Comment

Racism in science

Counter the weaponization of genetics research by extremists

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A memorial to the ten Black people who were killed by a shooter outside a shop in Buffalo, New York, in May 2022.

Geneticists must rethink how they conduct their research and how they communicate results.

Earlier this year, we were appalled to see a figure from a paper[1] co-authored by one of us (S.R.) displayed in a 180-page screed that was used by an avowed white supremacist to justify his massacre of ten Black people at a shop in Buffalo, New York.

Even before then, we had noticed that our work on patterns of global genetic diversity in humans was increasingly being invoked in online discussions among those who support white nationalist ideology. For example, a 2014 study on the origins of present-day Europeans[2] (co-authored by B.M.H.) continues to be mentioned regularly by Twitter users who deploy neo-Nazi symbols and imagery in their biographies.

There is growing awareness among geneticists and other researchers that the latest resurgence of white supremacy is being driven, in part, by the far right co-opting scientific findings. In fact, over the past five years or so, numerous scientists, editorial boards, scientific societies and research consortia have published statements denouncing the misuse of research by those who wish to feed racist ideologies.

Yet the actions proposed to deal with this issue are often vague. Take the Center for ELSI Resources and Analysis (CERA), a hub where stakeholders can learn about the ethical, legal and social ramifications of genetics and genomics research. CERA is currently urging "scholars, scientists, funders, policymakers, community advocates and others" to "recognize and address the racist use of genetic research", and provides a collection of resources to support this goal (see go.nature.com/3eebx3d). But even after we scrutinized the articles and other resources listed, we found it is frustratingly unclear exactly how scientists, clinicians or policymakers should tackle the issue.

We think that the efforts made so far by the scientific community to confront the latest resurgence of white supremacy are insufficient. Here, we lay out some concrete ways in which human geneticists could counter the co-option

and weaponization of primary scientific literature by the far right. These include changes to the way geneticists conduct their research, and to how that research is communicated.

History of hate

The misappropriation of research has been central to repeated attempts to revitalize the power of the far right since the Second World War.

For example, in the late 1970s and early 1980s, the National Front, a UK neo-fascist organization, produced a series of articles presenting findings from mainstream scientific research as evidence that racism was scientifically justified. Other white supremacist groups, including the US National Alliance (founded in 1974), have likewise been zealous consumers and promoters of primary scientific literature.

Around that time, many of the sociobiologists and other scientists whose work was misappropriated engaged in a series of heated exchanges in this journal and other venues. They insisted that their research was self-evidently incompatible with racist interpretations – in their view, any readers of their papers who came to racist conclusions had simply failed to understand the science[3–6].

Similar assertions dominate conversations among scientists today about the political weaponization of their work.

In tweets, editorials, blog posts and so on, geneticists often describe their work as being misused, misinterpreted and misappropriated to support far-right ideologies. When investigators and consortia publish human-genetics studies, they are urged to refute co-option of their research by using press releases or by listing answers to 'frequently asked questions' on consortia websites (see, for instance, www.thessgac.org/faqs and go.nature.com/3ssyoaa).

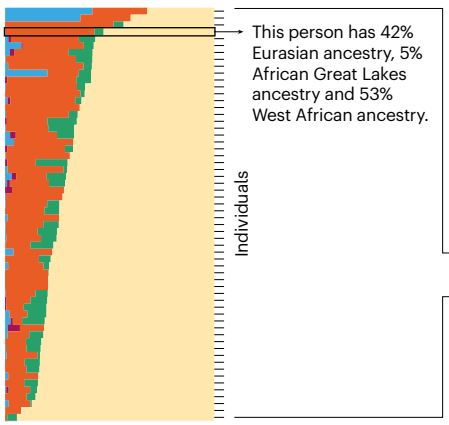
Yet the use of these post-hoc communications – especially answers to frequently asked questions – presupposes that non-specialist audiences might 'frequently' draw racist conclusions from the data. In our view, if we state that contemporary genetics research as a whole is incompatible with racist interpretations, yet acknowledge that human-genetics studies might foster racist interpretations, then something is awry with how we are conducting those studies and communicating the results.

With all its benefits, the growth of open-access publishing is making it easier for non-scientists to engage in what are essentially online journal clubs. Social-media platforms, such as Twitter and Facebook, enable non-specialists to communicate directly with

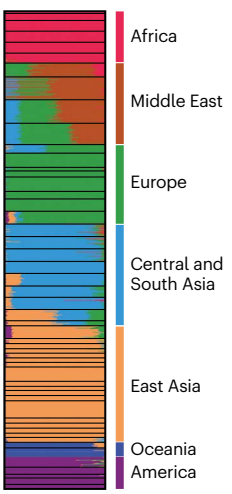
RACISTS USE GENETICISTS' INFOGRAPHICS

Compiling genotype data from individuals can show the genetic diversity of populations (**A**). A 2008 analysis* (co-authored by S.R.) suggested significant genetic differences between seven continental populations (**B**). But only 13.5% of the populations represented were from Africa. Boosting representation to 85% and sampling more broadly across the continent (**C**) underlines that the level of genetic variation within Africa is equivalent to that seen between continents.

A Individual genomes
Each horizontal bar corresponds to the genome of a single person, in this case from a population identified or self-identified as African American.



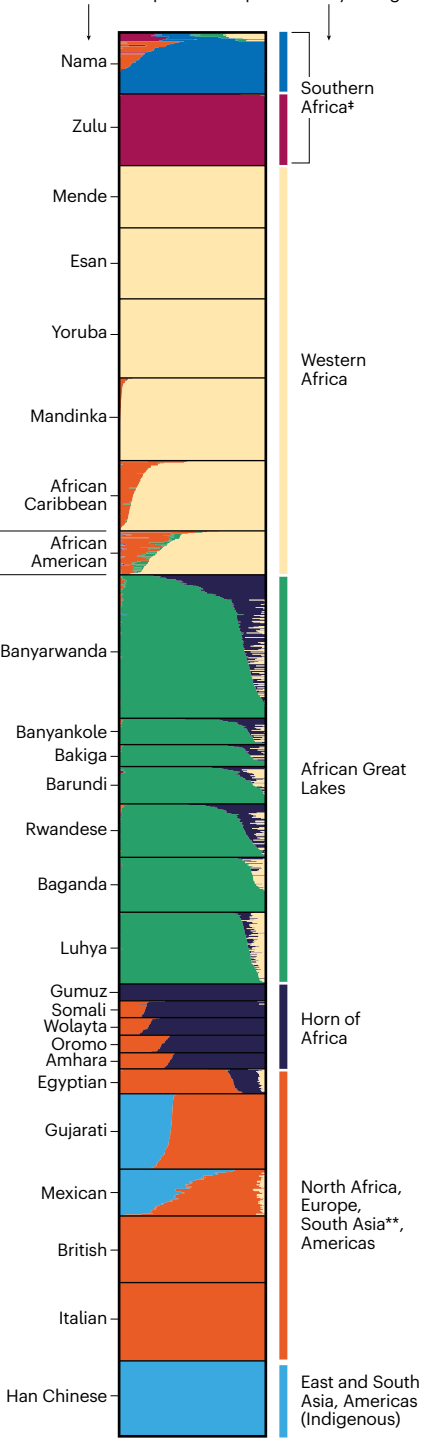
B Populations from Africa sampled: 13.5%
Part of the 2008 analysis was reproduced in a screed posted online by the gunman who killed ten Black people in Buffalo, New York, in May 2022.



C Populations from Africa sampled: 85% (unpublished)
Adjusting the sampling and using an African-centric data set creates a more representative view.

Population names are sample providers' self-identifications, or the descriptions used by those who collected the samples.

Six geographical labels correspond to the recent origins of the populations that fall mainly into the seven ancestry clusters produced by an algorithm†.



*J. Z. Li *et al. Science* **319**, 1100–1104 (2008).
†An algorithm divided genotype data from 1,900 individuals into seven clusters to mirror the 2008 study; 85% of the populations represented are from Africa (see Supplementary information). With this division, genetic differentiation across Eurasia and the Americas is low (blue and orange), relative to differentiation within Africa.
‡Southern Africa: South Africa, Namibia, Botswana, Mozambique; African Great Lakes: Kenya, Uganda, Rwanda, Burundi, Tanzania, Democratic Republic of the Congo, Malawi; Horn of Africa: Ethiopia, Somalia, Eritrea.
**South Asia appears twice because Gujarati people in India have intermediate allele frequencies.

SOURCES: A & C: ANALYSIS BY J. CARLSON *ET AL.*; DATA FROM THE AFRICAN GENOME VARIATION PROJECT (D. GURDASANI *ET AL. NATURE* **517**, 327–332; 2015) & THE 1000 GENOMES PROJECT (THE 1000 GENOMES PROJECT CONSORTIUM *NATURE* **526**, 68–74; 2015); B: REF. 1.

scientists and disseminate their own interpretations of the research (see 'Tracing racists' weaponization of research'). Meanwhile, far-right audiences are tracking particular fields and broadcasting flawed interpretations of scholarly research papers as soon as they are published. Certain scholars with far-right ideologies are also exploiting principles of open science to promote scientific racism on preprint servers and in peer-reviewed journals.

As such, we think a different approach is warranted.

Taking action

So what should human geneticists be doing to counter white supremacy?

Many of the denunciations of racism by scientists, scientific societies and editorial boards invoke decades of human-genetics research debunking the idea that human 'races' are biologically distinct, and repeatedly emphasize instead that race is a shifting social, historical and political construct. They stress that most human genetic variation is distributed as a gradient; that there is considerable genetic overlap between members of different populations; and that today's patterns of genome variation can be explained by migration and mixing of populations during human history[7].

But despite such denunciations, the past 15 years of population genetics have also unwittingly provided fodder for the concept that differences between so-called 'races' have a biological basis.

Take the genomic-data collections that are publicly available, such as the 1000 Genomes Project[8] and the Human Genome Diversity Project[9] (HGDP) – both international efforts to establish catalogues of human genetic variation from diverse populations and ancestries. These collections disproportionately represent populations outside Africa, which is problematic because Africa harbours the greatest human genetic diversity of all the world's continents. Of the 52 groups included in the HGDP, for instance, only 7 are groups from Africa.

The rich genetic diversity across the African continent continues to be neglected – in part because of implicit bias, small data sets and a perception by grant reviewers and funding agencies that studying this variation is not a priority.

Such sampling schemes can end up producing graphs or figures that downplay the extent of genetic diversity in African populations, and can reinforce the erroneous interpretation that discrete continental population labels reflect discrete genetic differences between samples.

One example is the widely distributed figure from a 2008 study (co-authored by one of us) that was included in the Buffalo shooter's screed. In the figure, which uses HGDP data, genetic ancestry seems to correspond to seven major continental designations: Africa, Middle East, Europe, central and south Asia, East Asia, America and Oceania[1]. This purported finding is based on an analysis in which 86.5% of the populations represented were from outside Africa and only 13.5% were from within Africa. It does not align with results from genetic data sets that use broader sampling across the continent. Those data indicate that the level of genetic variation in Africa is equivalent to that in many intercontinental comparisons, such that it does not make sense to label a single reference group or ancestry as 'African'.

Our unpublished analysis shows that if the authors of the 2008 study had had access to a more diverse data set – with 85% of the populations selected from within Africa, and the other 15% from outside the continent – and had allowed for seven subdivisions of genetic ancestry as in the original study, the data from African populations would no longer fall into a neat cluster that lies apart from all the others (see 'Racists use geneticists' infographics' and Supplementary information).

There has already been much discussion about the need to diversify the groups represented in genomics databases. In an ideal world, all populations would be represented equally. Until that happens, we geneticists should think more carefully about what data we select for our analysis – and how our

Tracing racists' weaponization of research

How common is the co-option of scientific studies by the far right?

Meta-research (which uses scientific methods to study science itself) and sociological studies from the past five years or so have demonstrated that the co-option of papers and concepts in disciplines from human genetics to neuroscience is not just happening at the fringes.

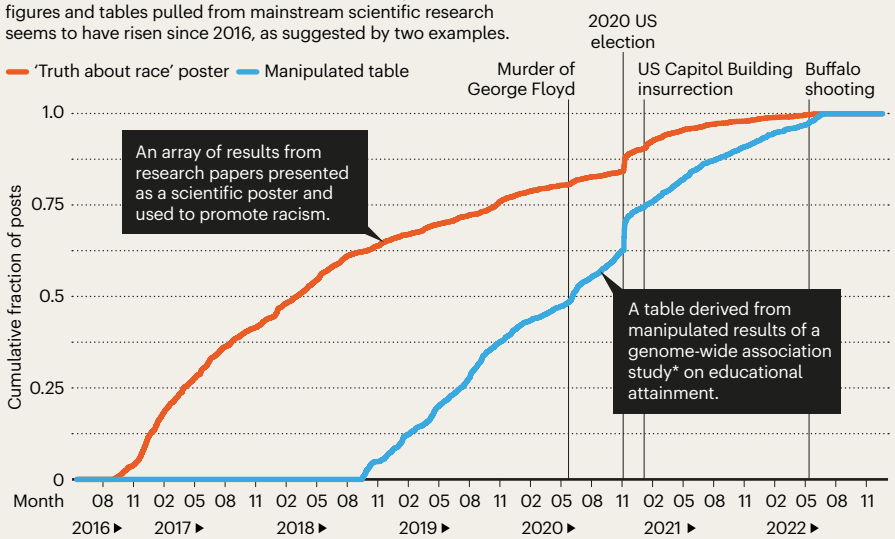
For instance, a study co-authored by one of us (J.C.)[17] analysed 1,800 preprints (published between 2013 and 2020) that had been tweeted about at least 50 times. For 10% of these papers, at least 5% of the tweets were from users associated with far-right extremist networks. (For 12 papers, including preprints that went on to be published in high-profile, peer-reviewed journals, more than one-third of the tweets about each paper were written by people with far-right ideologies.)

In fact, researchers who study political extremism postulate that the racist appropriation of scientific language and visualizations plays an important part in far-right ideology and recruitment[18,19].

Many of the pseudoscientific memes in the Buffalo shooter's screed can be traced to discussions about research papers on 4chan, an anonymous forum popular with the far right that the shooter says was influential in his radicalization. Our unpublished analysis of more than 5,000 4chan posts containing two of these memes demonstrates that the deployment of the memes on the platform has risen steadily in the past six years (see 'The spread of a meme').

THE SPREAD OF A MEME

On the online forum 4chan, the dissemination of quotes, figures and tables pulled from mainstream scientific research seems to have risen since 2016, as suggested by two examples.



*J. J. Lee *et al. Nature Genet.* **50**, 1112–1121 (2018).

SOURCE: ANALYSIS BY J. CARLSON *ET AL.*

choices could lead to misappropriation of our work.

Another action geneticists can take is to overhaul how they present their analyses visually.

Human population-genetics articles routinely include figures showing either the clustering of genotype data using analysis techniques such as principal components analysis (PCA)[10], or the distribution of 'ancestry' inferred from a modelling approach called structure and ADMIXTURE[11,12]. (According to Google Scholar, the three studies[10–12] published between 2000 and 2009 describing the techniques used to produce these figures continue to receive a combined total of more than 4,000 citations annually.) Such figures are compelling for press releases, and help specialists to communicate their results to other specialists. But they are easily co-opted by people with extremist views.

A practical step the genetics community can take to curb the decontextualization and misinterpretation of scientific figures is to develop standards for visualizations. For instance, journals could require that the axes of a cluster plot obtained from PCA are labelled to make it clear what proportion of total human genetic variation is explained by the variation in the analysis. (Although this suggestion has been made in the past[13], it is rarely followed[14].) PCA is often applied to subsets of the same data in the same paper, with the same visualization panel size. This amplifies fine-scale structure, but gives no context for the absolute differentiation or genetic similarity between individuals in each figure.

In short, more human geneticists need to anticipate that any visualization they generate could be stripped from the context and nuance of the study itself. Encouragingly, some pioneers, such as the group led by geneticist John Novembre at the University of Chicago, Illinois, are coming up with new visualization paradigms that are both informative and less susceptible to misinterpretation than the ones most commonly used today.

Steps to robustness

Such a rethinking of how human genetics studies are conducted — and how results are communicated — will have most impact if it happens in conjunction with changes at many other levels.

As many have written before[15], ensuring that scientific teams include and are led by people from groups harmed by weaponized science is one step that will make science more robust to misinterpretation and appropriation.

Also, a substantial amount of human-genetics research is subject to scrutiny by an institutional review board (IRB), a group formally designated to assess biomedical research involving human participants. Again, as noted by others, the IRB review process could include a more explicit evaluation of risks and benefits to groups beyond those immediately affected by DNA sampling or other interventions used in the study (see, for example, go.nature.com/3swtvju).

As scientists, we are constantly asked to articulate the positive impacts of our research on society. We reflexively focus on the potential benefits of our research in grant writing, publications and job applications, or when talking to journalists.

"All scientists should be asked to consider the potential harmful impacts of their work."

To help counter the repeated resurgence of scientific racism, all scientists (including ecologists and environmentalists, who are grappling with the resurgence of eco-fascism[16]) should be asked — just as routinely — to consider the potential harmful impacts of their work.

Efforts to claim the superiority of some people on the basis of genetics have no scientific evidence. Ultimately, we as scientists need to ensure that our analyses are conducted and presented to underscore — not undermine — the biological reality of our shared humanity.

CHIP SOMODEVILLA/GETTY

White nationalists march towards anti-fascist protesters in Charlottesville, Virginia, in 2017.

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