

Peer Review

Review of: "Genomic Testing of Clark's Theory of the British Industrial Revolution: A Monte Carlo Analysis of Statistical Feasibility"

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The paper is thorough and well-argued. One minor point I'd flag is the assumption that a 1 SD difference in polygenic scores (PGS) equates to a 1 SD difference in IQ between populations. While I've used similar simplifications in past work, this remains an open question. To clarify: 1. Within groups, trait variance scales with the square root of h^2 (heritability). 2. Between groups, the relationship is far more complex. To my knowledge, no formal model exists for scaling PGS to phenotypic differences across populations. This is why frameworks like Berg & Coop (2014) use PGS divergence as a proxy for QST, assuming that uncaptured causal variants (those not in the PGS) follow proportional between-group divergence under selection. In other words, if selection acts uniformly on the trait, the PGS (even with low within-group R^2) reflects relative genetic divergence. Critically, we're not estimating real-world phenotypic gaps (which would require environmental adjustments). Instead, we're asking: How much would populations differ genetically under equal environments? Here, scaling by $\sqrt{h^2}$ is unnecessary because we're isolating genetic divergence. Unfortunately, a lot of researchers still commit this fallacy. Missing heritability (uncaptured variants) introduces noise, but not systematic bias, if selection acted proportionally on all causal loci (and this is the framework my work since 2013 is based on, and which is the most misunderstood part). The common fallacy arises when conflating 1) prediction of observed differences (requires heritability/environment adjustments) with 2) Estimation of genetic divergence (assumes environmental parity, as in QST frameworks). This nuance is often overlooked, but it's central to interpreting between-group PGS differences. Unfortunately, to the best of my knowledge, we still do not have a method to solve this problem (although my intuition is that a 1 to 1 correspondence is usually a fair approximation). In other words, there is a lot of random error, but the error variance is unknown.

Declarations

Potential competing interests: No potential competing interests to declare.