58.6 % Asian), the authors compared these quantities against different sets of options for individual self-report (see Duster (2011) for more discussion of the flawed assumptions behind these percentage claims). First, they claimed to evaluate the practice of the one-drop rule of hypodescent by determining the proportion of “African ancestry” needed to self-classify or be classified by the interview as black. Second, they compared changes in racial self-identity against bio-ancestry estimates to report, for example, that for individuals who self-identify as black, an increase of “1 % bio-ancestry” (here they are referring to “African ancestry”) leads to a 6 % lower likelihood of a racial self-report classification change across surveys (from a survey in which only a single race is allowed to a survey in which a multiracial categorization is allowed).

These findings were then used to conclude the following: “our work demonstrates that in the case of race, social construction could be analyzed and examined *against a measurable continental and biological ancestry*” (p. 169, emphasis added). In doing so, the article promotes the perception that “race is rooted in one’s DNA—rather than being an artifact of sampling strategies, contrasting geographical extremes and the imposition of qualitative boundaries on human variation” (Bolnick et al. 2007:400). So while the authors concluded that “social forces trump biology in racial classification” (p. 141), the entire article ends up being an exercise in the opposite—essentially illustrating that there is a “logical basis for race/ethnic classifications” (p. 142), and that basis is in one’s DNA (i.e., an estimation of one’s genetic bio-ancestry).

A white paper by the American Society of Human Genetics predicts that “genetic ancestry inference (in particular, the use of AIMS and admixture mapping techniques) could reveal the nuances of ancestry and dispel the notion of race in humans and/or the practice of equating race with ancestry. Paradoxically, it is equally capable of giving credence to the idea that humans subdivide into distinct biological races and implying that there are clear-cut connections between DNA and specific geographic regions or ethnic groups” (Royal et al. 2010:670). The Guo et al. article, despite giving lip service to the first objective, ends up accomplishing the second in its insistence on using racialized ancestry estimates as the hard objective measure against which racial self-identity is continually compared.

Returning to the pitfalls and promises of combining a social science perspective with recent advances in human molecular genetics, a recent review piece on the challenges of using genetic data to augment anthropological knowledge reminds us that “genetic facts are not natural” but instead have “cultural information (values, ideologies, meanings) integrated into them” (Marks 2013:247). In the Guo et al. article, genetic contributions (in the form of “bio-ancestry estimates”) are represented as value-neutral genetic facts situated in a cultural context; that is, it is against this “logical” basis of racial/ethnic categories that the accuracy of racial self-identities are assessed. Marks (2013) would argue that the bio-genetic ancestry estimates Guo et al. presented would be more appropriately conceptualized as inherently biocultural facts imbued with values, ideologies, and meanings. Flipping the Guo et al. article on its head, this would

involve recognizing the social construction of the genetic ancestry estimates, questioning their production and the interpretations we give them. Only then will we begin to move beyond racial essentialist thinking and start to harness the promise of incorporating recent advances in human molecular genetics into social science research.

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