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PERSPECTIVE

The methodological and ethical concerns of genetic studies of same-sex sexual behavior

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Summary

Same-sex sexual behavior has long interested genetics researchers in part because, while there is evidence of heritability, the trait as typically defined is associated with fewer offspring. Investigations of this phenomenon began in the 1990s with linkage studies and continue today with the advent of genome-wide association studies. As this body of research grows, so does critical scientific and ethical review of it. Here, we provide a targeted overview of existing genetics studies on same-sex sexual behavior, highlight the ethical and scientific considerations of this nascent field, and provide recommendations developed by the authors to enhance social and ethical responsibility.

Genetic studies of same-sex sexual behavior

Since the early 1900s, researchers have sought to identify a genetic basis for same-sex sexual behavior (https://www.hrc.org/resources/the-lies-and-dangers-of-reparative-therapy). Though there is evidence that variation in the trait is partly attributable to genetic variation,[1,2] this area of study has been mired in fierce scientific and ethical debate. For example, some LGBTQIA+ activists have expressed concerns that this research extends a long history of pathologizing same-sex sexual behavior, and could be used to try to "fix" same-sex sexual behavior (https://www.hrc.org/resources/the-lies-and-dangers-of-reparative-therapy).[3] At the same time, other activists are more supportive of the research, provided that the results are communicated accurately.[4,5] Scientists have also voiced concerns over the limitations and replicability of these studies and how they are conveyed as an evolutionary framing of research on identities.[6] Meanwhile, other researchers claim that their findings will lead to greater understanding of human sexuality but often fail to reduce stigma against sexual minorities. Throughout this debate, a number of genetic studies of sexuality have been misused. For instance, a direct-to-consumer genetic testing platform released an app offering to calculate "how gay are you?"[7] based on the published results of a genome-wide association study (GWAS) on same-sex sexual behavior. Additionally, there are concerns regarding the use of this research in the criminalization of same-sex sexual behavior, conversion therapy, and stigmatization of individuals who participate in same-sex sexual behavior.

To summarize arguments being made about, and to mitigate the risks of, same-sex sexual behavior studies, we begin by providing a targeted overview of existing same-sex sexual behavior research, highlighting the methodological and ethical issues within these studies. These issues broadly include the following themes: lack of replication, over reliance on European genetic similarity, overuse of the UK BioBank (UKBB), lack of consistent definitions of same-sex sexual behavior, not considering confounding variables or environmental factors, and not working with affected communities to consider risks of the research. Next, we discuss the responsibility of scientists as well as systemic flaws within the scientific process itself. Finally, we propose recommendations for the scientific community to consider.

Throughout this manuscript we use "same-sex sexual behavior" while discussing studies that may have used different terminology in their own publications (e.g., "same-sex behavior," "homosexual behavior," "gay," and others). We use same-sex sexual behavior in order to be more specific and not conflate with community labels, as well as to standardize discussion of the behavior being examined and avoid terms that are not inclusive or not selected by communities impacted by the research. Phrases from specific studies will be shown in quotes when used. We recommend that researchers use specific labels and inclusive, community-selected language.[8]

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Evolving methodological and ethical issues of research on same-sex sexual behavior

Lack of replication

Many studies have sought to identify genes associated with same-sex sexual behavior by focusing on familial analysis and pedigrees.[7] Such studies have calculated that individuals participating in same-sex sexual behavior are more likely to have a sibling (particularly a brother) who also participates in same-sex sexual behavior than those participating in only opposite-sex sexual behavior. Twin studies have subsequently supported these results, indicating that there is a higher concordance of same-sex sexual behavior among people who have a twin.[1] These studies estimated the heritability of same-sex sexual behavior to be about 60%.[9] It is crucial to note that heritability is *not* a measure of genetic susceptibility to a given phenotype. Rather, heritability is a population-level statistic that quantifies the fraction of phenotypic variation among members of a population that is attributable to genetic variation among those individuals. As such, heritability estimates can be highly context-dependent and sensitive to the environment, historical time, and social structure. Virtually all traits, including behavior, have non-zero heritability.[10] It is also important to note that genes and environments are inherited together; individuals with more genetic similarity, such as families or groups from the same region, are also exposed to more environmental similarity, which can confound heritability estimates.[11–15]

While the heritability of same-sex sexual behavior has been replicated, efforts to identify specific genetic associations have been inconclusive. In 1993, a linkage study of 40 families[16] drew a connection between a genetic marker at Xq28 with male same-sex sexual behavior, which colloquially became known as the "gay gene," a phrase that oversimplifies the extent to which many genes play a role in the development of same-sex sexual behavior.[3] Later, in 2005, the first major genome scan for linkages with same-sex sexual behavior in men from 146 families was performed.[17] It failed to replicate the Xq28 region but reported others. A larger study on 409 pairs of brothers participating in same-sex sexual behavior was carried out in 2015 that identified Xq28 as being partially involved and suggested that a region on chromosome 8 was involved as well.[18] Taken together, these studies provide contradictory results that do not provide insight into how genetics play a role in same-sex sexual behavior.

Stemming from these early studies, the idea of a gay gene captivated the popular imagination.[19] Research into the genetic etiology of same-sex sexual behavior resulted in the narrative that those engaging in same-sex sexual behavior are "born this way" rather than making conscious choices.[6,20,21] While not all of the LGBTQIA+ community has adopted this narrative, and the argument itself is a logical fallacy,[3] the support for it has damped critique of these studies. A review from 1995, a few years after the 1993 gay gene publication, suggested that genetic studies of human sexuality should (1) report "valid and precise measures of individual differences," (2) employ "appropriate methods to ascertain biological relationships," (3) investigate "research subjects who have been randomly recruited," (4) use "appropriate sample sizes," (5) conduct "appropriate genetic models to interpret the data," and (6) exercise "caution in interpreting biosocial effects from the observed phenotypic correlations."[22] At the time it was written, the author was of the opinion that no study fully met these criteria. A review from 2023 of literature relating to human sexuality came to the same conclusion: no study had fully met all six criteria.[23]

A crucial limitation of these early linkage studies was that results were inconsistent. Additionally, the 1993 gay gene study was explicitly criticized[23] for its study design, which primarily aimed to compare non-same-sex sexual-behavior-participating siblings to same-sex sexual behavior participants.[3] Because the authors did not conduct DNA linkage analysis of the siblings, there was no control group for the study, which precluded the validation of differences seen specifically in individuals participating in same-sex sexual behavior.

The results of these initial studies demonstrated that same-sex sexual behavior is impacted by many different genetic processes.[21] As molecular genetic data became easier to obtain, the field shifted to conducting GWASs. In 2013, the first GWAS of human sexuality was published.[24] In this study, the authors identified variation upstream of *SMOC1*, a gene that potentially regulates prenatal sex hormones and digit ratio (ratio of lengths of the index and ring fingers). Prenatal sex hormones and digit ratio have been connected to a wide range of complex traits and behaviors, including same-sex sexual behavior. The 2013 GWAS was followed by another in 2017 on male sexual orientation.[25] Analysis identified a number of hits, including a SNP near *SLITRK5*, a gene whose protein product regulates neurodevelopmental pathways, which had been previously implicated in male same-sex sexual behavior.[23]

The largest ever GWAS of same-sex sexual behavior was published in 2019. The research team used data from the UKBB and the direct-to-consumer genetic testing company 23andMe.[2] The study estimated that 8%–25% of the variance in same-sex sexuality could be associated with genetic factors—indicating that same-sex sexual behavior is highly polygenic and predominantly impacted by environmental factors. Most recently, in 2021 a GWAS in Han Chinese participants followed by a postmortem and animal study looking at male same-sex sexual behavior was published.[26] Through this, they found two genetic loci strongly associated with male same-sex sexual behavior (*FMR1NB* and *ZNF536*). *ZNF536* was shown through the postmortem study to be down-regulated in the brains of individuals participating in same-sex sexual behavior, and an increase

in same-sex sexual behavior was observed in *FMR1NB*-knockout mice.

Replication issues have continued into the GWAS era. Ganna et al. only replicated findings for three of the five identified SNPs.[20] Similarly for Sanders et al.,[18] no individual SNPs were statistically significant. These problems were not unique to these studies; the same issues plagued many searches for genes associated with behavioral phenotypes.

Over reliance on European genetic similarity

The shift to GWAS brought with it additional limitations, which are shared by other studies using these methods. Ganna et al.[2] suffers from self-selection bias since less than 6% and 2% of UKBB members and 23andMe members, respectively, consented to be part of the study.[23] The authors additionally excluded individuals whose gender identity did not match their sex at birth, or transgender individuals. While gender is separate from sexuality, transgender individuals can participate in same-sex sexual behavior. In addition, these studies are further limited by their overreliance on data from individuals of European ancestry (or more precisely, European genetic similarity)—indicating that the findings are not generalizable.[14,20]

Overuse of the UKBB

In follow-up studies, a research team published papers in in 2023[27] and 2024.[28] In the 2023 paper, the authors aimed to evaluate the impact of oral contraceptives on the genetic maintenance of same-sex sexual-behavior-associated alleles using the UKBB. The authors summarize previous work hypothesizing that individuals carrying same-sex sexual-behavior-associated alleles who participate in opposite-sex sexual behavior have more sexual partners than those not carrying such alleles. Same-sex sexual-behavior-associated alleles are hypothesized to have been maintained through a positive impact on reproductive success. As posited by the authors, the use of contraception since the 1960s may have decoupled the number of sexual partners from the number of offspring. Therefore, the authors propose that the mechanism of genetic maintenance of same-sex sexual-behavior-associated alleles could be abolished.

This was followed by a 2024 publication looking more closely at the evolution of bisexual behavior.[28] The authors hypothesize that bisexual behavior is evolutionarily advantageous as it leads to more offspring compared to strictly same-sex sexual behavior. They then separated individuals by sex and determined that specifically male bisexual behavior was correlated with higher numbers of offspring. Subsequently, they turned their attention to risk-taking behaviors, which had been associated with same-sex sexual behavior in another study,[29] and found that male bisexual behavior was also correlated with risk-taking behavior. Finally, they showed that exclusively same-sex sexual behavior was negatively correlated with the number of children.

The UKBB has become a primary dataset used by researchers conducting genetics studies due to the breadth of data available. However, researchers need to keep in mind that the UKBB is primarily made up of individuals who are generally older and were receiving medical care while same-sex sexual behavior was stigmatized and discriminated against, including by medical doctors and the medical establishment.[14] Even now, 1 in 8 LGBT individuals in the UK say that they have experienced discrimination within healthcare (https://www.stonewall.org.uk/lgbtq-facts-and-figures). Disclosing to a medical professional that one participates in same-sex sexual behavior still runs the risk of discrimination. Therefore, it is plausible that a large number of people in the UKBB (as high as 65%) participated in same-sex sexual behavior but did not disclose the information.[30,31] As a result, this database is insufficient for identifying genetic trends underlying sexual behavior without several caveats, as participation bias creates the possibility that any trends identified are not related to the trait but to the subset of individuals who enroll in the database. We refer to a National Academies of Sciences, Engineering, and Medicine (NASEM) consensus report, which warns that if the pre-existing data do not meet a number of quality control checks, then careful consideration should be given to whether it should be used in research.[32] This appears to be the case with studying same-sex sexual behavior and the UKBB. As Song and Zhang[28] state, "the phenotypes analyzed here are self-reported, so they may contain substantial errors … if such errors are non-random, then they could create spurious genetic correlations." Since there is strong evidence that same-sex sexual behavior is both underreported and impacted by participation bias, it puts these results into question.

Lack of consistent definitions

Throughout all of this work, genetic studies of same-sex sexual behavior consistently lack clear definitions for what exactly same-sex sexual behavior consists of, and research treats this trait as an unchanging phenotype (when it is not).[20] This means results cannot be directly compared, and there is a lack of clarity over what researchers are studying. For example, Hamer et al. based their definition of same-sex sexual behavior on a single question[16] while Sanders et al. used self-reported identity and a Kinsey scale questionnaire.[18] Later on, Ganna et al. would define same-sex sexual behavior as having ever participated in same-sex sexual behavior.[2] These studies fail to capture the many complex facets that make human sexuality both variable and personal by reducing it to a binary trait (https://www.scientificamerican.com/article/is-bisexuality-genetic-its-more-complex-than-some-studies-imply).[2,23]

Not considering confounders or environmental factors

In Song and Zhang,[27] the initial hypothesis of this study is that same-sex sexual-behavior-associated alleles are

genetically maintained through increased offspring number. However, the authors never provide evidence to support this hypothesis, and the only support for this idea comes from a cited paper mentioning it as a possibility.[29] The authors' secondary hypothesis is that this mechanism of maintenance is abolished with the rise of oral contraceptives. In their analysis, the authors focus on oral contraceptives becoming available in 1960 yet overlook any other confounding variables. Many things changed in the 1960s, including gender roles, women's education, the feminist movement, and family structure.[33] In addition, the availability of oral contraceptives varied among different populations.[34] The authors failed to consider these factors as part of their studies, even though they are indeed raised in papers that the authors cite.[33] In fact, one such paper admits that "current associations between the number of mates and reproductive success (number of children) are unlikely to be informative" because contraceptives were not present for much of evolutionary history.[29] The study concludes with the idea that contraception is causing a decline in same-sex sexual-behavior-associated alleles—an "unfounded interpretation" of the data they presented.[20] Until these confounding variables are explored, concluding that oral contraceptives caused any changes remains unsubstantiated.

Additionally, the authors did not report the number of individuals they separated into different categories: individuals participating in same-sex sexual behavior and those participating in opposite-sex sexual behavior, which should have been included to facilitate replication of their work, so it is difficult to figure out how undercounted their analysis is (the authors also have not released summary statistics of their results, which is common practice for GWAS research, so it is impossible to know how they utilized the data).

Furthermore, investigating a connection between bisexual behavior and risk-taking behavior in Song and Zhang[28] requires significant justification since these are stigmatized behaviors. The authors note that a previous study found a connection to same-sex sexual behavior,[29] but that same study also found a connection to "openness to experience" and "physical attractiveness," two traits that are not investigated. Given that disclosing participation in same-sex sexual behavior is a risk by itself, this could be a confounding factor. In addition, the genetic correlation between exclusive same-sex sexual behavior and risk-taking behavior is not shown. This correlation is likely to be high as well, putting into question their finding that it only correlates with male bisexual behavior. It is also not clear what "risk-taking behavior" consists of as it is a single question in the UKBB survey, and definitions are likely inconsistent between participants. This selection of traits to compare both assumes that previous research is high quality and that therefore the comparison will be informative, which may be premature.[20]

The Song and Zhang[28] study raises a number of ethical concerns because it also stereotypes bisexual individuals as more sexually promiscuous (https://www.ambi.org/pressblog/bisexual-community-helps-break-stereotypes). The idea that individuals who participate in bisexual behavior are more likely to participate in risk-taking behaviors implies that they are more likely to take risks sexually. This has the potential to not only further the stereotype's prominence in society but also give it dangerous scientific backing. Given these concerns, further justification was needed to include risk-taking behaviors in this study.

Many studies do not acknowledge environmental impacts on same-sex sexual behavior.[2,35] To use Song and Zhang[27] as an example, when environmental impacts are acknowledged by the authors they state that same-sex sexual behavior has become more acceptable and that these behaviors will not disappear entirely as a result. This contradicts the main conclusion of their publication, which is that same-sex sexual behavior alleles will disappear from human populations. The authors themselves note that "increased birth rank of same-sex sexual behavior males arises from phenotypic plasticity instead of genetic effects," indicating that they are aware of factors beyond genetics, yet they do not include them in their study design.[27] Neglecting to mention a major factor in the development of same-sex sexual behavior does not adequately convey the limitations of the analysis being presented.

Not working with affected communities

An article published alongside Song and Zhang[28] included the following quote from the authors: "Many studies that were once considered dangerous propelled the progress of science, technology, and society."[36] This indicates that the authors recognize that their study carries risks. Furthermore, there does not appear to have been any meaningful or substantial involvement of the queer community in this research; the authors refer to an informal discussion with colleagues, but these colleagues are not acknowledged in the paper and are only credited with input into word choice at the end.[36] If there was substantial inclusion and discussion with queer individuals, those who this research places at greatest risk, there may have been better awareness of how this research could be used to discriminate against a community.[20] Greater engagement is increasingly what members of the LGBTQIA+ community want,[4] and a recent NASEM consensus report recommended that researchers "work in ongoing partnerships with study participants and community experts."[32] Crucially, any approach to community and/or public engagement should adhere to existing guidelines such as the Belmont Report and assess not only risks and potential benefits but whether benefits could be obtained by other means.[37]

The responsibility of scientists

As scientists, we have a direct responsibility to consider the social implications of our research and to safeguard against

potential harm. Indeed, a 2021 American Association for the Advancement of Science (AAAS) survey of scientists and engineers found that many agree they have a responsibility to take into account and minimize the risks of their research to society.[38] Unfortunately, there are ample examples of poorly conducted studies that have had a major impact on science and society and how genetic studies can impact extremist views and attacks. This includes the Buffalo shooting, where the perpetrator posted a manifesto citing behavioral genetics and evolutionary genetic studies.[39,40] This highlighted the potential negative uses of scientific studies, and sparked calls for increased responsibility among scientists.[40] Unfortunately, many scientists remain unaware of the social implications of their research.[8,41] Given that multiple mass shootings have already occurred targeting the queer community, it is possible that a study perpetuating stereotypes could lead to another act of hate (https://www.sandyhookpromise.org/blog/news/facts-and-statistics-about-the-impact-of-gun-violence-on-lgbtq-people/). Previous insights into the biological causes of same-sex sexual behavior have already resulted in gruesome attempts to "cure" individuals of this trait, including sterilization (https://www.hrc.org/resources/the-lies-and-dangers-of-reparative-therapy).[42]

Behavioral genetics studies are highly controversial.[43] The language used in studies like these, whether intentional or not, is often rooted in notions of genetic essentialism, or the idea that behaviors clearly divide humans into different groups that are "stable, immutable, and based in biology."[41] Same-sex sexual behavior genetics studies divide participants into two groups, one that participates in same-sex sexual behavior and one that does not, and assumes those groups to be inflexible. Similarly, genetic determinism, or the idea that genes determine every aspect of an individual, also comes into play if the results are not communicated in a way that makes limitations clear.[14,41] Further, the majority of these studies demonstrate genetic reductionism, or the idea that sexual behavior is best understood at the level of genetics rather than the environment, when the environment is not highlighted as another factor impacting variation in human traits.[41] These ethical issues are not inconsequential as same-sex sexual behavior was explicitly flagged as a "sensitive phenotype" in the 2023 Hastings consensus report on social and behavioral genomics[13] because it is a trait essential to the identity of a minoritized community. The report concludes that genetics research on sensitive phenotypes requires dedicated effort into responsible research conduct and communication.

When studies with inadequate scientific rigor go unchallenged, public perception of science and scientists may be harmed. It is rapidly becoming the responsibility of scientists to oppose anti-scientific rhetoric; currently, only 57% of Americans think that science has a positive impact on society.[44] In the US, confidence in science continues to decline and become more polarized, making it essential that the scientific community address bias and discrimination in its processes. Unfortunately, scientists encounter many barriers to thinking about societal impacts of their work. This can range from well-meaning scientists navigating barriers[45] to less-interested scientists finding ways to morally disengage from their social responsibilities to prevent harm.[46] However, "minimizing one's responsibility to mitigate against the social risks of a body of research does not make these risks go away."[40] Research can pose real risks; it is imperative that scientists start taking them more seriously at every level of the scientific process.

Systemic flaws within the scientific process

Methodologically and ethically flawed papers on same-sex sexual behavior beg the question: why do studies with key methodological limitations and significant ethical concerns keep happening? Here, we present an overview of stakeholders who are involved in the process and bear a responsibility (summarized in Table 1).

Funders

Funding bodies should take care when funding studies that investigate "sensitive phenotypes" and monitor the studies performed with grant funding carefully. Oftentimes, scientists use funds to perform research that is not connected to what they originally proposed in a grant application because of exciting findings during the course of research. Funders should consider developing mechanisms specifically for grants funding the study of sensitive phenotypes to more effectively observe how funding support is being used and if it aligns with the original proposal. Scientists are monitored in many ways throughout the research process (institutional review boards [IRBs], annual reports, conflict of interest statements, etc.), and we would recommend adding sensitive phenotypes as another element to consider when placing additional requirements on research.

Groups operating within academic institutions

As scientists, research groups are subject to a certain amount of oversight. Institutional committees such as IRBs and research ethics committees composed of bioethicists and diverse community and research members should be empowered to conduct regular reviews of lab research topics and flag projects that pertain to sensitive phenotypes. As the IRB focuses on human subjects research, many GWASs may not need to undergo an IRB review process, and additional review mechanisms for non-human subjects research are needed. One such example is the Ethics & Society Review at Stanford, which was developed for the review of artificial intelligence research (https://casbs.stanford.edu/ethics-society-review-stanford-university). In addition, IRBs largely focus on risks to study participants and are prohibited by federal laws like the Common Rule from considering broader impacts, such as the risks to communities

Table 1. Summary of stakeholder responsibilities and recommendations for research involving sensitive phenotypes

Stakeholder	Role in research overview process	Recommendations
Funders	monetarily support research	1. monitor how funding is being used to study sensitive phenotypes 2. withdraw funding from studies that are methodologically and ethically flawed
Groups within academic institutions	institutional review boards and research ethics committees that regularly review research projects	1. develop additional review processes for research on sensitive phenotypes akin to the Ethics & Society Review at Stanford University 2. provide resources for researchers to learn about scientific communication and community engagement
Biobanks	provide data for researchers to use	1. develop approval processes to examine studies before allowing access to data 2. provide limitations of their available data to help when deciding to use a given dataset
Academic journals	publish results of scientific research	1. make use of review processes to ensure studies being published are scientifically and ethically rigorous 2. provide greater recognition of studies that model rigorous methodology and clear, careful use of terminology
Media journalists	allow for wider dissemination of scientific research to the public	1. highlight studies that exemplify best practices within their methodology and demonstrate clear scientific communication with their results 2. portray studies (including the ethics behind them) accurately when presenting them
The public	engage with research results and are, ultimately, the group being studied within human research	1. engage in meaningful bidirectional partnerships with researchers 2. reconsider how we think about human sexuality

(https://www.ecfr.gov/current/title-45/subtitle-A/subchapter-A/part-46/subpart-A/section-46.111). Academic institutions can provide greater education about topics like research communication, risks to communities, and the importance of community engagement; a recent AAAS survey highlighted that more scientists rate these skills as very important but have limited access to resources to develop these skills.[38]

Biobanks

As biobanks continue to expand in size and scope, bioethicists are wrestling with issues such as how consent works with major biobanks. Data sharing can have benefits such as encouraging collaboration with diverse groups and enabling larger sample sizes to be collected (https://www.ashg.org/wp-content/uploads/2023/10/ASHG_Success_Stories-Data-Sharing-Final.pdf). But these benefits come with many responsibilities and risks since individuals need to have trust in scientific institutions to participate in data collection, and once violated, that trust is hard to rebuild. Biobanks need to revisit their approval process and rethink how access is given, particularly to ensure that the use of a biobank to study a specific trait is paired with collaboration with a community that has a stake in how that trait is perceived (https://www.ashg.org/wp-content/uploads/2023/10/ASHG_Success_Stories-Data-Sharing-Final.pdf). Previously, it has also been demonstrated that researchers with a political agenda are eager to access biobank data through both established access protocols and otherwise.[47] Biobanks need to take care that their procedures are protecting individuals and communities while also allowing for exciting research to take place.

Academic journals

In theory, the peer review process should weed out methodologically and ethically flawed science. Many journals have begun creating guidelines to mitigate the potential for stigmatizing research.[48] However, there are key limitations to the academic peer review process, including few protections against reviewer bias and peer review being an ineffective deterrent for plagiarism.[49] Editorial processes need to take care to prevent non-rigorous science from gaining publication.

Media journalists

Multiple press releases followed the publication of many of these studies, giving such research more legitimacy and a larger platform for attention. Since the lay public primarily engages with science in this way, more oversight needs to be taken to ensure that studies are carefully selected and presented accurately. Media journalists act as a bridge between the scientific community and the public by covering science in an accessible way, which is hugely important, but can result in oversimplification of the research they cover.

The public(s)

Community and public engagement is frequently offered up as a commendation for supporting more ethical and socially responsible research. For instance, some researchers set up websites with FAQs and outreach videos to help clarify the limitations and interpretation of the results (https://geneticsexbehavior.info/). However, members of the public and, in particular, communities that have historically been exploited by scientific research shoulder many of the burdens that come with the implementation of emerging technologies. These communities are often left out of upstream decision-making processes about whether, how, and what kind of research should be conducted. Examples of excellent upstream engagement include work done by the Native BioData Consortium to empower Indigenous groups, which can be used as a model

for future research frameworks.[50,51] In service of more equitable benefit sharing, it is necessary to bring in those who are often excluded from upstream decision making in the scientific process.

Recommendations for future studies

Establish meaningful partnerships with affected communities

Any study including human populations and human identities needs the input of those populations and identities in order to represent them accurately and respectfully. This engagement should be present from the conception of the study up until publication.[32] Importantly, there is concern among some researchers and activists that community and public engagement are becoming box-ticking exercises and that there are few opportunities to evaluate the goals and outputs of any given engagement.[52,53] While engagement with communities that have a relevant stake in research is vitally important, these efforts should take care to do so in a meaningful manner that supports power sharing, reciprocal relationships, and co-learning.[54] Furthermore, assessing who is being engaged, how, and what the outcomes of an engagement are will be vital for identifying both successful approaches and failures.

Reconsider how to conceptualize and study human sexuality

As a scientific community, we need to reconsider how we conceptualize and study human sexuality. This can be mitigated by partnerships with the queer community since, for decades, the queer community has had an understanding that human sexuality is fluid and constantly changing.[55] We need a research framework that recognizes how sexuality is highly dynamic and personal to each individual, and some recommendations have been put forward by queer scientists that primarily highlight the need for flexible self-identification.[56] Additionally, sexuality is highly dependent on the environment, and environmental factors continue to be understudied (partly due to the fact that it is harder and can be more costly to study).[57] Reconceptualizing how we think of sexuality might mean reconsidering whether genetics is the best lens to view this trait, as existing results have contributed minimally to our understanding of the phenotype.[20,23] This could mean supporting research within the realms of sociology or psychology until the field is better equipped to study this behavior through a genetic lens.

Recognize heightened responsibility in behavioral genetics research

Researchers need to take the lead in evaluating and communicating the limitations of their studies in behavioral genetics research. Previous work has shown that scientists communicating their findings attenuates science denialism online.[58] As the 2023 Hastings consensus report on social and behavioral genomics concluded, research into sensitive phenotypes like same-sex sexual behavior requires increased responsibility from researchers to engage with stakeholders, justify research parameters, and prioritize responsible conduct and communication.[13] Additionally, researchers should interrogate if their study could be interpreted in determinist, reductionist, or essentialist ways to not further these misconceptions.[41] As has previously been discussed, the risks of scientific research continue to exist even if individual researchers absolve themselves of responsibility.

Evaluate the appropriateness of the dataset

When scientists analyze data they did not personally collect, it is important to ask how well-suited the dataset is for their proposed study. Are the labels well defined, appropriate, meaningful, and community selected? Do they directly support the research question? Biobanks could highlight the limitations of their data to aid in decisions pertaining to its use. A NASEM consensus report includes a discussion of this, as well as a flowchart for deciding whether to use a given dataset or not.[32]

Think about the language used

Language has a large impact on how studies are received, and any quote can easily be pulled out of context and misinterpreted. As a result, scientists need to carefully think about how their work is presented. In a 2023 article dedicated to the discussion of language in science, Cho et al. suggest that the following questions be considered: "What is the evidence that racial, ethnic, sex, gender, or other differences are essential and relevant to the research question, and are there other types of differences that are being overlooked? What is the evidence that the differences are accurately measured or ascertained? Is the validity of the classification systems based on assumptions or evidence? Are labels respectful, accurate, and derived from community input?"[8] Racial, ethnic, sex, gender, or other labels may also have overlap and examining their intersectionality is equally important.[59]

Think about downstream implications of the research

Similarly to how a quote can be taken out of context and misinterpreted, figures from a study can also be taken out of context of the paper and misused.[39,47] Additionally, data from a study can be used by other researchers who may not be conscious of risks and reach harmful, misleading, or inaccurate conclusions. Before collecting or publishing data, scientists should think about minimizing its abusive uses, whether through study design or a review process. Existing datasets such as All Of Us have policies for researchers requesting to use the data, including training. They also have a designated committee called the Resource Access Board that evaluates if potential projects could be stigmatizing (https://www.researchallofus.org/frequently-asked-questions/). We recommend that

other biobanks consider using these methods to minimize and prevent misuse.

Conclusion

As indicated by recent research, science needs to overhaul how studies of same-sex sexual behavior are conceived, carried out, analyzed, and presented. These studies present very real risks to individuals who participate in same-sex sexual behavior, particularly those within the LGBTQIA+ community. This can lead to supporting conversion therapy, stigma, discrimination, and/or violence against LGBTQIA+ individuals. We recommend that changes occur at every level of the scientific process to mitigate these risks and ensure that science is a process that continues to benefit, and not hurt, the people that participate in it.

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Declaration of interests

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Supplemental information

Supplemental information can be found online at https://doi.org/10.1016/j.ajhg.2024.08.007.

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