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Peer Review

Review of: "Admixture Regression, Cognitive Ability, and Educational Attainment: A Social Science Application Using the Add Health Survey"

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This paper presents novel results on the relationship between continental ancestry and cognitive ability in admixed samples, using robust statistical methods.

Here are a few specific comments:

- Re "**Ancestry PCs as measures of continental ancestry.**" The section should more clearly distinguish three steps: validation of within-ancestry PCs as ancestry proxies, alignment of Add Health PC axes to the training-sample axes, and rescaling of standardized PC coefficients into hypothetical 0%–100% ancestry effects. The current description is difficult to audit, especially the PGS-based alignment and truncated-beta rescaling. The authors should report the exact PCs used, their signs, ancestry-proportion SD estimates, observed ancestry ranges, and sensitivity of results to imperfect PC-ancestry correlations.
- It's not clear what the difference between ADMIXTURE and tADMIXTURE is. Is this a typo? If they used ADMIXTURE, this should be cited "D.H. Alexander, J. Novembre, and K. Lange. Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 19:1655–1664, 2009."
- The authors do address the non-significant African ancestry coefficient in the Hispanic sample, attributing it to restricted African ancestry variation. This is plausible, since
  the implied full-range African coefficient remains large and similar to that in the African-ancestry sample. However, the manuscript should report confidence intervals for the
  rescaled B coefficients and avoid implying equivalence across samples without a formal heterogeneity

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or interaction test. Comparing significance in one group with non-significance in another is not itself evidence that the effects differ.

- The effect of PGS on phenotypic g is interesting. However, Table 12 reports only betas, not SEs, CIs, or p-values.
- The authors do not show whether polygenic g attenuates the ancestry coefficients when included in the same model.
- The authors rely on precomputed Add Health PGSs, but appear to construct the composite polygenic g score themselves using SMTpred. They should clarify whether the SMTpred combination was performed by the authors or taken from Add Health, and provide the exact component scores and weights used.

Declarations

Potential competing interests: No potential competing interests to declare.