

Please cite as: Veit, W. & Browning, H. (2022). Polygenic Scores and Social Science. Preprint.

Check www.walterveit.com for citation details once published

Polygenic Scores and Social Science

Walter Veit & Heather Browning

Abstract:

It is a hotly contested issue whether polygenic scores should play a major role in the social sciences. Here, we defend a methodologically pluralist stance in which sociogenomics should abandon its hype and recognize that it suffers from all the methodological difficulties of the social sciences, yet nevertheless maintain an optimistic stance towards a more cautious use.

Main text:

It is a hotly contested issue whether polygenic scores (PGSs) and genome-wide association studies (GWASs) should play a major role in the social sciences. As described in the target article, what we see is both (over)hype and a staunch opposition, with harsh accusations thrown around, straw man arguments, and ad hominem attacks. All this makes it difficult to not only evaluate the positions, but even to ask important methodological questions about the potential uses of these genetic tools within the social sciences.

Here, Burt (2022) offers an elegant methodological target article with the aim of addressing just this problem. In it, Burt objectively criticizes the hype that has often accompanied heritability research, without committing any of the above sins, drawing attention to the methodological limits and challenges of adding genetics research to the social sciences. While we agree with many of Burt's points, however, we can't help but feel that she ends up overstating her conclusions and overplaying the differences between sociogenomics and traditional research within the social sciences.

In her conclusion, Burt (2022) states that "GWASs and PGSs may be powerful tools for identifying genetic associations, but they are not the right tools for understanding complex social traits" (p. 25). Naturally, we wholeheartedly agree. However, our reasons for accepting this claim aren't a belief that these tools cannot at all help us to understand genetic influences or social outcomes, but rather that there is no such thing as *the* right tools for understanding complex social traits. That is, we do not think that there is some kind of unique or privileged combination of scientific tools for investigation of whatever complex social trait we are interested in, whether that is poverty, educational attainment, or criminal behavior. Let us elaborate.

As philosophers of science (and in particular, philosophers of the social sciences) have long recognized, complex phenomena are not to be understood through the competition of various methods with the aim of finding the ideal one, but rather through use of a broad range of tools that complement each other in various ways (Wimsatt 2007, Mitchell 2009, Ylikoski & Aydinonat 2014, Veit 2019, 2021). While there are often conflicts within scientific disciplines regarding what sets of methods, models, experiments, and the like should be employed, these often appear to be driven by ‘indoctrination’ into the methodology of a lab and ideological disputes over the correct methods. As the saying goes: if all you learn is how to swing a hammer, all problems will start to look like nails. But from a higher-level perspective, it is precisely due to the pluralism of different methods that science has flourished. And this conclusion, we think, likewise applies to the use of genome-wide association (GWASs) studies and polygenic scores (PGSs).

These methods should not act as a replacement for standard social science tools, nor should they be seen as competitors to RCTs that investigate environmental factors. Instead, we argue that they can provide us with a useful complement for research into the main targets of the social sciences, i.e. complex causal systems with great heterogeneity and no strong generalizations. Just as the study of genome-wide associations bears the danger of falsely attributing causality to observed correlations, so too does standard social science. Burt (2022) is right in her criticism of the hype around polygenic scores: that they are often seen as deterministic, fail to control for a wide range of potential confounds, risk reviving the unfortunate gene-culture war, etc. But it is possible to arrive at such a critical stance by highlighting that sociogenomics will of course suffer from all the methodological difficulties of the social sciences - causal indeterminacy, the complexity of the social world, looping effects, and so forth. Within such an alternative picture, however, sociogenomics could still play a valuable role, within its own limited sphere.

Rather than simplifying the complexity of social phenomena, we argue that sociogenomics can help us to highlight how complex and causally interdependent social phenomena truly are. That is, we can buy into the main criticisms of the usefulness of PGSs in the social sciences, without being led to the strong conclusion that sociogenomics is methodologically doomed. Rather than returning to old and unhelpful discussions of social vs genetic causes, we think that sociogenomics might in fact help us towards a recognition of the complexity of our social traits and their myriad bases. This is how one should understand the argument that PGSs may improve randomized controlled trials by finding further variables to be controlled for (Harden 2021). It’s an embrace of a supplementary and pluralistic stance in the face of complexity. Rather than eliminating sociogenomics, or buying into the mistaken hype that it is going to replace and revolutionize standard social science, we can see its role instead as a complementary method to be added to the vast toolkit of the social sciences. Burt rightly points out that the methods as they are currently used too often fail to appreciate their own limitations, but this can be used as a starting-point, with these careful criticisms forming the basis for refining and strengthening the methods to better fit the contexts of use.

We therefore think that neither the majority of advocates nor the majority of critics of polygenic scores hold an adequate epistemic stance towards their use in the social sciences. Instead, we have here advocated for something of a mid-level approach, in which proponents of sociogenomics are urged to recognize the methodological difficulties of social science research and familiarize themselves with the philosophy of the social sciences in order to improve their own methods. Once the hype dies

down, what remains will be better science, one practiced with adequate attention paid to the current problems and limitations of the methods. At the moment, without knowing exactly how this will unfold, we would like to avoid making any firm predictions regarding the likely payoffs of sociogenomics, however we hold a (cautiously) optimistic stance regarding its future use.

Conflict of interest statement:

The authors have no conflicts of interest to report.

Funding Information:

WV's research was supported under Australian Research Council's Discovery Projects funding scheme (project number FL170100160).

References

Ylikoski, P., & Aydinonat, N. E. (2014). Understanding with theoretical models. *Journal of Economic Methodology*, 21(1), 19-36.

Burt, C. H. (2022). Challenging the Utility of Polygenic Scores for Social Science: Environmental Confounding, Downward Causation, and Unknown Biology. *Behavioral and Brain Sciences*.

Harden, K. P. (2021). *The genetic lottery: why DNA matters for social equality*: Princeton University Press

Mitchell, S. D. (2009). *Unsimple truths: Science, complexity, and policy*. University of Chicago Press.

Veit, W. (2021). Model Diversity and the Embarrassment of Riches. *Journal of Economic Methodology*, 28(3), 291-303.

Veit, W. (2019). Model Pluralism. *Philosophy of the Social Sciences*, 50(2), 91–114.

Wimsatt, W. C. (2007). *Re-engineering philosophy for limited beings: Piecewise approximations to reality*. Harvard University Press.