

Thank you for submitting this article - it is a step in the right direction for ancestry determination in large-scale, complex cohorts. Please find some feedback below:

- **Title and abstract**
 - Does the title clearly reflect the content of the article? Yes
 - Does the abstract present the main findings of the study? Not completely, expansion of the abstract is needed
- **Introduction**
 - Are the research questions/hypotheses/predictions clearly presented? Yes
 - Does the introduction build on relevant research in the field? No, a more detailed interrogation of prior literature is needed.
- **Materials and methods**
 - Are the methods and analyses sufficiently detailed to allow replication by other researchers? Yes
 - Are the methods and statistical analyses appropriate and well described? Yes

Further suggestions:

1. Perhaps build in a step to convert large-scale whole genome sequencing VCFs to binary plink files.
2. A more detailed explanation on what preprocessing steps are assumed to be completed is necessary. This will affect the algorithm's accuracy.
3. I would recommend increasing the sample number for each demographic scenario used for the simulations.

- **Results**
 - In the case of negative results, is there a statistical power analysis (or an adequate Bayesian analysis or equivalence testing)? N/A
 - Are the results described and interpreted correctly? Yes

Further suggestions:

1. Whilst I understand the rationale behind not including the results for the ADMIXTURE run for full 1000 Genomes dataset, I still think including the results is needed for transparency. How long did ADMIXTURE take to run the full 1000 Genomes dataset? Please include the log-likelihood in Table S3.
2. An explanation of the admixture plot population abbreviations is needed.

- **Discussion**
 - Have the authors appropriately emphasized the strengths and limitations of their study/theory/methods/argument? Yes
 - Are the conclusions adequately supported by the results (without overstating the implications of the findings)? Yes