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Adjusting for principal components can induce spurious associations in genome-wide association studies in admixed populations

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Abstract

Principal component analysis (PCA) is widely used to control for population structure in genome-wide association studies (GWAS). It has been shown that the top principal components (PCs) typically reflect population structure, but deciding exactly how many PCs to include in GWAS regression models can be challenging. Often researchers will err on the side of including more PCs than may be actually necessary in order to ensure that population structure is fully captured. However, through both analytic results and application to TOPMed whole genome sequence data for 1,888 and 2,676 unrelated African American individuals from the Jackson Heart Study (JHS) and Chronic Obstructive Pulmonary Disease Genetic Epidemiology Study (COPDGene), respectively, we show that adjusting for extraneous PCs can actually induce spurious associations. In particular, spurious associations arise when PCs capture local genomic features, such as regions of the genome with atypical linkage disequilibrium (LD) patterns, rather than genome-wide ancestry. In JHS and COPDGene, we show that careful LD pruning prior to running PCA, using stricter thresholds and wider windows than is often suggested in the literature, can resolve these issues, whereas excluding lists of high LD regions identified in previous studies does not. We also show that the rate of spurious associations can be appropriately controlled in these data when we simply adjust for either the first PC or a model-based estimate of admixture proportions. Our work demonstrates that great care must be taken when using principal components to control for population structure in genome-wide association studies in admixed populations.

1 Introduction

Considerable variability in global ancestry—the genome-wide proportion of genetic material inherited from each ancestral population—has been observed in many studies of admixed populations such as African Americans and Hispanics/Latinos[1,2,3,4,5]. It has been widely documented that heterogeneous global ancestry, as with other types of population structure, can lead to spurious associations in genome-wide association studies[6,7,8,9]. In fact, some authors have even cited the ancestral heterogeneity of admixed populations, and the statistical challenges it poses, as one of many reasons why these populations have been historically underrepresented in genome-wide association studies (GWAS)[10,11,12,13,14].

Spurious associations can arise in GWAS in ancestrally heterogeneous populations when global ancestry confounds the association between genotypes and the phenotype of interest (Figure 1). This confounding occurs when the genetic variant being tested differs in frequency across ancestral populations (i.e., global ancestry is associated with genotype) and global ancestry also has an effect on the phenotype. Global ancestry may be associated with the phenotype if, for example, there are environmental factors or causal loci elsewhere in the genome that differ in frequency across ancestral groups.

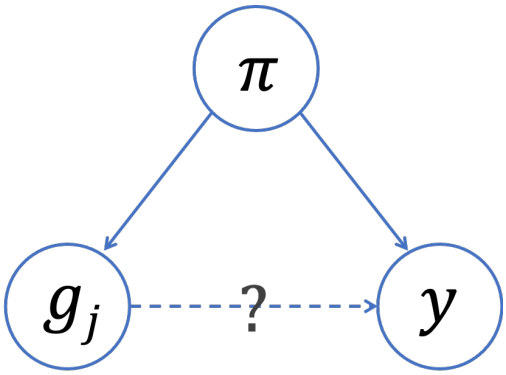

Figure 1: Global ancestry ($\boldsymbol{\pi}$) confounds the association between the genotype at position j ($\mathbf{g}_j$) and the phenotype of interest ($\mathbf{y}$) if ancestry is associated with both the genotype (e.g., the allele frequencies differ across the ancestral populations) and the phenotype (e.g., there are environmental or other factors that affect the phenotype and differ across the ancestral populations).

A number of methods for detecting and controlling for ancestral heterogeneity in genetic association studies have been proposed. Early approaches included restricting analyses to subsets of ancestrally homogeneous individuals[15], performing a genome-wide correction for test statistic inflation due to ancestral heterogeneity via *genomic control*[6], and using family-based designs[16]. More recently, approaches based on mixed models have been proposed[17,18,19], using random effects to control for both close (e.g., due to family-based sampling) and distant (e.g., due to shared ancestry) relatedness across individuals. When studies do not include closely related individuals, a simpler approach is to include inferred global ancestry as a fixed effect in marginal regression models[7,20]. This fixed effects adjustment for global ancestry is currently used extensively throughout the literature, with global ancestry inferred using either model-based ancestry inference methods (e.g., `frappe`[21], `STRUCTURE`[22], `ADMIXTURE`[23]) or principal component analysis (e.g., `EIGENSTRAT`[7], `SNPRelate`[24], `PC-AiR`[25]).

Principal component analysis (PCA) is a widely-implemented unsupervised approach for inferring global ancestry that does not require reference panel data or pre-specification of the number of ancestral populations of interest and is capable of capturing sub-continental structure[26]. To infer global ancestry using PCA, we preform a singular value decomposition of the matrix of standardized genotypes (i.e., $\mathbf{X} = \mathbf{UDV}^\top$) or, equivalently, an eigenvalue decomposition of the genetic relationship matrix (i.e., $\mathbf{XX}^\top = \mathbf{UD}^2\mathbf{U}^\top$). It has been shown that top eigenvectors, or *principal components* (PCs), $(\mathbf{u}_1, \mathbf{u}_2, \dots)$ tend to reflect global ancestry[27,28]. To adjust for ancestral heterogeneity, we choose some number of PCs to include as covariates in our GWAS regression models.

Determining the number of PCs needed to capture global ancestry can be difficult. Numerous techniques have been proposed for selecting this number, including formal significance tests based on Tracy-Widom theory[27,7], examining inflation factors[29,5] and/or the proportion of variance explained by each PC[30,29,5], comparing PCs to self-reported race/ethnicity[5], and keeping PCs that are significantly associated with the trait[31,32]. Typically, the number of PCs selected is on the order of 1–10[33], but in practice it is not uncommon to see applica-

tions in which more PCs are used than may actually be necessary to capture global ancestry. This could be due in part to work that has suggested that including higher-order PCs can provide the safeguard of removing "virtually all stratification" [34] at the cost of only "subtle" decreases in power [35].

Another challenge that can arise in using PCA to adjust for ancestral heterogeneity involves ensuring that PCs actually reflect global ancestry and not some other features or artifacts of the data. Prior work has shown that PCs can capture relatedness across samples [27,9,36,25], array artifacts or other data quality issues [27,7,9,37], and/or small regions of the genome with unusual patterns of linkage disequilibrium (LD) [27,7,38,39,40,9,37,41,42,36,43]. To address this last issue, some authors have suggested running PCA on a reduced subset of variants, after first removing regions of the genome that are known to have high or long-range LD (see Table 1) [38,44,26,40,45,37,30,5] and/or performing LD pruning (i.e., using a program such as `PLINK` [46] to remove variants that are in high LD) [38,44,26,47,48,45,37,42,36,49,25,29,50,5,32]. However, these suggestions are not universally implemented and the downstream implications of adjusting for PCs that capture features other than global ancestry are not fully understood. Furthermore, the work cited above has primarily been conducted in populations of European ancestry, so recommendations on how best to implement principal component-based adjustment for ancestral heterogeneity in admixed populations is lacking.

In this paper, we investigate the impact of LD filtering and pruning choices, as well as choices of the number of principal components to include in analyses, on genome-wide association studies in admixed populations. Through both simulation studies and analytic results, we show that including too many PCs can actually induce spurious associations in GWAS, particularly when those extraneous PCs capture local genomic features rather than genome-wide ancestry. To conclude, we provide suggestions regarding best practice for appropriately controlling for ancestral heterogeneity in genetic association studies in admixed populations.

Chr	Start (bp)	End (bp)	References
chr1	48000000	52060567	45,40,37
chr2	85941853	100500000	45,40,37
chr2	129600000	140000000	40,26,37,30,5,51
chr2	182882739	190000000	45,40,37
chr3	47500000	50000000	45,40,37
chr3	83500000	87000000	45,40,37
chr3	89000000	97500000	40,37
chr3	163100000	164900000	51
chr5	44000000	51500000	44,45,40,37
chr5	98000000	100500000	40,37
chr5	129000000	132000000	45,40,37
chr5	135500000	138500000	40,37
chr6	23800000	39000000	44,45,40,26,37,30,5,51
chr6	57000000	64000000	45,40,37
chr6	140000000	142500000	45,40,37
chr7	55000000	66193285	45,40,37
chr8	6300000	13500000	44,45,40,26,39,37,30,5,51
chr8	43000000	50000000	45,40,37
chr8	112000000	115000000	45,40,37
chr10	37000000	43000000	45,40,37
chr11	45000000	57000000	44,40,37
chr11	87500000	90500000	45,40,37
chr12	33000000	40000000	45,40,37
chr12	109500000	112021663	40,37
chr14	46600000	47500000	51
chr17	37800000	42000000	26,5
chr20	32000000	34500000	45,40,37

Table 1: Regions of the genome with high, long-range, or otherwise unusual patterns of linkage disequilibrium (LD) that are often recommended for exclusion prior to running PCA. This list of regions was generated on the basis of an extensive literature review. Start and end physical (base pair) positions are provided with respect to genome build 36. Also available for download (in builds 36, 37, or 38) at https://github.com/kegrinde/PCA/.

2 Material and Methods

2.1 Adjusting for ancestral heterogeneity in genome-wide association studies

To perform genome-wide association studies in samples of unrelated admixed individuals, we use marginal regression models, regressing the trait of interest on the genotype at each position across the genome. At a given position j, we quantify genotype g_{ij} as the number of copies (0, 1, or 2) of some pre-specified allele (e.g., the minor allele) carried by individual i at that position. Considering a quantitative trait y_i, we fit one linear regression model at each position ($j = 1, \ldots, m$):

$$E[y_i \mid g_{ij}, \mathbf{z}_i] = \beta_0 + \beta_j g_{ij} + \boldsymbol{\beta}_z \mathbf{z}_i,$$

where $\mathbf{z}_i$ is a vector of additional covariates (e.g., potential confounding variables) that we want to include in the model. This linear regression model can be replaced with a logistic regression model in the case of a binary trait (e.g., disease status). In either case, we test for an association between the trait and genotype by testing the null hypothesis $H_0 : \beta_j = 0$ at each position $j = 1, \ldots, m$.

To adjust for ancestral heterogeneity, we include inferred global ancestry in the vector $\mathbf{z}_i$ of potential confounders in our regression models. We infer global ancestry using one of two techniques: model-based global ancestry inference of principal component analysis.

Note: should some of the following should perhaps go to the Introduction section instead?

2.1.1 Model-based global ancestry inference

Various model-based approaches have been developed for estimating global ancestry proportions in admixed populations. We represent global ancestry via the vector $\boldsymbol{\pi}_i = \begin{pmatrix} \pi_{i1} & \ldots & \pi_{iK} \end{pmatrix}^\top$, where π_{ik} denotes the genome-wide proportion of genetic material inherited by individual

i from ancestral population k and $\sum_{k=1}^{K} \pi_{ik} = 1$. Note that the total number of ancestral populations, K, typically must be pre-specified, and the definition of global ancestry is typically restricted to the autosomes. Admixture proportions can be estimated directly using a program such as `ADMIXTURE`[23], or by calculating the genome-wide average local ancestry (i.e., $\hat{\pi}_{ik} = \frac{1}{2m} \sum_{j=1}^{m} a_{ijk}$), where local ancestry a_{ijk}—the number of alleles (0, 1, or 2) inherited by individual i from ancestral population k at position j—was first inferred using a program such as `RFMix`[52]. To adjust for ancestral heterogeneity, we include $K-1$ of these estimated admixture proportions as covariates in our GWAS regression models:

$$E[y_i \mid g_{ij}, \hat{\boldsymbol{\pi}}_i] = \beta_0 + \beta_j g_{ij} + \beta_{\pi,1}\hat{\pi}_{i,1} + \cdots + \beta_{\pi,K-1}\hat{\pi}_{i,K-1}.$$

Many model-based global ancestry inference programs are supervised, requiring data from individuals from each ancestral population of interest to form a reference panel. However, some approaches such as `ADMIXTURE` can also be run without a reference panel.

2.1.2 Principal component analysis

Principal component analysis (PCA) is an unsupervised dimension-reduction technique that is widely used for inferring population structure in genetic studies, with a number of software programs available for running PCA on genotype or sequence data (e.g., `EIGENSTRAT`[7], `SNPRelate`[24], `PC-Air`[25]). To run PCA, we perform a singular value decomposition of the matrix of standardized genotypes (i.e., $\mathbf{X} = \mathbf{U}\mathbf{D}\mathbf{V}^\top$) or, equivalently, an eigenvalue decomposition of the genetic relationship matrix (i.e., $\mathbf{X}\mathbf{X}^\top = \mathbf{U}\mathbf{D}^2\mathbf{U}^\top$). The top principal components $(\mathbf{u}_1, \mathbf{u}_2, \dots)$ typically capture global ancestry[27,28]. To adjust for ancestral heterogeneity, we choose some number of principal components, P, needed to capture global ancestry (typically $1 \leq P << n$) and include those PCs as covariates in our GWAS regression models:

$$E[y_i \mid g_{ij}, u_{i1}, \dots, u_{iP}] = \beta_0 + \beta_j g_{ij} + \beta_{u1} u_{i1} + \cdots + \beta_{uP} u_{iP}.$$

A number of techniques have been proposed for selecting the number of PCs, P, including formal significance tests based on Tracy-Widom theory[27,7], examining the proportion of variance explained by each PC[29], comparing PCs to self-reported ancestry[5], and/or keeping PCs that are significantly associated with the trait[31,32].

[... also some people just include how ever many PCs another paper included ...]

[... Mention that many people will include more than necessary? ...]

[... state what approach we take in this paper to choosing P ...]

2.1.3 Variant- and sample-level filtering

It is often recommended that filtering be performed at the variant and/or sample level prior to inferring global ancestry. Prior work has shown that both model-based estimates of global ancestry [... cite Tim's GAW paper ...] and principal components[25,7,27] [... check patterson, maybe add more refs: Price 2010 ...] can reflect family structure and/or cryptic relatedness rather than global ancestry when a sample includes related individuals, but restricting analyses to a subset of unrelated individuals (e.g., using the iterative procedure proposed by[53]) can circumvent that issue. At the variant level, it is common to perform filtering based on minor allele frequency [... find references ...], as prior work has shown that methods such as `EIGENSTRAT` can perform poorly when applied to rare variants[54].

Other variant-level filters have been recommended to address the sensitivity of model-based and PCA approaches to the presence of linkage disequilibrium (LD). This can include *LD pruning*, using a program such as `PLINK` [... CITE ...] to remove variants that are "highly" correlated (e.g., pairwise-correlation $r^2 > 0.2$) with nearby variants (e.g., within a window of size ??) [...[23], ADD MORE ...], and/or excluding regions of the genome that are known to have extensive, long-ranging, or otherwise unusual patterns of LD [... CITE ...]. A list of previously-identified high LD regions is provided in Appendix ??. [... say something about how not everyone does this, it's not always clear which parameters should be used, and/or much of this work has been performed in European pop and not clear what should

be done in admixed pop ...]

[... Add missing rates (SNPs and people) here? Or just frame as QC step?) ...]

2.2 Simulation study using TOPMed whole genome sequence data

Are we sure we want to use TOPMed? Or should we switch back to WHI?

We implement a simulation study using whole genome sequence data from the Trans-Omics for Precision Medicine (TOPMed) program to compare different approaches for adjusting for ancestral heterogeneity and explore the impact of different variant-level filtering choices, particular with respect to linkage disequlibrium.

2.2.1 TOPMed whole genome sequence data

TOPMed is [... describe TOPMed ...]. Whole genome sequence data for contributing TOPMed studies is available on dbGaP. We focus on two such studies, the Jackson Heart Study (JHS) (accession number: phs000964) and the Chronic Obstructive Pulmonary Disease Genetic Epidemiology Study (COPDGene) (accession number: phs000951).

- describe TOPMed
- describe sequencing methods
- how many samples in each study

2.2.2 Quality control

We process the sequence data for quality control, keeping only those variants that are bi-allelic, have a minor allele count of at least one, and pass standard variant filters (Mendelian or duplicate genotype discordance $< 3/5\%$, Hardy-Weinberg Equilibrium p-value $> 1 \times 10^{-6}$, etc.). [... Add filter for missing rates! ...] After all exclusions, we are left with ??? and ??? variants in JHS and COPDGene, respectively.

After variant-level filtering, we then use the iterative procedure suggested by Conomos et al.[5] and implemented in the TOPMed analysis pipeline to identify a subset of ?? mutually unrelated individuals. [... more details about iterative procedure; e.g., sing a kinship threshold of 0.044 ← double-check (i.e., excluding first, second, and third degree relatives) ...] Next, we run an unsupervised `ADMIXTURE` analysis with $K = 2$ and $K = 3$ and plot inferred global ancestry proportions to identify admixed (African American) and non-admixed (European) individuals. [... more details about thresholds used ...] After sample-level filtering, ??? and ??? individuals remain in JHS and COPDGene, respectively.

QC for JHS (dbgap accession phs000964):

- filtering
  - bi-allelic SNPs
  - minor allele count at least 1
  - pass variant filters (in VCFs that were downloaded from dbgap): overlaps with SNP, overlaps with indel, overlaps with VNTR, failed SVM filter, high (3/5% or more) mendelian or duplicate genotype discordance, excess heterozygosity with HWE p-value ¡ 1e-6
- merge the two subsets (cg1 and cg3)
- convert from VCF to GDS
- remove close relatives
  - run king (LD r threshold: 0.32, LD window size: 10, MAF threshold: 0.01, exclude PCA corr: TRUE, build: hg19)
  - run PC-AiR
  - run PCRelate
  - run PC-AiR again

  - run PCRelate again

- find African Americans
  - run stricter LD pruning (MAF = 0.01, window size = 0.5, rsq = 0.01, regions = TRUE, build 37)
    - List of regions stored here: `/projects/browning/brwnlab/kelsey/spurious_assoc/highl`
  - convert GDS to BED
  - run ADMIXTURE (K = 2 and K = 3)
  - plot proportions
  - exclude 40 people inferred to be 100% European; left with 1888

QC for COPDGene (phs000951):

- filtering
  - bi-allelic SNPs
  - minor allele count at least 1
  - pass filtering (from GDS annotation info, I inferred this to include: variant located in centromeric region, variant failed SVM filter, mendelian or duplicate genotype discordance is high (3/5% or more), excess heterozygosity in chrX in males, excess heterozygosity with HWE p-value ¡ 1e-6)
- convert from VCF to GDS
- remove close relatives
  - run king (LD r threshod = 0.32, LD window size = 10, MAF threshodl = 0.01, exclude PCA corr = TRUE, build = hg38); regions = see table below
  - run PCAiR

name	chrom	start.base	end.base	comment
2q21	2	129883530	140283530	LCT
HLA	6	24092021	38892022	includes MHC
8p23	8	6612592	13455629	inversion
17q21.31	17	40546474	44644684	inversion

Table 2: TOPMed hg19 high corr regions

name	chrom	start.base	end.base	comment
2q21	2	129125957	139525961	LCT
HLA	6	24091793	38924246	includes MHC
8p23	8	6755071	13598120	inversion
17q21.31	17	42394456	46567318	inversion

Table 3: TOPMed hg38 high corr regions

  - run PCRelate
  - run PCAiR again

- find African Americans
  - run stricter LD pruning (exclude PCA corr regions = TRUE, build = hg38, LD R threshold = 0.1, LD window size = 10, MAF threshold = 0.01); regions = `/projects/browning/brwnlab/kelsey/spurious_assoc/highLD_regions/`
  - convert from GDS to PLINK
  - run ADMIXTURE with K = 2 and K = 3
  - plot proportions and use cut-off of 30% to identify (and then remove) Europeans : Parker et al. 2014 "Admixture mapping identifies a quantitative trait locus associated with..." `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4190160/` (reduced from 8406 to 2676)

2.2.3 Genetic ancestry inference

- ADMIXTURE
  - JHS: ran with both K = 2 and K = 3

  - COPDGene: ran with both K = 2 and K = 3
  - unsupervised for both

- PCA using SNPRelate

- what filtering was performed, and how many variants left after filtering
  - JHS, ADMIXTURE: see above
  - JHS, PCA: exclude regions (TRUE/FALSE), r-squared (1, 0.1, 0.2, 0.05), window size (0, 0.5, 10), and MAF (0, 0.01)
    * no filtering: FALSE-1-0-0
    * MAF filtering: FALSE-1-0-0.01
    * exclude but no prune: TRUE-1-0-0.01
    * prune but no exclude: FALSE-0.1-0.5-0.01 and FALSE-0.1-10-0.01 and FALSE-0.2-0.5-0.01 and FALSE-0.05-0.5-0.01
    * prune and exclude: TRUE-0.1-0.5-0.01 and TRUE-0.1-10-0.01 and TRUE-0.2-0.5-0.01 and TRUE-0.05-0.5-0.01
  - COPD, ADMIXTURE: see above
  - COPD, PCA: exclude regions (TRUE/FALSE), r-squared (1, 0.1, 0.2, 0.05), window size (0, 0.5, 10), MAF (0, 0.01)
    * no filtering: FALSE-1-0-0
    * MAF filtering: FALSE-1-0-0.01
    * exclude but no prune: TRUE-1-0-0.01
    * prune but no exclude: FALSE-0.1-0.5-0.01, FALSE-0.1-10-0.01, FALSE-0.2-0.5-0.01, FALSE-0.05-0.5-0.01
    * prune and exclude: TRUE-0.1-0.5-0.01, TRUE-0.1-10-0.01, TRUE-0.05-0.5-0.01, TRUE-0.2-0.5-0.01

  - COPD, also ran SNPRelate on Europeans with different levels of filtering (FALSE-0.1-0.5-0.01, FALSE-0.2-0.5-0.01, FALSE-1-0-0.01, FALSE-1-0-0, TRUE-0.1-0.5-0.01, TRUE-0.2-0.5-0.01, TRUE-1-0-0.01)

2.2.4 Evaluating population structure adjustment approaches

- plot PCs vs global ancestry proportions
- plot SNP loadings
- simulating traits (effect sizes, choice of causal SNPs)
  - find loading peaks from "naive" approach
  - simulate trait that is beta * x + rnorm(0, 1), where beta = 1 or 2 and x = genotype at one of the peaks
- running GWAS
  - for each of 188*2 simulated phenotypes
  - for each set of PCs
  - including 1, 4, or 10 PCs
- defining spurious associations

3 Results

3.1 Ancestral heterogeneity in TOPMed African American samples

- quickly summarize ancestral heterogeneity (barplots of ADMIXTURE proportions)

3.2 Confirming the importance of adjusting for population structure

- show an example manhattan plot with no adjustment
- compare average number of spurious associations
- tie in theoretical results

3.3 Comparing different approaches for adjusting for population structure

Part 1: how does FWER compare?

- manhattan plots for one or two simulated traits
- overall summary of rejection rates
- is it appropriate to use same significance threshold for all?

Part 2: how does rate of spurious associations compare? (and alpha-adjusted spurious assoc?)

- manhattan plots for one or two traits
- overall summary of rejection rates

Part 3: why is this happening?

- are admixture proportions and PCs capturing similar information?
  - correlation between PCs and admixture proportions (PC1 highly correlated with admix prop)
  - correlation between PCs and genotypes (without pruning, later PCs highly correlated with genotypes in small regions)
- mathematical results

4 Discussion

Global ancestry = confounder

- Summarize conditions under which global ancestry is a confounder
- Relate to current understanding in literature

Be careful with PCs!

- Summarize conditions under which PCs can be problematic
- Relate to current understanding in literature (what have others shown can happen if you include a PC that captures local LD? how are things different in admixed populations, where LD is more extensive?)
- Relate to concept of collider bias
- Suggested diagnostics

5 Appendices

5.1 Regions Removed Prior to PCA

- a list of all "high-LD" regions removed prior to running PCA

5.2 Mathematical Derivations

- theoretical results
- proofs
- simulations validating theory

Supplemental Data

Supplemental Data include [... ?? ...] figures and [... ?? ...] tables.

Declaration of Interests

The authors declare no competing interests.

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Web Resources

GitHub Repository: lists of regions to exclude, code for LD pruning, excluding, and plotting loadings

Data and Code Availability

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Figure Titles and Legends

Tables