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PERSPECTIVE

The X-Axis: The Scientific and Ethical Issues of Race and Sex/Gender as Biological Categories in Research, Teaching, and Society

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Synopsis Race and binary sex/gender categories shape Western society. These systems of categorization preceded scientific study but were historically taken up by the biological sciences and currently appear widely in biology research, teaching, and society. Such biological categorization distorts our perception of variation and makes categories seem natural, immutable, and genetic in origin. These effects of biological categorization are in fundamental opposition to the nature of biological diversity and so may not accurately summarize or explain biological variation. Additionally, and more importantly, biological systems of race and sex/gender categorization have the potential to cause significant harm. In order to interrogate our ongoing use of race and sex/gender categories in the biological sciences, we take an interdisciplinary approach to answer the questions of whether these systems of categorization are robust, whether they are useful, and whether they cause harm. We conclude that biological race and sex/gender systems of categorization have little to no biological robustness or usefulness, and have caused great historical and ongoing structural harm. In moving forward we suggest that we apply these three questions to any usage of race sex/gender categories in biology research and teaching; reconceptualize race as a social category with biological consequences and initially eliminate binary sex/gender categories; fundamentally change how we conceive of variation; and make scientific reparations to address the past and ongoing harms caused by these systems of biological categorization.

Introduction

Race and binary sex/gender categories (Table 1) shape Western society, and inclusion in, or exclusion from, these categories is a fundamental part of existence (Morning 2011; Stryker 2017). These systems of categorizing humans preceded scientific study and were largely social, political, and material (Table 1) in origin (Boas 1912; DuBois 1940; Laqueur 1990; Morrison 1992; Fausto-Sterling 2000; Kendi 2016; DiTomaso 2024). However, with some historical antecedents (Kendi 2016), these systems of categorization were taken up as objects of study by the biological sciences (Table 1), including the fields of systematics, comparative anatomy, genetics, evolutionary biology, neuroscience, and medicine, during the ascent of science as a system of power in the late eighteenth and early nineteenth centuries (Haraway 1991; Marks 1995; Gould 1996; Fausto-Sterling 2000; Somerville 2003; Morning 2011; Roberts 2011; Subramaniam 2014; Gill-Peterson 2018; Donovan 2022; Smiley et al. 2024). "The themes of race, sexuality, gender, nation, family, and class have been written into the body of nature in western life sciences since the eighteenth century" (Haraway 1989, p. 1), and now "[t]he cultural logic of Western social categories is based on an ideology of biological determinism" (Oyěwùmí 1997, p. 10). We see ongoing evidence of the use of race and sex/gender as systems of biological categorization (Table 1) in research, teaching, and society; they are often the categorical x-axis. In the US, the National Institute of Health (NIH) requires binary sex to be included as a biological variable in all animal and cell studies (Clayton and Collins 2014), and "members of racial and ethnic minority groups" to be included in clinical research (Clayton and Blome 2018).

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Biology textbooks largely describe bodies according to binary sex categories (Bazzul and Sykes 2011; Donovan et al. 2024) and rely on racialized genetic diseases to teach introductory genetics (Morning 2011; Donovan 2022). Many people, including ~40% of medical students (Lujan and DiCarlo 2024), view race as a biologi-

Table 1 Glossary defining interdisciplinary terms used throughout the paper and highlighting our particular usage of them.

Term	Definition
Biological categorization	A process enacted by the biological sciences to impose order on the natural world. Carries the cultural authority of the biological sciences.
Biological diversity	The range of naturally occurring organisms and all of their structural, functional, and behavioral complexity. Does not fully exist in absence of the cultures and methods of the observers of this diversity (Haraway 1989; Subramaniam 2014).
Biological sciences, the	A human endeavor that uses the scientific method to understand biological diversity and processes. Has the assumptions and prejudices of the culture in which it is embedded (Marks 1995). Is part of a system of power and holds cultural authority (Hall 1997; Conner 2005).
Categories	Variously described as groups with something in common, ways of describing structures of variation in populations, and arbitrary, culturally specific ways of dividing continuous data (Alessandroni and Rodríguez 2020; Goyal et al. 2020).
Colorblindness	The belief that since racial differences are superficial, race-neutral policies are the best way to achieve a nonracist society, without accounting for the effects of either past or ongoing structural racism (Crenshaw et al. 2019).
Essentialization	An epistemology in which natural kinds are understood to have essences and to share deep similarities. In a biological context this is often taken to assume a fixed and deterministic genetic basis (Haslam et al 2000; Keller 2005). A form of prejudice that rationalizes the social order (Dambrun et al 2009; Donovan 2022).
Intersectionality	A critical theory stating that the effects of multiple systems of oppression on groups at their intersections are not just cumulative but emergent. First described with regards to black women at the intersection of racism and sexism (Crenshaw 1989).
Intersex	Describes people whose sex characteristics, including genitalia, reproductive organs, and chromosomes, do not fit into the male/female binary due to any one of at least 20 known biological causes (Davis and Murphy 2013).
Male/Female	Terms which refer to organisms based on their biological sex characteristics. In evolutionary biology, these terms are grounded in anisogamy. In feminist theory, female and male are sometimes taken to describe objective, physical sex differences, in contradistinction to terms like man, woman, and other gender identities. However, other theorists have shown that, like gender identity and expression, biological sex also has socially constructed and normalized aspects, and there exist embodiments that defy the binary (Butler 1993; Fausto-Sterling 2000; Davis and Murphy 2013). Since sex characteristics such as genitalia, reproductive organs, sex hormones, and chromosomes do not always all align with either only male or only female within a single organism, the defining criteria of being male and female are the object of debate.
Material	Pertaining to the physical, thus including both economic relations as they describe access to physical resources, and direct violence inflicted on bodies.
Nonbinary	A gender identity in which an individual does not align with either of the binary man/women gender categories. Here we also use this term more expansively, but consistently with the core values of a nonbinary identity, to reflect any organism or component of an organism that does not align with a binary system of sex/gender categorization.
Normalization	The scientific tendency to delimit a population, measure the mean levels of its various characteristics, and reify each mean as a norm that "compares, differentiates, hierarchizes, homogenizes, [and] excludes" (Foucault 1995, p. 183–184).
Race	Socially constructed categories dividing humans into distinct groups based on ethnicity, origin, and physical traits such as skin pigmentation. Divisions are not supported by genetic evidence, but made material by social, political, economic, and violent relations.
Reparations	Payment or material restitution made to a group of people in recognition and redress of past harm. In the US, it often refers to the proposal to redress the harm to black Americans caused by slavery, segregation, and ongoing discrimination (Coates 2014).

Table 1 Continued

Term	Definition
Sex, gender, and sex/gender	In the biological sciences sex is considered to be aspects of the genotype and phenotype involved in sexual reproduction. It is often grounded in anisogamy (Roughgarden 2004) but also variously encompasses genetic, molecular, cellular, physiological and behavioral levels of biological organization (Smiley et al 2024). Gender may be considered to be the social expression of sex and has been defined variously as "the set of arrangements by which a society transforms biological sexuality into products of human activity" (Rubin 1975), a "concept developed to contest the naturalization of sexual difference" (Haraway 1991), "the appearance, behavior, and life history of a sexed body" (Roughgarden 2004), and a social category based, in Western cultures, on body type (Oyěwùmí 1997). Gender is generally assumed to be socially constructed. However, it has also been suggested that binary sex categories are also shaped by social factors (Fausto-Sterling 2000; Stryker 2017). Here we largely use sex/gender both to reflect their continuity–a social expression of sex is a behavior and thus part of the phenotype albeit one that has strong human and cultural components–and also to highlight the lack of a clear biological/cultural divide in both binary gender and binary sex.
Structural harm	Anything that reduces life chances and enacts violence and suffering in systematically unequal ways, not as punishment for individual infractions but rather according to categorization within a political, social, economic, and material structure.
Transgender	Describes people whose gender identity or expression does not match the sex they were assigned at birth. An umbrella term including many identities.
Transsexual	Usage varies but most often describes people who identify as a sex or gender different from the one assigned at birth and seek medical transition, for example gender affirming surgery or hormone treatment. Now considered out-of-date by most trans communities and therefore often considered offensive unless used as a reclaimed word or a term of self-identification.

cal categorization system (Graves 2005; Morning 2011). And biological arguments are prevalent in contemporary anti-trans rhetoric and legislation (The White House 2025a, 2025b, 2025c; Lewis and Sharpe 2023; Watkins and DiMarco 2025).

Categorical thinking is considered, by psychologists and anthropologists, to be a pillar of human cognition. It enables the processing of large amounts of information by summarizing variation and supporting inductive and deductive reasoning (Hall 1997; Sloutsky 2010; Alessandroni and Rodríguez 2020). However, in Western societies, where scientific epistemology has enjoyed a distinct, if sometimes contested, ascendancy for centuries (Hall 1997; Conner 2005), categorical descriptions of living things have also been shown to skew perceptions of the structure and causes of variation. The use of biological categorization minimizes perceptions of within-category variation and increases perceptions of between-category variation, so artificially differentiating between members of categories. Moreover, it makes these categories seem fixed, natural, immutable, and to have a heritable (usually genetic) basis, so essentializing them (Table 1) (Haslam et al. 2000; Keller 2005; Noyes and Keil 2019; Donovan 2022; Sanchis-Segura and Wilcox 2024).

The perceptions of the structures and causes of biological variation evoked by biological categorization are fundamentally anti-Darwinian (Mayr 1982, 1997; Roughgarden 2004; Subramaniam 2014). Organisms are not discrete, fixed entities with essential natures. They are emergent, multiscale collections of many traits arising from the interactions of genes and the environment through development and over a life history. They have evolutionary pasts and futures predicated on their variation and thus are, perhaps uniquely, poorly suited to categorization (Fausto-Sterling 2000; Haslam et al. 2000; Roughgarden 2004; Kültz et al. 2013; Subramaniam 2014; Forsman et al. 2015; Prum 2023; Watkins and DiMarco 2025). Hence, our understanding of biological variation may benefit from greater interrogation of the use of biological categorization in general; even the most fundamental categorization of organisms into species requires delineation along a continuum of evolutionary divergence (Cadena and Zapata 2021). However, this is of particular importance in biological race and sex/gender systems of categorization as not only do these categories likely not effectively summarize and explain biological variation, but they also have the potential to cause significant harm.

The differentiated, essentialized perceptions of biological variation that arise from biological race and sex/gender categorization systems obscure the social origins of these categories and make them appear naturalized and immutable. In humans, this leads to the hierarchical ranking of categories and the rejection or pathologization of variation (Marks 1995; Fausto-Sterling 2000; Morning 2011; Wilkins 2013; Donovan 2022; Sanchis-Segura and Wilcox 2024), which may then be used to justify enormous harm (Morrison 1992; Somerville 2003; Dambrun et al. 2009; Miranda 2010;

Alexander 2012): "the institution of science reified social power and privilege into claims of natural and biological difference" (Subramaniam 2014, p. 14) in ways that have been central to histories of injustice (Subramaniam 2014).

Thus, given the social origins of race and sex/gender categories, the inadequacies of biological categorization for summarizing and explaining biological variation, the absence of immutable essential natures of biological entities, and the enormous potential for harm, we interrogate the use of these systems of categorization. The essentialist biological basis of race and sex/gender categorization systems has not gone entirely unchallenged in biology literature (Lewontin 1972; Roughgarden 2004; Fujimura et al. 2014; Lewis et al. 2022; Lewis and Sharpe 2023; Prum 2023) and has long been rejected by the humanities (Haraway 1989; Butler 1990; Fausto-Sterling 2000; Subramaniam 2014). However, these biological categorizations of race and sex/gender continually, and often uncritically, recur in research, teaching, and society. Thus, here we review and summarize literature from the sciences, humanities, and social sciences and ask: (1) are these categories robust—do they meaningfully summarize biological variation?; (2) are these categories useful—do they have high inferential potential and support our understanding of biological variation?; and (3) are these categories harmful—have they caused historical or contemporary structural harm (Table 1)? We then make recommendations for the use of such categories to limit future harm and call for scientific reparations (Table 1) to address past harms. We consider both race and sex/gender to highlight how the cognitive benefits and essentializing nature of categorization systems can contribute to their pervasiveness and harm, and to allow us to consider the intersectional (Table 1) nature of harms.

Are the categories robust?

If one of the functions of categories is to summarize variation, we should interrogate how robustly race and sex/gender categories summarize biological variation. When considering if a category is robust, we might ask to what degree data are continuously distributed and if there are any notable discontinuities. And for any measured trait, we might ask if there are statistical differences between categories, if those differences are biologically meaningful, and how much the categories overlap (Maney 2016; Sanchis-Segura and Wilcox 2024). Moreover, given the multiscale nature of biology, we might also ask whether systems of categorization based on things like allele frequencies at a single locus, genetic distance, or single traits are equally robust across a meaningful number of genes, traits, life-histories, species, and environments. If data are entirely continuous, there are no meaningful places to draw divisions between categories. If there is extensive overlap between measured trait values for individuals from different categories, a new individual cannot be reliably assigned to a category. If categories are not applicable across genes, traits, life-histories, environments, and species, we cannot infer anything about an entire individual based on their membership in a category. Thus, we argue that in these cases, categories are not robust, do not summarize data well, and lack inferential power.

Are human racial categories robust?

The biological categorization of humans has a long and troubling history of attempting to partition geographical variation into discrete racial categories (Roberts 2011; Kendi 2016). Early taxonomic efforts using morphological characters—such as Linnaeus's division of humans into four races aligning with the major continents based on skin color and other traits (Linnaeus 1758) and Morton's ranking of humans based on skull size (Morton 1839)—treated human variation as if it could be organized into natural, hierarchical biological categories. However, these morphological classifications lacked any scientific rigor and were subsequently discredited (Gould 1996).

Starting in the 1960s-1970s biologists moved from morphological characters to genetic data to describe biological diversity and applied this to humans (Lewontin 1972). Two key results emerged. First, humans, as a species, have exceptionally low levels of genetic diversity, so limiting the absolute amount of group/population differences possible (Lewontin 1972; Li and Sadler 1991; Przeworski et al. 2000; Auton et al. 2015). Second, analyses of these early genetic data did not support the existence of discrete racial categories of humans in any formal statistical sense. Lewontin (1972) used a variance-partitioning method to examine the frequency of gene variants in human populations and asked if most genetic variation was found within local populations, among populations within larger geographic regions, or among the broad continental groupings historically treated as races. His key finding was that the great majority (88%) of human genetic variation occurs within populations, whereas only a relatively small fraction (12%) is distributed among the broad continental groupings. Hence humans, like all species, have population genetic structure, but the broad continental groupings historically treated as races explain only a minor proportion of the already low overall human genetic diversity. Therefore, as with morphological characters, human genetic diversity could not be robustly divided into discrete racial categories.

However, since this early study, the idea that humans assort into genetic categories has continually resurfaced (Roberts 2011). Edwards (2003) argued that even small allele-frequency differences across many loci can permit accurate classification of individuals by "ancestry", a nonbiological term for the ethnic/geographic origin of a person. Further, modern whole-genome ancestry-clustering methods such as STRUCTURE (Pritchard et al. 2000) seemed, to some, to show that when individuals are sampled from geographically distant populations, they can be partitioned into a specified number of "clusters" that often roughly correspond to discrete continental ancestry groups (Rosenberg et al. 2002, 2005). However, the ability to assign individuals probabilistically to ancestry clusters using genetic data from multiple genes (Edwards 2003) does not demonstrate the existence of natural, sharply bounded, biologically coherent races. Instead, it shows that human population, like all animals, are structured by geography, migration history, isolation by distance, and admixture, such that ancestry can often be inferred statistically when enough loci are considered together (Novembre et al. 2008; Lawson et al. 2018). Further, the "clusters" recovered by programs such as STRUCTURE are not *prima facie* evidence of natural racial divisions. Such programs are highly sensitive to sampling and when, as in these cases, continuous variation is sampled discontinuously, discrete clusters can appear in the absence of true underlying sharp biological boundaries (Serre and Pääbo 2004; Lawson et al. 2018). Subsequent genome-wide studies have reinforced the absence of clustering, showing that human genetic variation is generally low, continuous, and geographically patterned, with similarity often decaying gradually with geographic distance (Ramachandran et al. 2005; Novembre et al. 2008).

This lack of meaningful, robust categories only increases as we move through levels of biological organization. Another key discovery in genetics since the 1970s is that only a small amount (~10%) of the human genome is composed of functional genes and regulatory sequences. The rest of the genome is largely composed of neutrally evolving repetitive elements (Lander et al. 2001; Ponting and Hardison 2011; Graur et al. 2013; ENCODE 2020). The genetic variants used to infer ancestry clusters are most often of this neutral class and so do not typically underlie any adaptive phenotypic difference between populations of humans. Further, when analyses are focused on coding/regulatory regions, they often do not recover the clustering patterns seen in neutral-marker datasets (Yi et al. 2010). Thus, there is little evidence that natural selection has produced a small number of deeply genetically differentiated, locally adapted human races. Instead, modern scans for geographically based selection have revealed adaptation at a very small number of genes, which affect highly specific traits in very particular environments (e.g., high-altitude adaptation in some populations), without generating the kind of genome-wide differentiation that would support biological races (Hancock et al. 2010; Simonson et al. 2010; Fan et al. 2016). Even analysis of the genetic basis of skin color variation does not support the idea of discrete biological races. While there is strong evidence that skin pigmentation has been shaped by natural selection during human evolutionary history, its genetic basis is highly complex and does not neatly align with racial categories. Instead, skin color is determined by variation at many loci (as well as the environment) and varies continuously, and there exist multiple distinct genetic routes to lighter or darker pigmentation in different populations (Jablonski and Chaplin 2000; Norton et al. 2007; Crawford et al. 2017). Similar pigmentation can therefore arise through different genetic mechanisms, and the trait itself reflects both evolutionary and environmental context. Thus, even one of the most racially coded phenotypic traits fails to provide evidence for discrete biological races.

The history of racial classification and modern population genetics both point to the same conclusion. Human genetic variation is real, structured, and historically informative. However, this variation is low, predominantly continuous, overlapping, and only weakly partitioned among populations. Human genetic and phenotypic variation do not resolve into a small number of discrete, coherent "races". Thus, consistent with the history of race as a social category, we may definitively conclude that racial categories do not robustly summarize biological variation in humans.

Are sex/gender categories robust?

While the evidence is clear that human racial categories do not meaningfully summarize human biological variation and so are not at all robust, the case of sex/gender is more complicated. In the biological sciences, sex is often considered to be aspects of the genotype and phenotype that enable the fusion of gametes during sexual reproduction and is often viewed as having binary male/female categories. In the humanities, gender is often considered to be the social expression of sex and in dominant Western culture, gender is viewed as having a man/woman binary corresponding to the male/female sex binary (Table 1), although many individuals and groups view gender as neither binary nor determined by sex. Additionally, gender has also been defined more broadly as "the appearance, behavior, and life history of a sexed body" (Roughgarden 2004, p. 27), and so can be applied to aspects of the phenotype of nonhuman

species. Here we use sex and gender where the distinction is clear and helpful, but largely use sex/gender to reflect the lack of clear divides between the biological and cultural and the human and nonhuman (Table 1).

Evolutionary biology locates binary sex categories with anisogamy. By convention, the production of small motile gametes (sperm) is designated as "male" and large static ones (ova) as "female" (Table 1) (Roughgarden 2004; Bachtrog et al. 2014; Fuentes 2025; Watkins and DiMarco 2025). There are a few caveats to this anisogamy binary. It excludes isogamous fungi and other unicellular organisms. Sperm size varies within and between *Drosophila* species leading to more than two gamete sizes (Lüpold et al 2016). And we appear to lack a quantitative assessment of the degree of anisogamy across species. However, the vast majority of sexually reproducing species are anisogamous (Roughgarden 2004). And thus, in contrast to race, binary sex categories do appear to have some degree of robustness.

However, critically, binary sex/gender categories are not applied just to gamete production, and gamete size is exceedingly rarely actually examined when an organism's sex is determined. The essentializing nature of biological categories means that they are consistently applied to individual organisms over entire life-histories. Sex/gender has been defined variously by genes, chromosomes, hormonal profiles, gonads, genitalia, body morphology, behavior, and the social expression of sex (Rubin 1975; Butler 1990; Haraway 1991; Oyěwùmí 1997; Fausto-Sterling 2000; Stryker 2017; Donovan 2022; McLaughlin et al. 2023; Prum 2023; Smiley et al. 2024). And a variety of excellent reviews over the last 25 years have shown that binary sex/gender categories do not robustly describe biological variation across these levels of biological organization (Roughgarden 2004; McLaughlin et al. 2023; Subramaniam and Bartlett 2023). Individual bodies do not always produce a single gamete size over their entire life-history. Most plants and many fish species are hermaphroditic (Roughgarden 2004; Kuwamura et al. 2020; Subramaniam and Bartlett 2023). And even in gonochoric species, in which individuals produce only one gamete size, individuals do not produce gametes their whole life (Prum 2023). A diversity of sex chromosomes and polygenic sex lead to more than two genetic sexes (Moore and Roberts 2013). The white-throated sparrow is said to have four genetic sexes because of an autosomal super gene that influences color morph and parental behavior independent of gamete production (Thomas et al. 2008). The so-called sex steroid hormones estrogen and testosterone are not sex-specific (Oudshoorn 1994) and their levels and effects vary widely with environment and across species. Estrogen causes singing in sperm-producing zebra finches (McLaughlin et al. 2023) and cichlid fishes remodel their neuroendocrine system with social environment (Francis et al. 1993). Genital morphology is not consistently binary with no individuals having phalluses in the majority of bird species while all hyenas do (Roughgarden 2004; McLaughlin et al. 2023). And broader morphological and behavioral reproductive strategies vary widely with many species having multiple morphs associated with a single gamete size, such as the three sperm-producing morphs in the side-blotched lizard (Sinervo and Lively 1996). Thus, across the tree of life, a gamete size binary is associated with vast genetic and phenotypic variation within and across species that is not robustly summarized by binary sex/gender categories.

Even in mammals, which are easily the most sexually conserved class of vertebrates, and even at the level of the sex chromosomes and genes that are assigned the decisive roles in sexual differentiation, binary sex/gender categories are not particularly robust. Mammalian sex/gender is traditionally presented as a linear, ratchet-like process in which the presence of an X or Y chromosome determines gonadal sex in the developing embryo, which then determines steroid hormone levels, all other morphological and behavioral sex differences, and thus assignment to one of two discrete, binary sex/gender categories (Nelson 2011; Arnold 2020). However, across species, Y chromosomes and the Y-linked gene (*Sry*) that initiates testis development are not always restricted to, or present in, individuals with testes. At least 10 species of mammals have lost *Sry* and/or the entire Y chromosome, and in at least 14 others some XY individuals are fertile ova-producers (designated X∗Y) (Hughes et al. 2024). In 3 rodent species from the latter group, X∗Y individuals have higher reproductive output than XX individuals (Espinosa and Vitullo 1996; Fredga et al. 2000; Saunders et al. 2014). These examples could be bizarre exceptions to an otherwise robust male/female binary in mammals. However, the much more general processes of sexual development and maintenance suggest otherwise. The gene regulatory pathways that initiate gonadal differentiation are complex and intertwined. For example, *Foxl2* actively suppresses *Sox9* expression in newly differentiated ovaries, and antagonism between these transcription factors is such that ovarian silencing of *Foxl2* in adult mice results in conversion of ovarian somatic cells to testis-like cells (Uhlenhaut et al. 2009) whereas loss of *Dmrt1* expression in adult testis activates *Foxl2* and reprograms testicular somatic cells to ovarian cells (Matson et al. 2011). These facts, that Y chromosomes do not determine "maleness" and that minor adjustments

to adult gene expression can alter the identity of the most sexually differentiated cell types throughout life, do not refute the reality of sex and sex variation in mammals. Rather, they demonstrate that even the sex chromosomes and genes that are assigned the decisive roles in sexual differentiation lack a robust binary sex/gender categorization system, even in the most sexually conserved class of vertebrates.

In humans, an estimated ∼0.2–2.0% of people are born with an intersex variation related to their gonads, internal or external reproductive structures, chromosomes and hormones (Blackless et al. 2000; Fausto-Sterling 2000). And the vast majority of traits are characterized by continuous variation or extensive overlap rather than a clear, categorical sex/gender binary (Maney 2016; Sanz 2017). For example, pelvis shape is best represented as a gradient (Fischer and Mitteroecker 2017), height has a 32% overlap between binary sex/gender categories and brain interhemispheric connectivity has an 88% overlap (Maney 2016). Gender variation beyond the binary exists in diverse, nonhomogenizable ways, across cultures and time periods, including historical sapphists, sodomites, and inverts who combined nonbinary gender expressions with nonnormative sexualities (Herdt 2003), contemporary trans and nonbinary identities (Snorton 2017; Stryker 2017; Chiang et al. 2018; Gill-Peterson 2018; Rizki 2019), and non-Western identities, which often combine nonbinary gender with religious and cultural formations, including the aqi or joyas of the Chumash (Miranda 2010), the nádleehí of the Diné (Epple 2008), the muxes of the Zapotecs (Mendoza-Álvarez 2018), the mahu of Hawaii (Mock 2014), the hijra of India (Lal 1999), the bakla of the Philippines (Alegre 2022), and many more. Thus, even in humans, we fail to find evidence of a robust sex/gender binary across physical and behavioral traits and in social and cultural manifestations.

Hence—although sexual reproduction is clearly an important feature of biology; anisogamy is a very common strategy; a diversity of genotypes, morphologies, hormones, and behaviors have evolved to facilitate the fusion of gametes; and many societies have some form of gender structure—there is nothing robust, fixed, or binary about the often insisted upon "male/female" and "men/women" categories. Therefore, we may conclude that while sex variation is real and important, fixed, binary sex/gender categories cannot be robustly applied to individual organisms over entire life-histories. This conclusion is consistent with and in part arises from decades of the feminist study of science which critiques the notion of an essentialist, biological sex/gender binary. Simone de Beauvoir first stated that "One is not born, but rather becomes a woman" (Beauvoir et al. 1973, p. 301) and this was then extended to sex by Judith Butler and Anne Fausto-Sterling who emphasized that while there is a material nature of the sexed body, this cannot be separated from the social context in which it exists (Butler 1993; Fausto-Sterling 2000). We see this social imposition of a sex/gender binary on biological variation in the creation and inflation of "male/female" differences in skeletal anatomical drawing (Schiebinger 1986), the bias in the publication of significant binary sex differences (Anastasi 1981; Maney 2015; Fine and Fidler 2015; Sanchis-Segura and Wilcox 2024), and the lack of well-supported sex differences in the majority of published studies claiming such differences (Patsopoulos et al. 2007; Joel et al. 2015).

Are the categories useful?

We might consider categories to be useful if they help us to summarize variation (see previous section). Categories are also thought to enable inferential reasoning and highlight mechanistic links between category members. Hence, we might consider biological categorization systems of race and sex/gender useful if they enable us to make predictions about category members and help us to understand important biological phenomena that underpin category membership. In biology education, we may consider biological categorization useful if it increases students' understanding of, and ability to apply, biological concepts. And, if medicine is a major application of biology, we may consider biological categorization useful if it improves human health. Here, we interrogate the usefulness of biological systems of race and sex/gender categorization in these areas and show that the absence of biological robustness of racial categories, and the lack of a mechanistic link between gamete size and other aspects of the genotype and phenotype, limit the use of these categories for understanding biological phenomena. Moreover these categories likely lack usefulness for biology teaching and medicine as they reduce the ability to apply biological concepts, encourage antievolutionary essentialist thinking, and limit our understanding of the causes and treatment of pathology.

Are human racial categories useful for the understanding of biological phenomena?

The assignment of humans, or other species, to ancestry clusters in population genetics may be considered useful in summarizing and explaining patterns of relatedness. In human population genetics, methods such as model-based clustering are valuable because they compress high-dimensional genomic variation into interpretable summaries of population structure, allowing researchers to detect geographic pattern-

ing, reconstruct historical relationships, identify admixture, and generate hypotheses about the processes that produced present-day genetic diversity (Pritchard et al. 2000; Patterson et al. 2006; Novembre et al. 2008; Bergström et al. 2020). Thus, these types of clusters are useful not because they reveal fixed biological categories, but because they highlight evolutionary phenomena that mechanistically explain genetic diversity within and among groups. They are also important analytically, since accounting for ancestry structure is often necessary to avoid confounding genome-wide association studies and other genomic analyses (Pritchard et al. 2000). At the same time, the usefulness of this process is limited by the fact that inferred clusters depend strongly on sampling design, marker choice, and model assumptions, and they can easily be overinterpreted as evidence of essential or sharply bounded human groups when the underlying variation is often clinal and overlapping (Lawson et al. 2018). Thus, ancestry analyses are useful when treated as heuristic and historical tools for studying human evolutionary and contemporary history, but not as support for biologically discrete racial categories. Indeed, such analyses are very harmful when employed in this latter role, leading to the suggestion that the only use value of biological systems of racial categorization is racism (Graves 2005; Roberts 2011).

Are sex/ gender categories useful for the understanding of biological phenomena?

Sex may be useful, and even necessary, for the understanding of evolutionary processes. Evolution, including evolution by natural selection, does not require sexual reproduction or sexes; clonal lineages can adapt perfectly well. However, sexual reproduction and the evolution of individuals with different sexual morphologies and physiologies add complexity and diversity within species, promote the origin of new species (Chen and Wiens 2021), and are essential to the evolution of sexually selected phenotypes. Therefore, although evolution can be understood without consideration of sex or the use of sex/gender categories, much of the variation and diversity of eukaryotic life is the product of sexual reproduction and sexual selection only operates in systems with more than one sex. In these contexts, it is undeniably convenient to use categorical terms such as "male" and "female" to reference conspecifics that differ predictably in reproductive phenotypes of interest. Theories that generate robust predictions and explain widespread patterns in nature are inherently useful, and therefore these categorical terms would then be extremely useful for our understanding of biological phenomena if they denote some underlying feature of "males" and "females" that holds significant explanatory and predictive power. However, such theories could hinder our understanding if their predictive power is overextended. To try to understand the usefulness of binary sex categories, we summarize their predictive power and limitations in the action of sexual selection.

Sex/gender binaries are deeply embedded in theories of sexual selection, beginning with Darwin's proposition that the sexual preferences of "comparatively passive" females and the competitive abilities of "eager" males (Darwin 1871, p. 273) impose selection only on traits affecting reproductive success (Darwin 1871, chap. VIII). Post-Darwin, classic sexual selection theory became grounded in binary differences in gamete size (anisogamy) and the consequences of this initial asymmetry for all downstream reproductive investments (Bateman 1948; Trivers 1972). More recent work calls into question aspects of Bateman's Drosophila study and Trivers' interpretation thereof (Gowaty et al. 2012; Tang-Martínez 2016), and Darwin's sexual stereotypes are at least partially diffused by recognition of postcopulatory sexual selection and the commonness of polyandrous mating, and a more nuanced understanding of mating decisions (Rosenthal and Ryan 2022). However, whether anisogamy and its associated difference in energetic investment reliably predict binary sex differences in nongametic reproductive investment and the intensity of sexual selection are topics of unresolved debate (Schärer et al. 2012; Kokko et al. 2013; Ah-King and Ahnesjö 2013; Janicke et al. 2016; de Vries and Lehonten 2023; Evron 2023; Gourevitch et al. 2026).

The predictive power of anisogamy is supported by models (Lehtonen et al. 2016; Lehtonen 2022; reviewed in Kokko et al. 2006), and by meta-analysis of the relationships between sex differences in the strength of sexual selection, parental care, and sexual dimorphism across a broad taxonomic sample of animals (Janicke et al. 2016). However, as Darwin was painfully aware (Darwin 1859, chap. VI; Darwin 1871), the scientific usefulness of a theory breaks down when the "exceptions" that it fails to explain become too frequent. And there are a great number of exceptions. The premise of differential gametic investment may be fundamentally less applicable in plants where, for example, angiosperms require two sperm for fertilization (Subramaniam and Bartlett 2023). And, as we see above, there exists a plethora of examples in which sexual variation is nonbinary within a species and highly variable across species, suggesting a lack of consistent and binary response to differential gametic investment. Similarly, we see that a greater investment in large gametes does not always translate into "male" competition and "female" choosiness. For example, all wild rabbits fight to establish and maintain within-sex dominance (von

Holst et al. 2002) and all ornate jumping spiders are ornamented, engage in displays, and are choosy about who they mate with (Lim et al. 2007).

Thus, given that the production of small versus large gametes is widely used to delimit the categories of "female" and "male", the fact that anisogamy is an inconsistent predictor of reproductive genotypes/phenotypes and so-called "sex roles" limits the utility of these binary categories. Indeed, it has been argued that these categories may obscure or limit our biological understanding (Lewis and Sharpe 2023; Gourevitch et al. 2026). For example, the imposition of binary sex onto plants has been suggested to misrepresent important features and drivers of plant reproduction (Subramaniam and Bartlett 2023) and, despite being widespread, female-female aggression has only recently been studied (Rosvall 2008; Lipshutz et al. 2025). Moreover, *a priori* framing of biological and biomedical questions in the context of binary sex can obscure underlying mechanisms. For example, sex-based variation in stress responses is reported in lizards (Dupoué et al. 2020), and gender is often treated as a risk factor in knee pain (Silverwood et al. 2015). However, these effects are likely better explained by variations in hormone concentrations and pelvis morphology than by gamete size and would be better studied through these lenses. This is nicely illustrated in species with multiple morphs that produce a given gamete size. For example, the higher testosterone in the orange small gamete producing side blotched lizard morph is an important determinant of its greater territoriality (DeNardo and Sinervo 1994; Sinervo and Lively 1996) and the greater aggression of both the small and large gamete producing white-striped morph of the white-throated sparrow is mediated by differential allelic expression of an estrogen receptor located in the supergene (Merritt et al. 2020). Hence, we suggest that while differential gametic investment may have some explanatory power, binary "male/female" categories as applied to individual organisms are of limited value given the array of reproductive genotypes/phenotypes and absence of mechanistic links between gametic investment and many aspects of the presumed reproductive genotype/phenotype.

Are race and sex/gender categories useful for the teaching and learning of biology?

Race and sex/gender categories may also be considered useful if they can achieve the educational goal of acquiring biological knowledge that can be applied to novel situations. If biological categorization systems are to support teaching and learning in this way, then they must have high inferential power. Yet, we know this is largely inconsistent with the nature of biological variation, and as we see above a categorical approach often does not support understanding of biological phenomena (Mazzocchi 2012; DeDecker et al. 2022). Indeed it has been shown that the use of surface-level categories is a characteristic of novice thinking (Smith et al. 2013; Sung et al. 2022). Thus, biological categorization of race and sex/gender is likely to be of limited value. However, beyond this limited usefulness of categories in general, the particular use of biological race and sex/gender categories is likely to have deeper implications. Biology education materials often present sex/gender categories as binary, highly differentiated and essentialized (Bazzul and Sykes 2011; Donovan et al. 2024), and a basic genetics education often focuses on molecular genetics and links monogenic traits to social groups such as "diseases like sickle cell anemia in Africans" (Morning 2011; Donovan 2022). Such approaches have been shown, at least for racial categories, to interact with students' preexisting socio-cultural understanding of the world and increase genetically essentialist racial thinking (Donovan 2022). In addition to causing social harms, this likely also reduces biological literacy. Genetically essentialist thinking suggests specific, proximate, stable, and immutable relationships between genes and traits that lead to misunderstandings of the structures of variation, and is fundamentally antithetical to evolutionary thinking (Kampourakis 2020; Donovan 2022). Thus, we suggest that race and sex/gender categories have little use in biology teaching and learning and may in fact be detrimental.

Are race and sex/gender categories useful for human health outcomes?

Race and sex/gender categories have been argued to be critical clinical variables that could provide a step towards personalized medicine and improve health outcomes, particularly for oppressed groups, by acting as proxies for clinically relevant genetic and physiological variation (Risch et al. 2002; Gemmati et al. 2019). Superficially, this approach may be understandable given the existence of glaring racial health disparities (Levine et al. 2001; Bailey et al. 2017; Nnorom and Wilson 2022), differences in the binarily sexed or gendered prevalence and outcomes of various conditions (Gemmati et al. 2019), and worse health outcomes for transgender than cisgender people, particularly transgender people of color (Veale 2023; Jolly et al. 2025). To understand if biological race and binary sex/gender categorization systems are useful for improving human health, we must understand both how these categorical health disparities arise if these biological systems of race and binary sex/gender category (which are often

poorly and inconsistently defined in such studies) do not well describe biological variation, and the implications of the clinical use of these biological categorization systems.

There is strong evidence to suggest that health disparities arise from social factors rather than any inherent biological differences between category members. In racially stratified societies such as the USA, race is confounded by environmental factors to the extent that it has been suggested to create different ecological niches (Henry et al. 2023). And it is well established that racial health disparities arise from racial biases in medical care and the effects of interpersonal and structural racism on levels of oxidative stress and inflammation, neurohormonal systems, and epigenetic regulation of gene expression (Gravlee 2009; Roberts 2011; Bailey et al. 2017; Tsai et al. 2020; Norris et al. 2025; Smith et al. 2025; Stensland et al. 2025). There are demonstrated racial biases in medical professionals' assessment and treatment of pain (Smith et al. 2025; Stensland et al. 2025), racist microaggressions increase salivary cortisol (Nam et al. 2022), early-life stress affects leptin production (Yam et al. 2017), and immigration raids reduce self-reported health scores (Lopez et al. 2017). Moreover, the effects of sex-related components of biology are inextricably entangled with sexed/gendered experiences in Western societies (Fausto-Sterling 2000; Joel et al. 2015; Maney 2016). "Women" experience worse medical care than "men", often being diagnosed later (Westergaard et al. 2019). And binarily gendered disparities in a range of conditions have been shown to be better explained by social factors than by inherent biological differences with, for example, higher rates of COVID-19 infections in women best explained by gendered differences in testing (Boulicault et al. 2025). The more precarious existence outside of a sex/gender binary (Stryker 2017) increases negative interactions with medical professionals (Zeeman et al. 2019) and is beginning to be linked to increases in allostatic load and reduced health outcomes (Veale 2023). Thus, we see the impact that systems of biological categorization, mediated by structural oppression, interpersonal discrimination, and medical biases, can have on the health of members of categories deemed inferior such as people of color and cisgender women, and people excluded from categories such as trans and intersex people.

The lack of biological robustness of race and sex/gender categories, and the social causes of health disparities, limit the clinical use of these categories and may cause harm. Essentialist race and binary sex/gender-based medicine often attributes disease to explicitly or implicitly biologically essentialist causes (Pickering 2007; Gower and Fowler 2020) so ignoring the actual determinants of disease and limiting interventions (Risch et al. 2002), absolving dominant social groups of the responsibility for creating and addressing health disparities, and reinforcing deeply entrenched ideas of biologically essentialist race and binary sex/gender categories (Hall 1997; Gravlee 2009; Morning 2011; Roberts 2011; Joel et al. 2015; Maney 2016; Norris et al. 2025). Such approaches have also been shown to increase the fully justified medical mistrust in racially oppressed groups (Condit and Bates 2005; Gutiérrez 2008; Washington 2008). However, the study of health disparities also has the potential to demonstrate the profound impact that social factors can have on the health of oppressed people, thus illustrating how biological categories can be created through social systems (Fausto-Sterling 2000; Graves 2005; Roberts 2011). This understanding is foundational to addressing health disparities. Thus, if race and sex/gender categories are to be useful in improving health equity they must explicitly define nonessentialist race and sex/gender categories and be driven by overtly anti-essentialist hypotheses which center the role of systems of oppression and actively reject genetic explanations.

Are the categories harmful?

The cultural authority held by science and the effects of biological categorization have the potential to contribute to, justify, and perpetuate significant harm, specifically structural harm (Table 1). Structural harm may be defined as anything that reduces life chances and distributes violence and suffering in systematically unequal ways, not as punishment for individual infractions but rather according to categorization within a political, social, economic, and material structure. This harm may manifest both as violence against members of a category deemed inferior, and as violence against those who transgress category boundaries. And the intersections of these biological systems of categorization create not just cumulative but emergent forms of oppression (Crenshaw 1989). Here, we review evidence from the history of science, the humanities, and the social sciences to examine the interaction between biological race and sex/gender categorization systems and structural harm. We particularly highlight how scientific theories of race and sex/gender in the eighteenth and nineteenth centuries appealed to popular ideologies of racism and sexism to bolster their own credibility, and in turn rationalized and naturalized those ideologies and made biological race and sex/gender categories seem immutable, essential, and hierarchical. These systems of biological categorization then provided the justification for the structural harms of slavery and segregation (Jordan 1968; Morrison 1992; Alexander 2012), subordination of women (Showalter

1970; Russett 2009), pathologization of sex/gender variation (Fausto-Sterling 2000; Somerville 2003), current systems and persistent inequalities (Yzerbyt et al 1997; Bonilla-Silva 2006; Dambrun et al. 2009; Alexander 2012; Coates 2014; Fine and Fidler 2015), and anti-trans and anti-DEI legislation in our current political moment (The White House 2025a, 2025b, 2025c).

Harm caused by racial categories

Our discussion of racial categories will largely focus on the construction of black and white in US nineteenth and twentieth century history. While volumes could be written on the role of science in other examples of racial harm, such as colonization and genocide of native peoples and exile and exclusion of racialized immigrants, the tumultuous racial politics and the cultural ascent of science during this time period make this a foundational and highly consequential instance of the structural harm that biological categorization can cause, justify, and perpetuate. The categories of black and white, and with them the modern practice of dividing all humanity into racial categories, were born not of biological observation but of the political and psychological necessity of differentiating and hierarchizing categories of slave and free in Africa and the colonial Americas, as early as the fifteenth century (Kendi 2016) and more prevalently by the seventeenth century (Jordan 1968; Morrison 1992; DiTomaso 2024). Biology became a dominant epistemology and took up racial categories as objects of knowledge in the late eighteenth century (Haraway 1989) and throughout the nineteenth century (Somerville 2003). This rise was supported by the developing disciplines of craniometry, phrenology, and comparative anatomy (Gould 1996; Somerville 2003), and race as a biological category was enshrined.

In this formative era, the biological sciences were concerned with how different races of humans were created. The theory of monogeny stated that humans were created as a single species with a common ancestor and that the unquestioned biological difference between races arose from the supposedly greater evolution of the white race or the degeneration of other races, while the theory of polygeny stated that different human races were created in separate times and places as distinct species (Somerville 2003). While these theories shared the premises that biologically distinct human races exist and the white race is superior, they were differently useful to justify structural harms at different points in time. Monogeny was initially more popular as it was more consistent with dominant white Christian ideology (Keel 2018). Polygeny became increasingly dominant in the USA by the 1850s, as the risk of contradicting Christianity became less costly than what could be gained by a more compelling justification of slavery in the face of increased abolitionist challenges (Keel 2018). Preeminent scientists such as Louis Agassiz and Samuel Morton endorsed polygeny, and it "was one of the first theories of largely American origin that won the attention and respect of European scientists" (Gould 1996, p. 74). Thus, we see how theories of biological categorization waxed and waned in popularity among scientists and society based on the support they could provide both for the scientific institutions themselves and the structural harm of slavery.

After the Civil War, the maintenance of hierarchical systems of racial categorization and structural harm faced dual challenges. First, the end of slavery had eliminated the legal definitions of racial categories based on enslavement. And second, the new theory of evolution reduced scientific support for polygeny. In the late nineteenth century biologists swung toward a new iteration of monogeny compatible with evolution and applied the principle that "ontogeny recapitulates phylogeny" to human groups, arguing that despite a common ancestry, non-white races have somehow become stuck at an inferior, less-evolved stage (Gould 1977; Somerville 2003). These theories of evolution and recapitulation justified the fear that the white race could degenerate due to intermixing with others, and so endorsed the structural violence of the Jim Crow era by providing support for segregation, antimiscegenation, lynching, and the "race hygiene" logic of eugenics and involuntary sterilization (Somerville 2003). Thus, in the late nineteenth and early twentieth centuries we see new biological theories bolstering racial categories, and justifying the violent enforcement of their boundaries, even as these racial categories were legally altered and reinvented.

The end of Jim Crow segregation in the 1960s and the rise of molecular genetics ushered in the next era in the history of racial science, in which the central question was whether genetic evidence supports the existence of biologically meaningful races in humans. In 1996 Bill Clinton famously announced, "I believe one of the great truths to emerge from this triumphant expedition inside the human genome is that in genetic terms, all human beings, regardless of race, are more than 99.9% the same" (Roberts 2011, p. 50), a statement that continues to be supported by the modern scientific consensus. While this is undoubtedly a positive development within the biological sciences it is important to be cognizant of its potential to perpetuate structural harm through colorblindness (Table 1), a damaging ideology that emerged after the end of legal segregation. Colorblindness is exemplified from the antiaffirmative action movement beginning in the 1970s (Bonilla-Silva 2006) to the executive order of 2025 ordering "the termination of all discriminatory programs, including ille-

gal DEI [. . .] mandates, policies, programs, preferences, and activities in the Federal Government" (The White House 2025c). Michelle Alexander writes, "Saying that one does not care about race is offered as an exculpatory virtue, when in fact it can be a form of cruelty. . . We have become blind, not so much to race, but to the existence of racial caste in America" (Alexander 2012, p. 241). Colorblindness made it more discursively difficult to name the impact of race, even as the hierarchized racial categories established by slavery and cemented by the biological sciences continued to do massive structural harm, as evidenced by the racialized mass incarceration that is a literal legal extension of slavery (Alexander 2012); racial disparities in the Child Protective Services and foster care systems that continue slavery's annihilation of family bonds (Roberts 1997); modern policing as inheritors of slave patrols (Spruill 2016); discriminatory housing and lending practices and resulting wealth disparities (Coates 2014); white supremacy and antiblackness in education (Love 2019); and black vulnerability to gratuitous violence (Wilderson 2010) and sexual violation (Douglass 2025). Hence, while current antiracist approaches to human population genetics have much to offer in disruption of biologically essentialist racial categories, we should be mindful of the implications of the authority of biology pivoting to dismiss racial categories as "not real" without actively redressing the very real differences in distributions of wealth and violence, and indeed in the biology of racialized people itself, that have resulted from centuries of enslavement, segregation, and ongoing oppression previously naturalized and justified by systems of biological categorization.

Harm caused by sex/gender categories

Structural harm supported by biological sex/gender categories operates predominantly through the mechanism of normativity. As we see above, throughout human histories and cultures and across the tree of life, sex/gender is multiplicitous, fluid, and diverse. Yet systems of biological categorization have largely reduced sex and gender to two nonoverlapping options, "male" and "female" or "man" and "woman", and ignored or pathologized anything that does not fit perfectly into either category. This is a paradigmatic instance of what Michel Foucault calls "normalization": the scientific tendency to delimit a population, measure the mean levels of its various characteristics, and reify each mean as a norm that "compares, differentiates, hierarchizes, homogenizes, [and] excludes" (Foucault 1995, p. 183–184). Because, within this paradigm, the average human belongs perfectly to the category of either man or woman, anyone who does not is defective and must be corrected; because the average man is stronger than the average woman, for example, the categories can be hierarchized. What is called normalization at the individual level, Foucault names "biopolitics" when it extends to the societal level and becomes the practice of using statistics and demographics to manage entire populations. For human beings, to be included in the measured population means to be subjected to immense political, social, and material coercion to conform as closely as possible to the norm (Butler 1990), while to be excluded generally means to be left with only "bare life", excluded from participation in civil society (Agamben 1998).

This sex/gender normativity supported by biological categorization does structural harm in (at least) three distinct ways. First, biological sex/gender categories have harmed those who fit the binary norms of female and feminine by ranking them as categorically inferior to those who are male or masculine. Second, biological sex/gender categories have harmed those who transgress these binary categories, such as intersex, trans, nonbinary, and third gender people, by either erasing their existence or treating them as pathological aberrations to be corrected. Finally, as we will see in the next section, sex/gender categories do emergent types of harm in intersection with racial categories.

First, the scientific history of the sex/gender binary illustrates that biological categorization and normalization can be used to differentiate and hierarchize. While scientific precursors such as Aristotle and Galen identified differences between "men" and "women", the insistence on a rigid sex binary is a more recent development: "The dominant, though by no means universal, view since the eighteenth century has been that there are two stable, incommensurable, opposite sexes and that the political, economic, and cultural lives of men and women, their gender roles, are somehow based on these 'facts'" (Laqueur 1990). In the early nineteenth century, the scientific fields of anthropometry and comparative anatomy mobilized to produce data in support of this binary in precisely the way Foucault identified, with overlapping male–female distributions collapsed to a binary (Sanz 2017). These differences were then used to justify medical theories of the late nineteenth century stating that women were unfit to receive rigorous education in their formative years because it would interfere with reproductive system development, and unfit to do hard mental or physical work during menstruation (Showalter 1970; Bullough and Voght 1973). Thus, an essentialized, hierarchized, binary sex categorization system caused structural harm by giving ideological support to the dominant political positions that women were unfit to vote, work, or participate in public life (Russett 2009).

Second, the scientific history of a sex/gender binary also demonstrates that biological categorization

and normalization can be used to erase, pathologize, and eliminate some bodies. In the late nineteenth century, "Medical and sexological literature [. . .] held substantial definitional power within a culture that sanctioned science to discover and tell the truth about bodies" (Somerville 2003, p. 16). Sexology gave visibility and vocabulary to nonbinary gender identities, but also the authority to declare them pathological (Fausto-Sterling 2000): "Sexology. . . displaced the old view of sexual practices as sinful—and hence under the jurisdiction of the church—and imposed a new view of sexual perversions as disease and/or manifestations of degeneracy, and thus under the jurisdiction of medicine" (Bland 1998). Biological categorization can either completely erase minority existence, as in the biology textbooks that describe only "male" or "female" development as if no variation existed (Bazzul and Sykes 2011; Donovan et al. 2024), or Trump's decree, "'Sex' shall refer to an individual's immutable biological classification as either male or female. . . 'Women' . . . shall mean. . . human females. . . 'Men' . . . shall mean . . . human males" (The White House 2025b). Or, perhaps more insidiously, it can use the "discovery" of deviation from the norm to justify medical, normativizing, and biopolitical intervention, as in the examples of sexology (Somerville 2003), unnecessary surgery on intersex infants and young children (Fausto-Sterling 2000, Davis and Murphy 2013), and the medicalization of transsexual identity in the twentieth century, which collapsed a wide variety of trans identities and expressions into a treatable pathology with access regulated by doctors and scientists (Gill-Peterson 2018).

Intersectional harm

The first two modes of harm, described above, apply to white civil society; the normative ideals of sex and gender categories are, explicitly or implicitly, defined within whiteness. Finally, categories of sex/gender and race interact in their mechanisms of harm. Legal scholar and critical race theorist Kimberlé Crenshaw described this concept in the context of discrimination against black women: "The intersectional experience is greater than the sum of racism and sexism" (Crenshaw 1989). To broadly extrapolate the insight that harm at the intersection of categories is not just cumulative but emergent, we turn to postcolonial scholar Achille Mbembe, who updates Foucault's theory of normalization to consider its intersection with racism and colonialism by considering those who fall categorically and permanently outside of the measured, managed, normalized population, such as African people "left to die" when biopolitics becomes "necropolitics" under colonialism (Mbembe 2019). Similarly, in the US context, Hortense Spillers argues that slavery in the Americas "ungendered" black bodies (Spillers 2003). Rather than being subject to the same normalization that oppressed white women and white people who did not conform to sex and gender norms, enslaved black bodies were excluded categorically from the normalized population, and instead subjected to the logic of what Saidiya Hartman names fungibility and accumulation (Hartman 1997). Thus, the abolitionist questions posed by the Wedgwood medallion–"Am I not a man and a brother?"—and by Sojourner Truth–"Ain't I a woman?"—were far from rhetorical; they named a fundamental exclusion from sex/gender normativity at its intersection with race.

This exclusion at the intersection of race and sex/gender categories manifested in the biological sciences in instances such as the early nineteenth century use of the body of Saartje Baartman by the field of comparative anatomy as evidence that black bodies were always nonnormative in sex/gender, and the argument that supposedly greater sexual dimorphism among white populations than black ones proved that the former was more highly evolved (Somerville 2003). When scientists measured features of black populations in the eighteenth and nineteenth centuries, it was not to include them in the population that could become normative by embodying the mean traits of binary sex/gender categories, but rather to prove they were a separate species or irredeemably degenerate population, and this sex/gender nonnormativity was taken as proof (Somerville 2003). The support for intersectional exclusion by biological categorization persisted after the abolition of slavery in the form of eugenics. Eugenics was a dominant scientific theory and medical practice in the USA in the first half of the twentieth century that leveraged evolutionary principles to control reproduction. And while this movement also enacted ableist policies by advocating for "race hygiene" to keep the white race pure of disability and "degeneration", it enacted categorical violence in limiting the growth of non-white populations. The white feminist birth control movement colluded with the eugenics movement and supported the mass involuntary sterilization of black people (Davis 1983; Somerville 2003; Carter 2007). In summary, in different eras of history, scientific theories authorized intersectional violence in their categorical exclusion of blackness from sex/gender normativity.

On the use of race and sex/gender categories in biology and moving forward

Here we have considered the use of biological race and sex/gender categorization systems in research, teaching, and society. We have interrogated their robustness or ability to meaningfully summarize biological diver-

sity, their usefulness or inferential potential and contributions to understanding and application of biological principles, and their potential to cause structural harm including harm enacted based on the perceived inferiority of a category, exclusion from any category, or existence at intersections of multiple categories. We show, as is well established, that human racial categories have no biological robustness and that while population genetics methods can elucidate demographic history, they do not produce meaningful biological clusters that correspond to racial categories. Sex/gender is more complicated. Anisogamy is very prevalent and associated with differential energetic costs, and vast genetic and phenotypic diversity associated with sexual reproduction is observed. However, this relatively robust binary variation in gamete size does not give rise to consistent, binary sex/gender categories across levels of biological organization. Thus, to varying degrees, and unsurprisingly given their social origins, biological race and sex/gender categorization systems have little robustness or usefulness. However, these biological categorization systems, and the assumptions that arise from them, have caused significant historical and ongoing structural harm. The depths of this harm are so great that it has become embodied; surgeries on intersex bodies and the environmental creation of racial health disparities literally create biological variation that aligns with race and binary sex/gender categories. This highlights the findings of decades of feminist science and technology studies, known but not internalized in the same way by the biological sciences, that "organisms are co-constituted and co-produced by nature and nurture, genes and their environments" (Subramaniam 2014, p. 3) and that systems of oppression constitute a driving environmental force (Haraway 1989; Butler 1990; Fausto-Sterling 2000; Subramaniam 2014; Henry et al. 2023).

Given the weight of the history, and the ongoing impacts, of the structural harm caused by biological race and sex/gender categorization systems, we as biologists must take responsibility for past harms and be accountable for considering whether our current use of race and sex/gender categories contributes to or reduces structural harm. While some factions of the biological sciences community have argued that the potential for harm means that scientists studying human differences have a responsibility that goes beyond being neutral and technically correct (Marks 1995; Maney 2015; Fine and Fidler 2015; Prum 2023), we go one step further and reject the notions that while "biologists studying fruit flies certainly have the same cultural prejudices of an era and class, [. . .] it is more difficult to imagine those prejudices in their work as the basis of scientific authority to oppress or to degrade the lives of other people" (Marks 1995, p. 2–3), and that biological arguments can be decoupled from the society in which they exist: "[t]he biological understanding of sex has been shaped for the comparative study of reproductive systems across the diversity of life, not for making decisions about the social and legal status of human beings" (Griffiths 2021; Griffith and Spencer 2025). We see throughout this paper how categorical perceptions of biological variation, particularly in relation to socially important categories, can cause deep harm. We thus suggest deep interrogation of any proposed use of race and sex/gender categories in biology research and teaching, the reconsideration of the use of such categories in general, and a reparations-based framework to mitigate new harms as we shift our use of these categories.

In this paper, we have laid out a process for interrogating the use of biological categorization systems of race and sex/gender that asks how robust the categories are, how useful they are, and if they cause harm. We suggest this process should be applied every time the use of these categories is considered, and some summary of the results of this thought process communicated alongside any use of the categories. For example, when designing a study to test the effectiveness of a new drug we might consider whether racial groups are a good categorical x-axis, how robustly racial categories describe relevant biological variation, and whether there is any mechanistic rationale for any effect of racial category on the effectiveness of the drug. With this information, we can then make an informed decision about whether any use, in terms of explanatory power, outweighs the potential cost of inadvertently reinforcing the scientific and social perception that racial categories are biological in origin. And when preparing to teach sexual selection, we might ask how useful the differential energetic costs of large and small gametes are in predicting "male" and "female" phenotypes and dedicate class time to effectively communicating complexity. This would enable us to describe the currently understood basis of sexual selection while also highlighting the diversity of reproductive phenotypes and the limitations and harm of a sex/gender binary. We suggest that such approaches will prevent us from defaulting to inadequate systems of categorization, disrupt assumptions about structures of variation and essentialist notions, and force us to weigh any perceived benefits of these categories against the harm that they have and continue to cause (Watkins and DiMarco 2025).

As we move through the above process of interrogating biological race and sex/gender categories, we are likely to come to fundamentally reconsider their use. Given the information reviewed here we might first ask whether we should entirely abandon race and sex/gender categories in biology in what has been termed race, or sex, eliminativism (Noyes and Keil 2019;

Watkins and DiMarco 2025) or whether we should reformulate them. While not yet widely adopted, leading scientific and medical institutions have called for the rejection of biological race categories (Flanagin et al. 2021; National Academies of Sciences, Engineering, and Medicine 2023) and several authors have suggested, variously, multi-dimensional, nonbinary, life-history or population-level treatments of sex, and the operationalization of "male" and "female" for the particular purposes of the study (Roughgarden 2004; Griffiths 2021; McLaughlin et al. 2023; Prum 2023; Smiley et al. 2024; Watkins and DiMarco 2025). We certainly recognize the value in the above approaches, and they are huge improvements over the uncritical use of biological race and sex/gender categorization systems. However, we also make some additional suggestions based on our findings that may advance our thinking.

The social category of race gained substantial power from its entirely unfounded biological associations and, through persistent atrocities, has created profound and ongoing inequalities in the distribution of wealth and violence, and impacted the biology of racialized people. Hence, we suggest that to move to race eliminativism without addressing the biological sciences' role in the harms created would amount to biological colorblindness and so potentially cause new harm. In addition, the inability of racial categories to explain human biological diversity has been known for half a century, yet this is still not consistently reflected across biology research, teaching or society (Morning 2011). It may be that the biological manifestations of the deep harm that race has caused, in addition to the essentializing nature of biological categories and the benefits for white society of maintaining a racial hierarchy, make it hard to disrupt these notions (Gravlee 2009). Hence, we suggest that it may be most beneficial and ethical to, with extreme caution, retain race as an explicitly social-scientific category, as opposed to a natural-scientific one (Noyes and Keil 2019), actively disrupt comparisons to population structure and subspecies in nonhuman organisms, and treat this new social-scientific categorization system as an important site of biological inquiry for examining the effect of social structures on the biology of individuals and groups. For example, a recent study by Nam et al. (2022) starts from the perspective of structural racism and its effects on the neuroendocrine system and goes on to investigate racial disparities in salivary cortisol in response to racist microaggressions, so centering social structures and actively disrupting essentialist notions of biological race.

The effective reform of binary sex/gender categories is challenging for multiple reasons. First, the proximity of binary sex/gender categories to the biologically important process of sexual reproduction, the essentializing tendencies of biological categories, and the implication of the use of operationalized terms that there are benefits to consistent descriptions of "male" and "female" across species seem to make it hard to redefine these categories without slippage back to their current usage. Second, and in contrast to race, the assumed universal nature of sex across species means that any change to category usage has to be applied across all species. And lastly, given that binary sex/gender categories inflict their harm predominantly through exclusion, any efforts to limit harm would require additional categories which would move us further from the purported basis in anisogamy and likely require species- and culturally-specific categorization systems.

Given these complexities, we propose a layered approach that balances conducting biological inquiry and minimizing harm. We propose that all studies should begin from a perspective of sex eliminativism; as a default, we do not treat binary sex/gender categories as a biological variable. The decision to move to any inquiry using binary sex/gender categories should then be justified either by a direct and mechanistic link between the question and differential investment in gametes, which is likely rare, or a focus on the biological effects of the social categories of sex/gender. In the former, we recommend using terminology that centers the differential investment rather than "male/female" due to their repeated application to entire individuals. In the latter, we propose that gender categories may be appropriate but should be multiplicitous. If there is no direct link to gamete investment, we suggest that investigations be framed in terms of mechanistic questions related to components of the reproductive genotype/phenotype. For these studies, we suggest that rather than operationalizing binary sex/gender terms, we instead take the more trans- and intersex-inclusive approach of referring directly to variation in the aspect of the genotype/phenotype of interest, for example, "people who menstruate", "people with ovaries", "people with higher levels of testosterone", etc., as mechanistically relevant. For all of these approaches, we recommend that any analysis that pertains to sex/gender or any components of the reproductive genotype/phenotype should avoid the *a priori* assumption of binary categories and instead use unsupervised statistical methods with a range of possible numbers of categories (Smiley et al. 2024).

Finally, and maybe more importantly than whether we retain race and binary sex/gender categories, we should be concerned with how we fundamentally perceive and communicate variation and how our scientific method creates and reflects harmful processes such as normalization and hierarchization, especially with regard to socially important categories. How do we de-

sign studies, analyze and present data (Sanchis-Segura and Wilcox 2024), and conceive of and discuss variation (Subramaniam 2014)? Do we assume existing categories, or use unsupervised methods to explore data (Pritchard et al. 2000; Smiley et al. 2024)? Do we sample in ways which reflect the true variation, or do we allow preconceived notions and sampling bias to recreate presumed categories (Roberts 2011; Fujimura et al. 2014)? Do we present data in ways that accurately reflect within- and between-group variation, or do we compress variation and rely on mean comparisons, creating the illusion of discrete and fixed categories (Sanchis-Segura and Wilcox 2024) and promoting normalization (Foucault 1995)? Do we default to poorly defined essentialist hypotheses, or do we devise mechanistic hypotheses that consider the full scope of environmental effects and actively reject unfounded essentialist assumptions (Tsai et al. 2020; Henry et al. 2023)? Do we consider variation neutral, beneficial or pathological (Fausto-Sterling 2000; Subramaniam 2014; McLaughlin et al. 2023)? And do these approaches and perceptions change across systems of categorization based on their social importance (Fausto-Sterling 2000)? We suggest that the harm caused by scientific normativity and hierarchization may be reduced by statistical and illustrative approaches that better reflect variation (Donovan 2022; Sanchis-Segura and Wilcox 2024; Smiley et al. 2024), by gathering counterevidence within scientific epistemologies (Roughgarden 2004; See 2020), by attending to resistant, nonscientific or science-critical epistemologies within Western cultures (Haraway 1989, 1991; Harding 1991), and by learning from indigenous and non-Western epistemologies in which all beings are interrelated and nonhierarchized (Liboiron 2021; Hernandez 2022).

However, we argue that before we move forward, and for any of these approaches to have any hope of success, science must make reparations for the deep harm that it has caused through the biological categorization systems of race and binary sex/gender. Even if contemporary biology is beginning to move away from such essentialist categorization systems, this does not redress the prior harm done both materially and in terms of social perceptions. In "The Case for Reparations", Ta-Nehisi Coates writes, "Indeed, in America there is a strange and powerful belief that if you stab a black person 10 times, the bleeding stops and the healing begins the moment the assailant drops the knife. We believe white dominance to be a fact of the inert past, a delinquent debt that can be made to disappear if only we don't look" (Coates 2014). That is, dominant society cannot just change how it operates, but must also make commensurate amends for the enormous harm done. And this is as true in science as it is more broadly (Ogbunu 2020). Scientific reparations could take many forms including material support for data sovereignty (TallBear 2013, scientists from oppressed groups (Schell et al. 2020; Taffe and Gilpin 2021; Lewis and Sharpe 2023), and research that centers the embodiment of systems of oppression (Gravlee 2009; Nam et al. 2022); appropriate leveraging of genetic data to support reparations claims (Nelson 2016) and phenotypic data to highlight sex/gender diversity (Roughgarden 2004; McLaughlin et al. 2023); and the commitment of time and energy required to resist the allure and convenience of categorical thinking and fundamentally change how we conceive of variation in biology research, teaching, and society.

Author contributions

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