OXFORD

BIOLOGY Methods & Protocols

Biology Methods and Protocols, 2023, bpad032

https://doi.org/10.1093/biomethods/bpad032

Advance Access Publication Date: 11 November 2023

Methods Article

Getting it right: Teaching undergraduate biology to undermine racial essentialism

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Abstract

How we teach human genetics matters for social equity. The biology curriculum appears to be a crucial locus of intervention for either reinforcing or undermining students' racial essentialist views. The Mendelian genetic models dominating textbooks, particularly in combination with racially inflected language sometimes used when teaching about monogenic disorders, can increase middle and high school students' racial essentialism and opposition to policies to increase equity. These findings are of particular concern given the increasing spread of racist misinformation online and the misappropriation of human genomics research by white supremacists, who take advantage of low levels of genetics literacy in the general public. Encouragingly, however, teaching updated information about the geographical distribution of human genetic variation and the complex, multifactorial basis of most human traits, reduces students' endorsement of racial essentialism. The genetics curriculum is therefore a key tool in combating misinformation and scientific racism. Here, we describe a framework and example teaching materials for teaching students key concepts in genetics, human evolutionary history, and human phenotypic variation at the undergraduate level. This framework can be flexibly applied in biology and anthropology classes and adjusted based on time availability. Our goal is to provide undergraduate-level instructors with varying levels of expertise with a set of evidence-informed tools for teaching human genetics to combat scientific racism, including an evolving set of instructional resources, as well as learning goals and pedagogical approaches. Resources can be found at https://noto.li/YIlhZ5. Additionally, we hope to generate conversation about integrating modern genetics into the undergraduate curriculum, in light of recent findings about the risks and opportunities associated with teaching genetics.

Keywords: curriculum; science education; pedagogy; STEM; evolutionary genetics; teaching materials

Introduction

A working knowledge of human genomics has become increasingly important for navigating health care and reproductive decisions, as well as for engaging with science journalism and public policy debates [1–3]. Meanwhile, rapid advances in genome sequencing over the past two decades have transformed our understanding of how genetic and environmental factors shape human diversity [4]. Simple Mendelian genetic models consider a human trait as largely controlled by a single genetic variant, which primes the essentialist belief that genes determine the inherent and immutable characteristics of individuals. In contrast, we now know that most human traits are influenced by many genetic variants, each with a small effect and that these effects are likely modulated by myriad environmental factors [4–8]. Nevertheless, simple genetic models continue to dominate introductory textbooks at the secondary and undergraduate levels [2, 3, 9–13]. Although historically important and relatively simple to understand, these models do not describe the genetic basis for the majority of common phenotypes; nor do they provide students with the practical skills to engage with and interpret genetic health or ancestry test results, mass media, or academic reports on modern human genomics research [1–3, 10, 14, 15].

Worse still, simple Mendelian models may enable the spread of scientific racism. We are witnessing a surge in scientific racism in the USA and elsewhere and, in particular, the weaponization of human genomics by white supremacists facilitated by the Internet and a toxic culture that can thrive online [16, 17]. Importantly, many of our students will be exposed to racist disinformation simply as a result of time spent online [18]. A lack of modern genomics literacy can make this content difficult to critically evaluate. As with other forms of dis and misinformation, scientific racism relies on the authority of credentialed individuals who use their platform to perpetuate unfounded or untested ideological assertions about human differences [19]. In some cases, such individuals have established their own, non-mainstream, ostensibly "peer-reviewed" journals that have their own editorial boards and publication autonomy in order to create the illusion of vetted and robust science [20, 21]. Together, sharing of such race science alongside mainstream—albeit frequently distorted—human genetics articles results in a landscape of information, misconceptions, disinformation, and misinformation around human genomics that is challenging to navigate. Addressing this situation warrants the development of a framework for teaching genetics that equips students to better critically evaluate this information landscape.

Received: October 07, 2023. **Revised:** November 03, 2023. **Editorial decision:** November 08, 2023. **Accepted:** November 10, 2023

White supremacists, particularly in the USA, have long invoked the authority of science to support racist claims that racial hierarchies are an inevitable and acceptable consequence of innate human biology [12, 22, 23]. Specifically, three arguments presented as rooted in science have been advanced to support this premise. The first is race realism or racial essentialism. Race realism is the idea that humans naturally fall into biologically distinct racial groups. Racial essentialism assumes race realism and is related to genetic essentialism. Genetic essentialism is the belief that genetic make-up is the source of inherent, immutable, and essential characteristics of individuals. Racial essentialism understands races as differing in their essential characteristics. Racial essentialism has not always relied on a genetic understanding of race [23], but most contemporary forms of racial essentialism do [22]. The second is genetic determinism. Genetic determinism is another closely related concept that understands most phenotypes, including psychological and behavioral phenotypes, to be primarily genetically determined [23]. The third premise is hereditarianism, or the idea that phenotypic differences among racial groups are due to genetic differences.

Research indicates that an exclusive focus or overemphasis on simple and/or outdated genetic models can promote genetic essentialism and determinism and lead to disregard for environmental causes of human traits [11, 12, 22]. In addition, the use of racially inflected language (e.g. Caucasian, African ancestry) in teaching genetics has consequences for the reification or amelioration of racial essentialism. Donovan [24] found that educational materials about the genetic basis of sickle cell anemia and cystic fibrosis that were framed in racial terms primed middle and high school students to agree more strongly with racially essentialist statements about both physiological and psychological traits. Moreover, students expressing higher levels of biological essentialist beliefs were more likely to explain racial differences in life outcomes as driven by genetics rather than differences in the physical or social environment [24]. A similar study found that the use of racially inflected terminology when discussing genetic diseases increased middle and high school students' perceptions of the amount of genetic difference among people of different races and decreased students' support of programs aimed at redressing racial inequity in education [25].

Humans certainly exhibit allelic differences among individuals, families, and geographical regions; however, the genomics era has only further undermined race realism by demonstrating the ubiquity of migration and gene flow throughout human history [26–31] and further bolstering earlier findings that human variation is much higher within, rather than between, geographical regions [32–34]. Decades of research contradict straightforward genetic determinism in establishing the complexity of most human traits [4, 5, 8, 35], particularly psychological traits [36–38], where hundreds and even thousands of genetic variants interact with each other and environmental factors to produce a phenotype. Hereditarianism is viewed with deep skepticism in genetics, as experts appreciate the inherent conceptual and technical impediments to making inferences about group differences from heritability and polygenic score estimates [39–43].

Given that racial essentialism, genetic determinism, and hereditarianism are not considered legitimate hypotheses among geneticists, why do such beliefs persist among the public? [44] One likely reason, given the long history and influence of these beliefs, is that they are deeply culturally entrenched in the USA. Research indicates that young children do not hold essentialist beliefs about racial identity but that they begin to consider racial categories to be natural and static during elementary school [22]. While motivated cognition to endorse essentialism and rationalize exclusion is already present in undergraduates [45, 46], key aspects of the advanced knowledge of genetics that undergird experts' views are not typically conveyed in their biology curriculum. Ongoing alignment with racial essentialism, genetic determinism, and/or hereditarianism in older age groups may also result from receiving little or no genetics education. However, while not the root of such beliefs, simple, Mendelian models may inadvertently perpetuate these misconceptions [3]. Encouragingly, providing students with information about human genetic diversity can reduce such misconceptions [47], and an improved understanding of genetics appears to lead to a less essentialist interpretation of genetic ancestry information [14].

These findings raise important questions about how undergraduate-level biology and anthropology educators can best counteract harmful misconceptions about genetics and race to which our students have likely already been exposed. Human geneticists have responded to the misappropriation of their work with alarm and have taken and proposed various measures to try to prevent it [48–51]. In addition to these efforts, biologists and anthropologists in post-secondary education should actively contribute to combating the spread of harmful misinformation [22].

Here, we present a framework and example teaching modules we have developed to teach undergraduate students key concepts in genetics, human evolutionary history, and phenotypic diversity. Although these resources were developed within a US context, we believe they are generally applicable across many countries. Our aim is that this framework will provide undergraduate instructors with an alternative to traditional textbook approaches to teaching genetics and that these materials may motivate further conversation around how to best equip undergraduate students with a more up-to-date, non-deterministic, and non-essentialist understanding of human genetics that will help them navigate and critically evaluate genetics information they will encounter in their daily lives.

Overview of modules

We have organized material into four teaching modules, described below. The modules consist of slide decks, example student worksheets, and instructor's guides provided in editable Google Drive formats. The target audience is undergraduate students, both science, technology, engineering, and math (STEM) and non-STEM majors, in lower division biology and anthropology courses, although they may also be applicable to advanced secondary school students. We present the material both graphically and verbally, a pedagogical technique known as dual-coding that enables students to better learn and recall information because it is handled by both the visual and the linguistic pathway [52]. We also sought to reinforce the material through a combination of lecture materials, curated assigned readings, and worksheets. The combined key takeaways from the modules undermine the scientific basis of the core components of scientific racism (Table 1).

Our present goal is to promote discussion of how to align undergraduate-level teaching of genetics and human variation with the emerging findings that the pedagogical approach has a profound influence on student perceptions of scientific racism and genetics disinformation at the secondary level. Following calls by education researchers for geneticists and human biologists to contribute our expertise and effort to addressing this issue [22], we identify key learning objectives and provide the requisite background knowledge to understand them. Although

Table 1. Core tenets of scientific racism and the key genetics concepts that contradict them.

Misinformation	Key takeaways from learning modules that contradict false claims
Race realism: Race is biological and heritable	• Because of our species' recent common origins and pervasive geographic gene flow through much of our species' history, there is more genetic diversity within than between geographic regions [32–34, 53, 54]. • Human genetic variation among geographic regions takes the form of allele frequency differences. The majority of high-frequency alleles are observed at high frequencies in all regions, while regionally specific alleles tend to be both rare and observed at low frequencies [33, 34, 55]. • Geographic variation in allele frequencies shows a pattern of isolation-by-distance where nearer geographic regions are more similar and more distant geographic groups more diverged. This reflects the probability of migration scaling with geographic distance: on average, most individuals migrate shorter distances and fewer individuals migrate over longer distances [55–59]. • All ancestry is mixed and ancestry inference does not reflect deep time [56, 60]. • Continental-scale labels are applied to ancestry estimates for convenience, not because reference groups naturally group along continental lines. Ancestry is not a proxy for race, which is socially defined rather than biological [55, 56, 60].
Genetic determinism: Phenotypes, including behavioral and psychological phenotypes, are largely genetically determined	• Most phenotypes are polygenic and influenced by the environment [4–8] • We do not know the genetic architecture of most phenotypes and complexity in genotype–phenotype associations makes uncovering it challenging in most cases [35].
Hereditarianism: Phenotypes, like intelligence, show mean differences among racial groups that are genetic in basis	• Heritability is intrinsically specific to a given environmental context and is not an inherent attribute of a phenotype. It can change over time and across groups of study subjects [41, 42]. • Inherent and practical limitations in estimating heritability preclude its use in drawing conclusions about differences in group means [39, 41, 42].
Intended conclusion: Working for equity is pointless, racial socioeconomic hierarchies are acceptable	• Scientific racism is not a brave, politically incorrect, or commonsense view but rather a "zombie idea," or "a view that's been thoroughly refuted by a mountain of empirical evidence but nonetheless refuses to die, being continually reanimated by our deeply held beliefs" [61]. • In contrast to hereditarianism, there is good evidence that a long history of exclusion and disenfranchisement, justified in part by scientific racism, has contributed to current-day racial disparities [20, 21, 23].

we have incorporated the material presented in these modules in our own classes, we have not yet systematically assessed the effectiveness of using the slides and worksheets in their current form. We imagine other instructors may take inspiration from or flexibly use the resources we provide.

Human evolutionary history

Background

Our species, *Homo sapiens*, arose during the Pleistocene epoch ~300,000 years ago in Africa [53, 54]. The Pleistocene was characterized by cooling and drying of the global climate and periodic Ice Ages of several tens of thousands of years, separated by shorter "interglacial" periods in the Northern Hemisphere. During the Ice Ages, much of the temperate Northern Hemisphere was covered in continental ice sheets. Deserts expanded and sea levels dropped due to much of Earth's water being frozen, resulting in land bridges between many land masses, such as the British Isles and mainland Eurasia, that are separated by seas today. Thus, our species arose and migrated across the globe under extreme climatic conditions and shifting geographic connectivity.

The earliest known *H. sapiens* fossils outside of Africa were found in the Middle East and dated to at least 95,000 years ago [62]. Humans reached eastern Eurasia by at least 80,000 years ago [63] and covered the vast distance to Australia by ~65,000 years ago on a journey that would have required navigation of the open ocean [64]. The oldest evidence for *H. sapiens* in western Eurasia (Europe) is ~50,000 years ago [65]. The most widely accepted estimate of the earliest human occupation of the Americas puts it at ~15,000 years ago [27], though there is some evidence of earlier occupation [66]. Humans reached the Americas via the Bering Land Bridge, or Beringia, connecting northeast Eurasia and northwest North America.

Ancient DNA has provided many insights into human movement during the later Pleistocene and early Holocene over the last decade [27, 28, 67, 68]. For example, the spread of farming from several independent early agricultural centers over the last few thousand years involved multiple cases of extensive genetic turnover due to the replacement and assimilation of foraging groups by agriculturalist settlers [28]. Although most studies thus far focus on western and central Eurasia, more data are emerging from other regions supporting substantial interconnectivity over long distances, including between continents,

indicating that large-scale and long-range migration is not a recent historical phenomenon [28, 29, 67, 69–75]. Human movement has nevertheless been dynamic over the last 500 years with increasing trans-Oceanic travel and European colonialism [75]. Indeed, the current spatial distribution of human genetic variation has been heavily shaped on multiple scales due to mass movements including settler colonialism and forced displacements, in addition to demic replacements, admixture, as well as assortative mating and forced segregation due to institutionalized racism itself [76, 77].

The Human Evolutionary History Module provides a brief overview of this history and how it shapes the current-day distribution of human allelic variation. For example, the module explains how, due to our species' recent shared origins and subsequent pervasive geographic gene flow, most human allelic variation is found within geographic regions and, thus, shared across the globe. It also covers how genetic diversity decreases with distance from Africa and how, generally, allele frequencies are more similar between neighboring regions than more distant regions. These two dynamics provide a framework for the subsequent Ancestry Module (see below) in establishing how historical processes have resulted in two seemingly contradictory aspects of human global genetic variation: while most human genetic variation is shared across geographic regions, there is still a geographic signal in sufficiently large genomic datasets to predict ancestry.

Key takeaways

1. Most of *H. sapiens*' evolutionary history took place in Africa, where the highest human genetic diversity is found today.
2. Because of our species' recent common origins and pervasive geographic gene flow through much of our species' history, there is more genetic diversity within than between geographic regions.
3. Differences between geographic regions are almost exclusively in allele frequencies, and not in allele presence/absence. Most common alleles are found across all geographic regions, and alleles observed only in a single geographic region tend to be at very low frequency.
4. Geographic variation in allele frequencies shows a pattern of isolation-by-distance where nearer geographic regions are more similar and more distant regions more diverged. This reflects that the probability of migration scales with geographic distance: on average over time, most individuals migrate shorter distances and fewer individuals migrate over longer distances.

Content

The Human Evolutionary History Module slides are organized into four sections. The first starts with the basics of DNA biology and defining genetic variation. The second provides an overview of the basics of human evolutionary history, specifically: (i) that humans evolved in Africa and spent most of our evolutionary history there; (ii) that a subset of humans migrated out of Africa ~100,000 years ago, setting off a series of migratory events culminating in the peopling of the globe; and (iii) that long-range migration, including across and between continents, was fairly continuous following the migration out of Africa.

The third section covers how these events created the major patterns we observe in worldwide human genetic data today. In particular, it discusses why Africa harbors the greatest genetic diversity and why genetic diversity declines with distance from Africa due to serial founder events during the peopling of the globe [78]. It also discusses how frequent short-range and less frequent long-range gene flow has created a pattern of isolation-by-distance but few strong genetic barriers in humans globally. This section also discusses how our species' relatively recent diffusion beyond Africa and the pervasive gene flow among regions since has resulted in most human genetic variation being shared across geographic regions rather than distinguishing people living in different geographic regions. The key takeaway is that human genetic variation occurs primarily between individuals, not groups [32, 34, 39].

The final section discusses how to interpret two common visualizations found in human genomics research articles: principal components analysis (PCA) and STRUCTURE analysis [79, 80]. Both of these methods are powerful ways to maximize geography-informative signals from large datasets but are also prone to be misinterpreted and/or misappropriated in support of race realism [16, 23, 50].

The student worksheet provides reading questions based on an accessible article by human geneticist Noah Rosenberg on the geographic distribution of human allelic variation [33]. The Instructor's Guide includes additional resources, additional background information on PCA, and answers to frequently asked student questions.

Genotypes and phenotypes

Background

Research suggests that students taught standard Mendelian and classical genetic models have little practical understanding of the genetic contribution to human phenotypes, despite humans increasingly becoming the genomically best profiled and most studied species, and the growing relevance of human genetics to medical, reproductive, criminal justice, and other personal and policy decisions facing everyday citizens [1]. For example, students are typically very familiar with the concept of allelic dominance, but cannot explain it, and often mistakenly believe it to be a ubiquitous attribute of allelic variation [1]. Moreover, pre-genomics models of genotype–phenotype interactions (i.e. Mendelian model, classic beads-on-a-string model), tend to be highly deterministic [9, 13], and these models are often taught alongside illustrative examples, such as eye color as a monogenic trait, and deterministic phrasing (e.g. "control," "determine," and "cause") [9], that we now know to be inaccurate.

The Genotypes and Phenotypes Module seeks to replace a simplistic and deterministic model of genetics with real-world examples highlighting the high level of polygenicity and gene-by-environment interactions that shape familiar human traits. This module also introduces the concept of heritability, a foundational but widely misunderstood and misused concept in genetics [41, 42]. Importantly, heritability estimates have been fundamental to eugenic and hereditarian claims about the genetic basis of group differences in traits like IQ (perhaps most famously in *The Bell Curve*) [81]. Helping students to understand how heritability is measured and what can and cannot be inferred from it provides them with the knowledge to debunk hereditarian claims, which can often seem logical on the surface but are revealed to be scientifically fallacious on closer inspection.

In this module, we attempt to present a more complete and relevant model of the relationship between genotype and phenotype, still starting from the basics. This is by far the longest module, as understanding the relationship between genotype and

phenotype is complex, and grasping that complexity is essential to making sense of genomic information. Importantly, all the examples presented are in humans. This module provides the foundation for all subsequent modules and is intended to help remediate misconceptions for students previously exposed to genetics in other contexts.

Key takeaways

1. Most phenotypes are polygenic and influenced by the environment.
2. We do not know the genetic architecture of most phenotypes and the complexity in genotype–phenotype associates makes uncovering it very challenging in most cases.
3. Heritability is inherently specific to a given environmental context and is not an inherent attribute of a phenotype. It can change over time and across groups of study subjects.
4. Inherent and practical limitations in estimating heritability preclude its use in drawing conclusions about differences in group means.

Content

The Genotype–Phenotype Module slides are divided into four sections. The first discusses how genotypic variation contributes to phenotypic variation, starting with the example of eye color, a well-understood and moderately polygenic trait. This section then introduces the concepts of penetrance and variable expressivity, as well as how the environment influences phenotype, using the example of height.

The next section is on heritability. It explains the heritability equation and variance components and describes how heritability can be estimated using parent–offspring regression. It also presents some of the odd features and limitations of heritability analysis. Specifically, it introduces the familial fallacy and discusses how shared environment and shared genotypes are confounded in families. This section includes a historical case study about pellagra, a condition once thought to be heritable but now known to result from nutrient deficiency. This section also presents why heritability is inherently environment specific, which is illustrated by returning to the example of height.

The following section relates global geographic genetic variation to geographically structured human phenotypic variation through the case study of skin pigmentation. The major takeaways are that (i) even alleles related to a phenotype strongly associated with geography and group identity are largely shared geographically, although they do occur at different combined frequencies, (ii) the degree of geographic variation in allele frequencies contributing to skin color is not representative of human genetic variation more generally, and (iii) skin color variation is not an indicator of genotypes unrelated to pigmentation.

The final section is epistemological and discusses how scientists uncover the genetic contributions to phenotype. This includes a discussion of experimental genetics in model organisms, including hybrid cross and knockout studies, and why these approaches cannot be used in humans. The materials also cover trait mapping, a commonly used traditional method for linking genetic loci to phenotype, and genome-wide association studies, the most commonly used approach to linking genotype and phenotype in the genomics era, and their respective uses and limitations.

Notably, this module does not directly discuss psychological research on the heritability of traits such as IQ, a long-standing controversial area of inquiry that has been deeply linked with scientific racism for 100 years [21, 82, 83]. In our experience, the quantitative details of heritability estimation can be conceptually challenging for students. Thus, we choose to introduce it with more socially neutral examples first, as introducing it within an emotionally difficult context is likely to inhibit a deep grasp of the concept. Once students have mastered the concept, they will have the chance to apply their understanding to discussions of scientific racism in the Scientific Racism Module. Moreover, we do provide additional resources on the history and (mis)use of IQ in the Instructor's Guide.

The accompanying student worksheet includes an activity based on the wonderful website maintained by John McDonald, *Myths of Human Genetics*, which provides overviews of what is known about the heritability and genetic architecture of common human traits believed and often taught to be Mendelian (e.g. widow's peak, eye color) [84]. It also includes reading questions on (i) Gregory Radick's article *Beyond the "Mendel-Fisher Controversy,"* [85] which provides an accessible overview of the history of the Mendelian–biometrician debates and raises many pedagogically valuable questions about the process of science, and (ii) Graham Coop's blog post *Polygenic scores and tea drinking*, which provides an entertaining explanation of the challenging confound of genetic–environment covariance [86]. We encourage instructors to select from among these suggested materials, based on the level most appropriate to a particular course.

The Instructor's Guide includes genetics refresher materials, citations and resources on some of the human phenotypes mentioned in the slides, and answers to frequently asked student questions. We also provide additional slides discussing polygenic scores and the concept of "missing heritability" and some of its potential explanations.

Ancestry

Background

> They tell us race is an invention. That there is more genetic variation between two black people than there is between a black person and a white person. Then they tell us black people have a worse kind of breast cancer and get more fibroids. And white folk get cystic fibrosis and osteoporosis. So what's the deal, doctors in the house? Is race an invention or not? (Chimamanda Ngozi Adichie, *Americanah*) [87].

Ancestry is a term commonly used in human genetics and medical literature, as well as to sell consumer products. Direct-to-consumer ancestry tests are a primary way by which many students will engage with genetics and human genetic diversity [88]. However, ancestry is often not well defined, and the term is used in many different ways [60]. Most people have some sense of the concept of genealogical ancestry and family history. Genetic ancestry differs from genealogical ancestry in referring only to those ancestors from whom you have inherited DNA, which, due to the random nature of recombination, will be a subset of the genealogical ancestors [56, 60]. The discrepancy between genealogical and genetic ancestry has grown with each generation in the past, limiting the informativeness of genetic ancestry past about the last few hundred years [57].

Notably, however, genetic ancestry is generally not tractable to direct estimation and thus "biogeographic ancestry" is used as a proxy for genetic ancestry [60]. This is really a misnomer, as biogeographic ancestry actually quantifies an individual's relatedness to "reference groups" of people living in different parts of the globe today. This procedure is based on the reasonable

assumption that higher relatedness corresponds to a greater number of shared ancestors. Nevertheless, this distinction is often not made clear [60]. This method is limited by the reference groups available for comparison, which are not uniformly distributed around the world. Partly due to lack of resolution and partly for convenience, larger scale (typically continental-level) labels are often used to describe an individual's ancestry. For example, portions of an individual's genome with high relatedness to the Yoruba reference group will be referred to as "African ancestry" [56]. While not incorrect, this practice conveys the misimpression that continental-level ancestry is discrete and an inherently biologically informative level of ancestry categorization. It can also reinforce a misunderstanding of human migration history, leading people to believe that there has been a deep history of reproductive isolation between continents, with admixture occurring only within the past few hundred years. These erroneous impressions about human genetics have numerous consequences for the interpretation of medical information (e.g. generalization of an association between Yoruba ancestry and disease risk to all individuals with "African" ancestry) and for the average person's understanding of race (use of continent-level ancestry as a stand-in for racial categories reinforces the idea that race is biological) [16, 55, 61, 63, 89, 90].

Key takeaways

1. Genetic ancestry is only informative about fairly recent family history.
2. All ancestry is mixed ancestry.
3. Ancestry tests measure relatedness to a limited number of living human reference groups.
4. Continent-level ancestry is not inherently meaningful or informative for medicine.

Content

The Ancestry Module consists of three sections. The first section covers genetic versus genealogical ancestry and the concept of relatedness. It explains how the random nature of recombination makes the amount of DNA inherited from a given ancestor random as well, and, how with increasing numbers of generations in the past, an individual will have many genealogical ancestors with whom they share no DNA. This segues into a discussion of relatedness as a measure of biogeographic ancestry, and thus as a proxy for genetic ancestry.

The second section provides a brief overview of how ancestry tests typically work: measuring relatedness to "reference groups" of living people in different geographic locations using unphased biallelic single nucleotide polymorphism (SNP) data. It covers how ancestry tests assign geographic ancestry to blocks of chromosomes, emphasizing that this is a probability-based method. This section also covers the difference between ancestry tests and other types of DNA testing (such as paternity tests and forensic analyses) and considers how decisions about the presentation of consumer ancestry test results (e.g. contrasting colors for different continents) shape the way they are interpreted (labels as biologically meaningful rather than just for convenience). The third section addresses a common source of confusion: how to reconcile the idea that race is socially constructed with our ability to assign individuals to ancestry groups based on genetic variation. This section reiterates important content from the previous modules, reminding students that most variation across geographic regions is in allele frequencies, which can be predictive of relatedness when combined across many loci. This section also highlights how biogeographic ancestry can be used in medicine effectively or ineffectively, and how this distinction depends largely on whether or not it is being used as a proxy for racial categorization.

Scientific racism

Background

Scientific racism has a long history and has played an important role in the US and world history. Here we focus on the USA, as that is our area of experience and knowledge. Several excellent scholarly works have been dedicated to the study of the development of scientific racism and the major events and figures marking its history, for example [20, 21, 82]. Our intent with this module is not to provide an exhaustive overview of the subject but rather to (i) convey the far-reaching societal impact of scientific racism, (ii) highlight that throughout history various scientists and anthropologists have continually rejected the scientific basis of racist claims, and (iii) demonstrate the continuity in the concepts used by scientific racists for nearly two centuries despite considerable scientific advances that have invalidated scientific racism's core assumptions. This module was intended to be taught last so that students can bring the information they have learned about human evolutionary history, genetic variation, heritability, and the influence of genotype and the environment on phenotype to bear on critiquing racist arguments.

Key takeaways

1. Scientific racism is not a brave, politically incorrect, or commonsense view but rather a "zombie idea," or "a view that's been thoroughly refuted by a mountain of empirical evidence but nonetheless refuses to die, being continually reanimated by our deeply held beliefs" [91].
2. In contrast to hereditarianism, there is good evidence that a long history of exclusion and disenfranchisement, justified in part by scientific racism, has contributed to current-day racial disparities.

Content

The Scientific Racism Module consists of an online interactive timeline and accompanying guiding questions for students to independently apply what they have learned from the previous modules. The timeline includes historical events, scientific advances, major events and actors in the history of scientific racism, and contemporaneous scientifically based criticisms of scientific racism. The guiding questions encourage students to engage with the claims of scientific racism, including early, antebellum evolutionary arguments, eugenics, and arguments about racial IQ differences by identifying themes and applying the genomics knowledge they have gained from previous modules to evaluate the scientific bases of historical and contemporary claims rather than telling students these arguments are incorrect or unethical.

Discussion

In the above, we present a framework and four teaching modules that provide instructors and students with up-to-date learning materials on genetic concepts that will help students better navigate the genetic information they encounter during their lives, including misinformation wielded in support of white supremacy. This misinformation is able to spread because of poor

genomic literacy in the general public and educational and commercial discussions of genetics that inadvertently reinforce typological and deterministic thinking. By presenting these materials, we hope to encourage and support future conversations and efforts among instructors at the undergraduate level on how to use our courses and our expertise to contribute to combating this problem. Although the undergraduate curriculum has a narrower reach than the secondary school curriculum, it is certainly of considerable importance, for example, in diminishing racial essentialism in the next generation of physicians and teachers.

Moreover, there is reason to believe this approach to teaching can enhance inclusion in our classrooms and, hopefully, encourage broader participation in STEM. First, the perception that genetics is aligned with genetic determinism and racial essentialism is more likely to dissuade certain students, especially Black, Indigenous, Hispanic/Latino, and other people of color, from pursuing careers in biology [92]. Students may also experience cognitive dissonance as a result of conflicting content they are taught about race from the social sciences versus human genetics or medicine [93]. Thus, people who are already sorely underrepresented in STEM fields, including molecular biology and evolutionary biology [92, 94–101], may be further deterred, hampering efforts to broaden participation in STEM. Furthermore, a number of studies show that students from underrepresented groups are more likely to consider societal or community benefit in their choice of major [102–105]. If genetics can be aligned with debunking rather than reinforcing social inequity, these students may be more likely to see a meaningful career for themselves in science.

Representation in the field of genetics, with its long history of weaponization by white supremacists, is particularly important for the health of the discipline. For example, in addition to asking novel questions, researchers from currently underrepresented communities are often better equipped to prioritize community wishes regarding what research is conducted and not conducted and are more likely to be aware of issues of data sovereignty (i.e. the right of Indigenous people to have full control over their own biological samples and data) [106–108]. Indeed, modest gains in representation are already yielding new insights by, for example, taking a community-engaged approach to discover the erased histories of Indigenous and enslaved communities in the Americas [109–112]. Broader participation in human genetics can plausibly also act as a more effective firewall against scientific racism in mainstream science.

In closing, we believe that an undergraduate curriculum that places greater emphasis on human evolutionary history, complex trait architecture, and the global distribution of human genetic variation will better equip our students—and ourselves as instructors—to dismantle preconceived biases toward determinist and essentialist thinking. These learning opportunities at multiple levels will better enable the current and next generation of researchers, physicians, teachers, and engaged citizens to interact meaningfully with current research into human genetics. Developing this type of new curriculum will require expertise from across a wide range of disciplines, including not only biologists and anthropologists who want to teach about these topics, but also historians and sociologists who study race, psychologists who study biases, pedagogy researchers who can help us to understand how students are scaffolding new content into their existing knowledge, and many others. Here, we present a framework for this new curriculum, from our perspective as population geneticists and anthropologists. We hope publishing these materials will provoke broader discussion across expertise about how to do this well, in addition to providing slides and worksheets that can be directly used in the classroom.

Acknowledgements

We thank the Duke University Office of Faculty Advancement, the National Science Foundation (BCS-1944425), and the National Institutes of Health (R35-GM133481) for support of this project and Susan Alberts, the faculty of the Duke Department of Evolutionary Anthropology, Duke Learning Innovations, Angel Zeininger, Rachel Johnston, Leslie Digby, Megan Lancaster, Jenny Tung, Amy Goldberg, Hannah Rogers, and L.A. Heberlein for project assistance and helpful discussion.

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Conflict of interest statement. None declared.

Data availability

Materials are available via two options: (i) a peer-reviewed version from the time of publication is available on Dryad at https://doi.org/10.5061/dryad.2rbnzs7v3 and (ii) a version that we maintain and update at https://noto.li/YIlhZ5.

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