



Anti-Discrimination Working Group

Kick-off meeting

Friday 31st March 2022

9.30am, NCRR main meeting room (and online)

Agenda

1. Introduction round
2. Aims of the group
3. Jed's Twitter thread
4. Communication paradigms: a case study (Rosenberg et al., 2002)
5. Discussion
6. Ideas for next meeting



Aims of the group

1. To strive for **equality**
2. To strive for **diversity**
3. To be **open & transparent**
4. To be mindful that **the topics we discuss may be triggering and upsetting**, impacting on people in different ways.
 - This is not a passive intellectual topic. It takes time to install the correct support and find solutions. This is a learning process.
5. To discuss ongoing issues with **discrimination in research**
6. To recognize **harmful structures and practices** of discrimination in research
7. To **advocate for changes** that promote equity in research

Jed's Twitter thread

Problem	Action
1) Existence of extremist "journal clubs"	<ul style="list-style-type: none">• Familiarize yourself with how papers are appropriated• Conduct your research conscientiously assuming there's a chance it will receive a stamp of approval from a hateful terrorist
2) "Meme-ification" of figures (particularly PCA plots)	<ul style="list-style-type: none">• Understand how our communication can be (mis)interpreted• Improve established visualisation paradigms
3) Interest in research on the genetics of cognitive/behavioural traits (particularly IQ)	<ul style="list-style-type: none">• Be the "loudest voice in the room" discussing your own research• Defend your work, particularly against those with a warped appreciation (e.g., intervene, respond with factual information, address the faulty rhetoric)

Communication paradigms

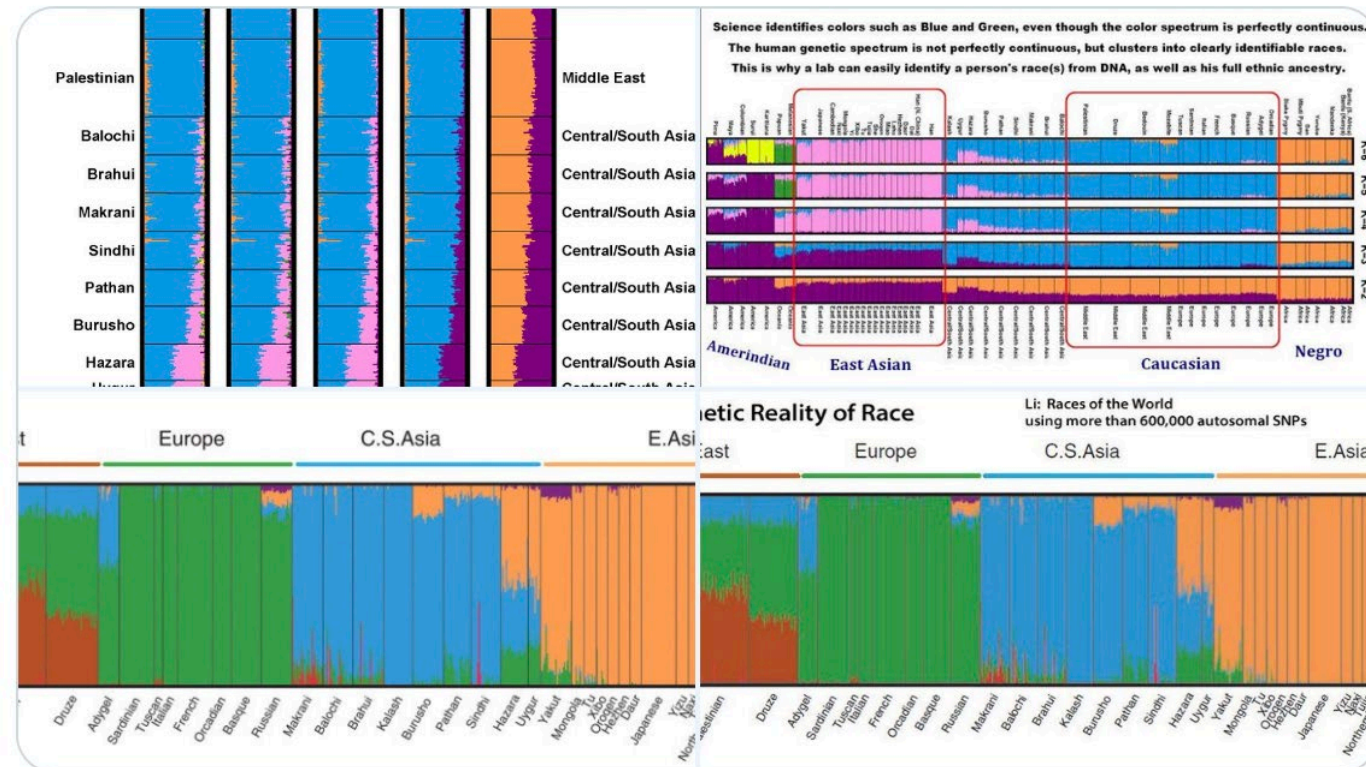


Jedidiah Carlson
@JedMSP



Replying to @JedMSP and @hoffsbeefs

Couple of prime examples, where figs are pulled directly from papers & subtly edited into nationalist memes--try a reverse img search!



Case study: Rosenberg et al., (2002)



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Are Clusters Races? A Discussion of the Rhetorical Appropriation of Rosenberg et al.'s "Genetic Structure of Human Populations"

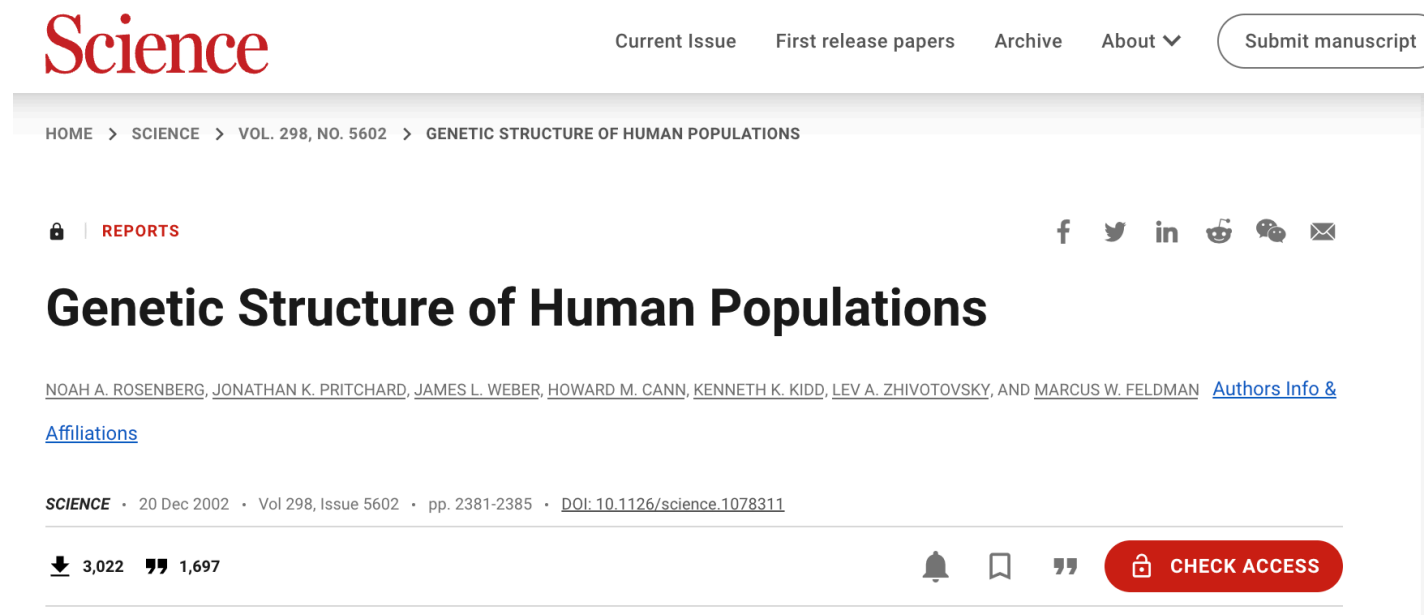
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Case study: Rosenberg et al., (2002)

- "Genetic Structure of Human Populations" (published in *Science*)
- Most cited paper in *Science* in its year of publication
- Continues to be cited in scientific and philosophical debates 20 years on



Case study: Rosenberg et al., (2002)

What did they do?

- Clustering algorithm *structure*
- Human Genome Diversity Cell Line Panel
- $N = 1,056$ individuals from 52 distinct global populations
- 377 microsatellite DNA

Case study: Rosenberg et al., (2002)

Abstract

"We studied human population structure using genotypes at 377 autosomal microsatellite loci in 1056 individuals from 52 populations. Within-population differences among individuals account for 93 to 95% of genetic variation; differences among major groups constitute only 3 to 5%. Nevertheless, without using prior information about the origins of individuals, we identified six main genetic clusters, five of which correspond to major geographic regions, and subclusters that often correspond to individual populations. General agreement of genetic and predefined populations suggests that self-reported ancestry can facilitate assessments of epidemiological risks but does not obviate the need to use genetic information in genetic association studies."

Case study: Rosenberg et al., (2002)

What did they conclude?

- Membership coefficient patterns tended to be consistent across individuals with predefined populations
 - *"...genetic clusters often corresponded closely to predefined regional or population groups or to collections of geographically and linguistically similar populations"*
- Inferred clusters tended to agree with geography (regional and worldwide)
- Genetic drift, geographical or linguistic isolation largely drive genetic differences between groups

Case study: Rosenberg et al., (2002)

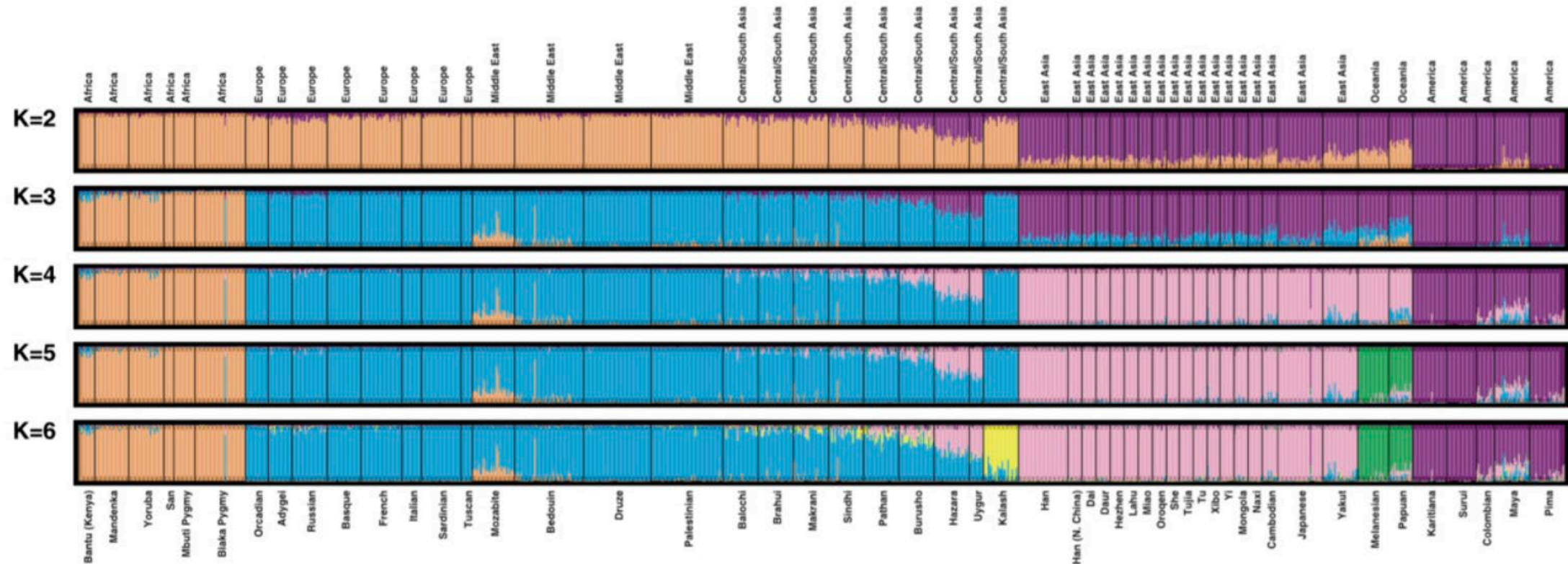


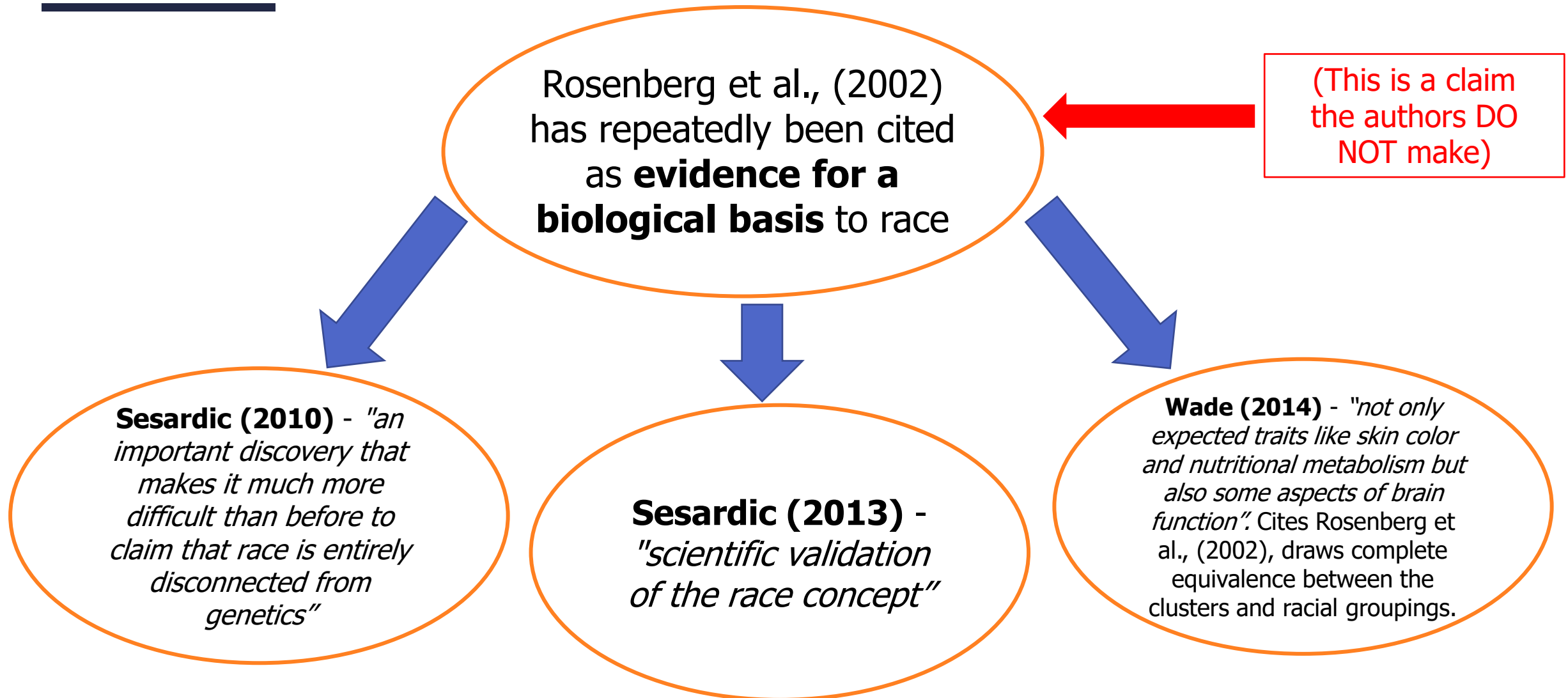
Fig. 1. Estimated population structure. Each individual is represented by a thin vertical line, which is partitioned into K colored segments that represent the individual's estimated membership fractions in K clusters. Black lines separate individuals of different populations. Populations are labeled below the figure, with their regional affiliations above it. Ten *structure* runs at each

K produced nearly identical individual membership coefficients, having pairwise similarity coefficients above 0.97, with the exceptions of comparisons involving four runs at $K = 3$ that separated East Asia instead of Eurasia, and one run at $K = 6$ that separated Karitiana instead of Kalash. The figure shown for a given K is based on the highest probability run at that K .

Case study: Rosenberg et al., (2002)

- K is variable, but they emphasise K=6
 - E.g., in abstract *"we identified six main genetic clusters, five of which correspond to major geographic regions, and subclusters that often correspond to individual populations"*
- Nowhere do the authors mention the term "race"
 - They exclusively refer to *"populations"* or *"clusters"*
- The end of the article reminds the reader of genetic similarity between individuals across the world
 - *"...because most alleles are widespread, genetic differences among human populations derive mainly from gradations in allele frequencies rather than from distinctive 'diagnostic' genotypes. Indeed, it was only in the accumulation of small allele-frequency differences across many loci that population structure was identified."*

Case study: Rosenberg et al., (2002)



Case study: Rosenberg et al., (2002)

- Authors have **completely rejected** these misinterpretations
- Many others have criticised Sesardic and Wade

Melissa Wills:

*"Critics of this misinterpretation have often suggested that it follows from interpreters' personal biases skewing the reception of an objective piece of scientific writing. I contend, however, that **the article itself to some degree facilitates this misrepresentation.**"*

*"While such rebuttals are vital in rejecting the racial interpretation, I challenge this tendency to scrutinize the language and motives of the interpreters **without considering their source material.**"*

Case study: Rosenberg et al., (2002)



Discussion time!

Can anyone think of any ways in which the authors could have facilitated this misinterpretation?

Case study: Rosenberg et al., (2002)

Melissa Wills points out:

- Emphasis on $K=6$, 5 of which map onto geographical clusters
- Labels above figure
- Wording
 - "Correspond"
 - "Anchored in"
 - "Match"

Discussion

- What do you think about having to keep these points in mind?
- Jed → The link between misappropriation of research and violence should factor into decisions made by IRBs, funders, and journal editors. What do you think about this?
- How do you feel about having to "intervene" with the rhetoric on social media?
- Any ideas about possible alternatives to visualization paradigms?

Ideas for next meeting

- Historical perspective
 - E.g., parallel development of genetics and eugenics
- Book club
 - E.g., *The Immortal Life of Henrietta Lacks*
- How-to: Active anti-discrimination
 - E.g., “racefile” for PC plots in a published [bioinformatics tool](#) → here is how one reviewer addressed it:

Reviewer response for version 1

[Stephanie M. Gogarten](#), Referee¹

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Competing interests: No competing interests were disclosed.

Review date: 2021 Aug 26. Status: Approved with Reservations. doi: [10.5256/f1000research.57243.r91453](https://doi.org/10.5256/f1000research.57243.r91453)

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The snpQT software is a useful resource for researchers working on Genome-Wide Association Studies (GWAS). It bundles a wide collection of software together and provides a clearly defined workflow based on best practices in GWAS quality control. It will be particularly useful for beginning researchers as it provides a straightforward entry point to learning how to work with GWAS data. The software is open source and comes with extensive documentation and tutorials, all available on the web.

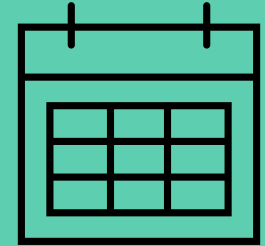
The manuscript is well written and clearly describes the use of the software and its benefits, with a few caveats as outlined below:

Major:

1) The term “**racefile**” as an argument name is inappropriate and should be changed. Race refers to a social category that is correlated with, but not the same as, genetic ancestry, and using it in this way goes against current recommendations in the human genetics community (Brothers, Bennett and Cho 2021 ¹; Birney *et al* 2021 ²). In fact, the allowed values in the “**racefile**” appear to be 1000 Genomes population labels, which are not races. A more appropriate term for this argument would be “popfile”, with the associated argument “racecode” instead called “popcode”.

2) Similarly, the term “ethnic outliers” should also be changed, both in the manuscript and in the snpQT online tutorial. Ethnicity is also a social category and its use is not appropriate in this context. The outlier removal performed by EIGENSOFT does not rely on any labelling of race, ethnicity, or population, but is instead described in the original publication (Price *et al* 2006 ³) as “Outliers were defined as individuals whose ancestry was at least 6 standard deviations from the mean on one of the top ten inferred axes of

Next meeting:
Early May



Thanks!

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Resources

- [*Science* piece on how papers are appropriated](#)
- [Article on how to be mindful in writing](#)