Getting genetic ancestry right for science and society

We must embrace a multidimensional, continuous view of ancestry and move away from continental ancestry categories


Glaring health disparities have reinvigorated debate about the relevance of race to health, including how race should and should not be used as a variable in research and biomedicine (1). After a long history of race being treated as a biological variable, there is now broad agreement that racial classifications are a product of historically contingent social, economic, and political processes. Many institutions have thus been reexamining their use of race and racism and stating intentions about how race should be used going forward. One common proposal is to use genetic concepts—in particular, genetic ancestry and population categories—as a replacement for race (2). However, the use of ancestry categories has technical limitations, fails to adequately capture human genetic diversity and demographic history, and risks retaining one of the most problematic aspects of race—an essentialist link to biology—by allowing genetic ancestry categories to stand in its place.

The process of racialization entails a dynamic cognitive process of identification based on phenotype that is often highly context dependent. Although research has found genetic variation correlated with phenotypes that have been historically used to assign race categories, such as skin pigmentation or hair texture, it is the case that such genetic correlates are not distributed in a manner that corresponds to racially defined groups. Race is a sociopolitical construct rather than a biological one. For example, in the United States, immigrants from southern and eastern Europe only began to be classified as “white” on the census in the 20th century (3); the American Indian/Alaska Native census category reflects colonizing histories and federal policies (4). As such, social scientists and others have argued that the strongest case for using race is limited to tracking the impact of racism on health outcomes, rather than as a proxy for anything biological (5).

Genetic ancestry, one of the main proposed alternatives to using race, is of relevance to statistical and population geneticists, epidemiologists, public health practitioners, physicians, and patients. In particular, genetic ancestry has renewed relevance for the clinical application of genetic technology because the accuracy of genetic risk scores varies across ancestries (6). Genetic ancestry and population categories are also relevant to the general public, as demonstrated by the tens of millions of individuals who have paid for ancestry reports from consumer companies. Across these different domains, a dominant description of genetic ancestry is associated with continents as meaningful groupings. Within genetics research, continental ancestry categories have become the most common type of group label (7). Similarly, consumer genetics products give customers a report with data based on a percentage of these continental groups from which an individual can trace their “ancestry.”

Systems of racial classification have historically regarded continents as meaningful group boundaries; thus, it is not surprising that racial categories and continental ancestry categories are often confounded. Whenever continental ancestry categories are used, the risk is high that a misconception of race as a biological attribute will reenter through the back door (8). Insufficiently nuanced thinking about continental categories, genetic ancestry, and racial groups can lead to the conflation of the three.

A Flattened Notion of Ancestry

Our genetic ancestry is defined by the stretches of the genome that we inherit from our ancestors (9). Geneticists have a concept for this known as the ancestral recombination graph (ARG). Put simply, an individual’s genetic ancestry is the subset of paths through the human family tree by which they have inherited DNA from specific ancestors. Most often, geneticists study the ARG of multiple individuals at the same time.

Crucially, this definition makes clear that there are two things that are not necessary to the definition of genetic ancestry. The first is any categorization by populations or groups. And the second is any contextualization of the individuals apart from their genealogical connections—for example, by labeling these individuals with geographical or cultural information. Yet current practices around ancestry estimation and reporting almost always impose categories and, when they do so, very often default to just one way to contextualize individuals: by continent of origin. Both practices limit the accuracy and reliability of claims being made by researchers about human genetic difference.

There are many statistical methodologies across subfields of genetics and genomics whose outputs are framed as “genetic ancestry,” most of which do not attempt to approximate the ARG and several of which only capture genetic similarity (9). The majority of these methods involve placing individuals into categories or modeling them as mixtures of discrete categories. For some methods, the categories are predefined and prelabeled. For others, the categories emerge from the analysis. In these cases, not only are the resulting categories very sensitive to which individuals are included in the analysis, they may not even represent shared ancestries (10). In other cases, categories and their labels are imposed in downstream analysis.

The concern about use of categories goes beyond these technical limitations. Imposing categories on genetic ancestry fails to adequately capture human genetic diversity and what we know of human demographic history. A standard way to visualize patterns of genetic similarity is by plotting results of principal components analysis of genetic variation data, a technique that reduces the dimensionality of that data. Most genetic analyses use data from reference populations to contextualize a study’s data. The most commonly used reference data were created by sampling individuals from a few dozen places spread across the globe. If individuals from these populations are graphed in this manner, distinct clusters roughly representing continental categories are visible (see the figure). A prominent early result was that genetic ancestry was strongly concordant with continental origins when ascertaining for individuals...
The continuous, category-free, nature of genetic variation

Colored dots (n = 4149) are reference panel individuals from 87 populations representing ancestry from seven continental or subcontinental regions projected onto the first two principal components (PC1 and PC2) of genetic similarity. Gray dots (n = 31,705) are participants from BioMe, a diverse biobank based in New York City. Clearly delineated continental ancestry categories (the islands of color) are shown to be a by-product of sampling strategy. They are not reflective of the diversity in this real-world dataset, which is made evident by the continuous sea of gray.

A MORE COMPLEX NOTION OF ANCESTRY

What are the implications for researchers who want to invoke genetic ancestry? They should first ask whether they need to impose categories at all to answer their research question. There are many situations in which categorization has been thought essential but has subsequently been shown to be avoidable, such as in correcting for population stratification in genome-wide association studies (14). In cases in which genetic ancestry categories can be avoided, they should be avoided. If researchers are able to justify a scientific need to impose categories, they should next think about whether they have to provide labels (be it geographic, ethnic, linguistic, or other) to the groupings they impose. If they do need to provide labels, they should give the scientific justification for that choice and show that they have considered potential disadvantages of imposing these labels.

Additionally, researchers should use multiple types of categories, reflecting that
genetic ancestry is a historical concept: We all have multiple ancestries depending on the time horizon considered. No individual has a single “ancestry”; the plural should always be used. Different geographical resolutions—for example, “Yoruban” versus “West African”—can serve as proxies for different time slices. Ancestry categories from different time points may be of medical relevance. The incorporation of ancient DNA information can also allow for probing different time slices, although the promise of this approach will depend on how much ancient DNA can actually be recovered and analyzed. The use of continental ancestry categories as a proxy for one of the time slices considered must be particularly carefully justified because of the conflation of continental ancestry categories with racial groupings. Additionally, future work should find better ways to conceptualize the genetic ancestry of individuals whose recent ancestors come from distant parts of the ARG.

For some diseases that have a different prevalence in different populations, genetic risk factors may indeed be at play, a result of differences in the chance arrival of new mutations, demographic history, and historical environmental exposures. But although it is possible that genetics is playing a causal role in such cases, genetic ancestry may also be serving as a proxy for differences in environmental effects, including the effects of discrimination. Whenever researchers invoke any categories in understanding health outcomes, they need to make careful efforts to jointly model genetic and environmental effects and acknowledge that a failure to explain differences could be due to unmodeled factors.

Science is reductive, and a model that uses simple continental categories has been useful in starting the process of understanding human genetic diversity. But all models have their legitimate domains of application and limits, and a much more complex set of models should now be the norm across a wide variety of use cases. This is particularly important because although human genetics falls under the biological sciences, it is in fact a science at the intersection of several disciplines, including anthropology, demography, epidemiology, history, and sociology. Even if the limitations of models used are well understood by statistical and population geneticists, others may take the models to be descriptive of realities rather than recognizing that they merely formalize approximations and estimates, using reductive categories to do so. Hence, one of the risks of using these categories is that others may interpret them as true natural kinds, which is inaccurate.

Instead, they are heuristics permitting the approximation or answering of very narrow sorts of questions. Because of the association of continental ancestry categories with racial groupings, this is particularly important for continental categories.

An individual researcher’s use of continental ancestry categories is not in and of itself racist, but the cumulative impact of this practice has led to and sustains racism. Typological thinking about human difference has had damaging social consequences. Continued reliance on continental ancestry categories contributes to failures of inferential, miscommunication between fields, and reported findings that are rooted in reductive and limited ways of understanding human difference. These are likely to exacerbate medical stereotypes about individuals and groups, contribute to health disparities rather than addressing them, and reify (mis)understandings of race as biological. Moreover, this problem is not limited to continental ancestry categories; national categories can and have been reified as biological for political goals (15).

The solution will require addressing the issues with how ancestry is conceptualized and used across the entire biomedical research ecosystem. This will involve the development, operationalization, and widespread use of a more complex notion of ancestry—one that disambiguates what is meant by genetic ancestry from related concepts, wherever possible does not treat ancestry as a categorical variable, and treats ancestry as reflecting a historical process, meaning that any study should use many different types of categories.

To aid this transition, a solid empirical understanding of how and why different fields use and operationalize the concept of ancestry is needed. To ensure that this more complex notion of ancestry is then used in practice will require systems-level change. New computational tools and data structures will be required—for example, a wider variety of proxies for genetic ancestry that do not impose categories, as well as easily accessible software tools to enable use of ancestry categories representing multiple time horizons. Further development and adoption of methodologies that directly estimate the ARG should be encouraged. Educational materials will need to be developed for scientists and physicians. Scientists of all stripes who engage in research that uses biological categories for humans should not work in isolation but as part of interdisciplinary teams, ideally including engagement with affected communities. In support of these efforts, journal editors should set standards, professional societies should publish best practices, and funders should carefully consider which research agendas they will support. It is paramount, as these organizations rightly critique the use of race as a biological variable, that use of continental ancestry categories does not become the new default. The US National Academies of Sciences, Engineering, and Medicine recently formed an ad hoc committee, “Use of Race, Ethnicity, and Ancestry as Population Descriptors in Genomics Research”; we are hopeful that this represents an opportunity for consideration and consolidation of the points raised here.

Adoption of a more complex notion of ancestry should in turn continue to inform the research agenda in population and statistical genetics and in ancient DNA research. It is in these fields, the home turf of the concept of genetic ancestry, that change in practice may have the largest overall impact. These changes are a prerequisite to any research that looks for connections between genetics and health disparities. More generally, with a more complex notion of ancestry that reflects continuous variation and historical depth, we can start to pave the way for a science that reflects the complex histories of human groups, including the power dynamics among them.

REFERENCES AND NOTES

8. T. Duster, Backdoor to Eugenics (Routledge, ed. 2. 2003).

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SUPPLEMENTARY MATERIALS

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