bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Biogeographic Ancestry and Socioeconomic Outcomes in the Americas: a Meta-analysis

Emil O. W. Kirkegaard[1]

Mingrui Wang[2]

John Fuerst[3]

Abstract

Admixture analyses attempt to infer if medical-related outcome differences between populations and self-identified race/ethnic (SIRE) groups have a genetic etiology by ascertaining whether biogeographical ancestry (BGA) is associated with outcomes in admixed populations. Narrative reports suggest that socioeconomic status (SES) covaries with BGA in the Americas. If this is generally the case, SES potentially acts as a confound and needs to be taken into account when evaluating the relation between medical outcomes and BGA. To explore how systematic BGA-SES associations are, a meta-analysis of American studies was conducted. 41 studies yielded a total of 166 datapoints and 76 non-overlapping effect sizes. An analysis of effect directions found a high degree of consistency in directions. The N-weighted directions were .97, -.95 and -.94 for European, Amerindian and African ancestry, respectively. An analysis of effect sizes found that European BGA was positively associated with SES r = .18 [95% CI: .13 to .22, K=27, N=34,233.5], while both Amerindian and African BGA were negatively associated at -.15 [-.20 to -.10, K=26, N=20,657.5] and -.11 [-.16 to -.07, K=23, N=28,813.5], respectively. There was considerable cross-study variation in effect sizes (mean I^2 =92%), but there were too few datapoints to permit credible moderator analysis. Implications for future studies are discussed.

Keywords: biogeographic ancestry, self-identified race/ethnicity, SES, admixture mapping, medical outcomes

1. Introduction

Admixture analysis is a potent tool for the exploration of the etiology of traits and trait differences in context to admixed populations. Admixture mapping (AM) is a form of admixture analysis that allows for the detection of specific disease and trait-associated genes (Shriner, 2013; Winkler, Nelson, & Smith, 2010). When biogeographical ancestry (BGA) groups differ in the frequency of disease or trait causing genetic variants, the phenotype of interest will be correlated with the degree of BGA near local regions of the genome in the admixed populations and self-identified racial/ethnic (SIRE) groups, a situation which allows for the identification of associated loci. Admixture analysis also permits global analyses, in which global BGA is correlated with a trait. An association between global BGA and a trait provides suggestive evidence that trait differences between parental BGA groups, and consequently between populations with different BGA component percentages, have a genetic etiology. Such methods have been utilized to investigate, for example, if the difference in Type II diabetes prevalence between White and African American SIRE groups has a likely genetic basis (Cheng et al. 2012). The finding of an association between global ancestry and a trait is often the launching point for AM analyses.

1Department of linguistics, University of Aarhus, Aauhus, 8000, Denmark. Email: emil@emilkirkegaard.com.

2Department of Biology, Beijing University of Agriculture, China. Email: mail@mingrui.wang

3Independent researcher, Cary, North Carolina, 27606, US. Email: j122177@hotmail.com.

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

As used here, BGA refers to ancestry with respect to BGA groups, where these groups are delineated, using ancestrally informative molecular markers, according to the relative genetic affinity of the members of reference samples. These groups have been called *ancestral groups*, *clusters*, and *ancestral populations* (e.g., Shriver and Kittles, 2004) and BGA has been referred to as "the heritable component of 'race' or heritage" (Frudakis & Shriver, 2003). With respect to studies of American populations, the reference BGA groups are typically indigenous Europeans, West Africans, and Amerindians, because they are the main source ancestry groups (Salzano & Sans, 2014). Here, the polyseme "population" refers to geographically delineated groups (for a list of alternative biological definitions, see: Waples & Gaggiotti, 2006). In contrast, SIRE groups are delineated in terms of self-identification and represent social identities.

SES inequalities between SIRE groups may lead to spurious associations between ancestry and outcomes and thus is a concern when it comes to admixture analyses. For this reason, controls for socioeconomic status (SES) are frequently incorporated into analyses, on the assumption that ancestry may covary with SES and that differences in SES may induce the medical related outcomes differences. Narrative reports have noted that SES covaries with admixture such that Amerindian and African BGA is associated with lower SES related outcomes than is European BGA (For example: González Burchard et al., 2005). If this is generally the case, it would be advisable for researchers to include, when possible, measures of SES as covariates in analyses so to provide lower bounds estimates of the ancestry-outcome associations. However, no meta-analysis has been conducted to date to establish whether SES outcomes are associated with ancestry in any consistent way. To explore the matter, a review was conducted.

Methods

Collecting studies and Data Exclusion

In 2014, phrases such as "admixture African socioeconomic" and "admixture Amerindian education" were searched using Google Scholar for years 2003 to 2014. In total, these searches turned up approximately 20,000 hits in descending order of relevance to the search terms. The first 1,500 abstracts were skimmed. Approximately 250 papers were identified as potential sources and read. Over the course of 2015, the search was expanded using the PubMed and BIOSIS previews databases.[4] At the beginning of 2016, the Google Scholar search was repeated for year 2015 and 2016. Many studies did not report effect sizes, or any other statistic which was convertible to an effect size. Some studies did not even report directions for relationships. In cases where an effect size could not be found or calculated, the authors were contacted and the data was requested. For 76% of the cases a reply was forthcoming. For 36% of the cases, the authors provided results not reported in the original papers. Two of this paper's authors reviewed studies and reached agreement on ambiguous cases. Relevant information from each study was recorded.[5] For the meta-analysis, we excluded

4 Searches such as the following were used: (admixture) AND (socioeconomic or education or income or SES or poverty) AND (African or European or Amerindian) AND (Antilles OR Latin America OR South America OR Central America OR Caribbean OR Anguilla OR Antigua OR Aruba OR Barbuda OR Argentina OR Bahamas OR Barbados OR Belize OR Bolivia OR Brazil OR Chile OR Colombia OR Costa Rica OR Dominica OR Dominican Republic OR Ecuador OR El Salvador OR Grenada OR Grenadines OR Guadeloupe OR Guatemala OR Guyana OR Haiti OR Honduras OR Jamaica OR Martinique OR Mexico OR Montserrat OR Nevis OR Nicaragua OR Panama OR Paraguay OR Peru OR Puerto Rico OR Saint Kitts OR Saint Lucia OR Saint Vincent OR Suriname OR Surinam OR Trinidad OR Tobago OR Uruguay OR Venezuela).

5 The following pieces of information were recorded for each datapoint: author-year (APA format), type of sample (medical, control, combined, etc.), country, first order administrative division within country, specific region such as city, the subpopulation examined (African American, Hispanic American, Puerto Rican, etc.), the sample name, a sample ID within each study, sample size, ancestry examined (European, Amerindian, African), mean level of admixture (arithmetic mean), standard deviation of admixture, number of genetic variants used to estimate admixture, outcome category (e.g. SES, income), outcome literal, type of outcome mentioned in the

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

cases in which the respective mean admixture was at or below 5% or the SD of admixture was at or below 2.5 because it makes little sense looking at the association between outcomes and admixture when there is little variance in the latter.

Descriptive statistics of studies

A total of 41 studies were coded for the meta-analysis yielding a total of 166 datapoints. About 60% of the datapoints came from the US. Studies often divided their samples into ethnic groups. Table 1 shows a breakdown by country and ethnic group.

Table 1: Independent datapoints by country and ethnic group

Ethnic group	**Frequency**	**Ethnic group**	**Frequency**	**Ethnic group**	**Frequency**
African American (US)	11	Multi-ethnic (Chile)	2	Afro-descent (T&T)	1
Hispanic (US)	10	Multi-ethnic (Mexico)	2	Multi-ethnic (Argentine)	1
Mexican (US)	6	Multi-ethnic (US)	2	Multi-ethnic (Colombia)	1
Multi-ethnic (Brazil)	6	Mestizo (Chile)	2	Not stated (Costa Rica)	1
Puerto Rican (PR)	6	Native American (US)	2	Puerto Rican (US)	1
Not stated (Mexico)	3	Not stated (Uruguay)	2	White American (US)	1
Multi-ethnic (Peru)	3	Not stated (Colombia)	2		

Searches were conducted for the years 2003 to 2016. For identified papers, references were also searched. For this reason, not all included papers were published at or after 2003. Most datapoints were from papers published in the last few years with the median being 2012. If the trend holds, more data can be expected to be published in the next few years. Studies varied widely in the size of their samples. Figure 6 and Supplementary Figure 1 show, respectively, a histogram of the publication year and a density-histogram of the sample sizes. Many studies had medical themes and often included both case and control samples. Table 2 shows the breakdown of independent data points by sample type.

Table 2: Independent datapoints by sample type.

Sample type	**Frequency**
case	11

source, outcome levels, the number of levels in ordinal outcomes, the association direction (positive, negative, null, not stated), the p-value, test used to derive the p-value, the correlation, the conversion method, if the correlation was derived from other statistics, notes on the method, details for the conversion, details for author contact attempts (multiple columns).

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

case and control	23
control	8
non-medical	23

Studies reported a large variety of specific outcome variables. These outcome variables were coded to broad categories. Table 3 shows the breakdown of all outcomes by broad category.

Table 3: Outcomes by category for all datapoints.

Outcome category	**Frequency**	**Outcome category**	**Frequency**
Education	63	Parental SES	6
Income	42	Parental education education	2
SES	34	Parental income	1
nSES	18		

Measures were mostly of individual education, income, or a combination of variables. A few datapoints were based on the socioeconomic level of the individual's neighborhood. Depending on the model of the proposed covariance, this could be a questionable index. For example, a recent study based on the UK Biobank (N≈112k) found a modest phenotypic correlation between individual and neighborhood-level SES (0.24) but a strong genetic one (.87) (Hill et al., 2016). While neighborhood-level measures are included in the meta-analysis, it is advisable that investigators conduct moderator analyses to estimate the effect of using neighborhood versus individual indexes in future works. Additionally, several studies reported parental SES. Because most children are the biological offspring of both of their parents, their admixture will index the average of their parents. These results can then be seen as showing the correlation between the parents' SES and the parents' BGA.

Methods

Directions and Effect size meta-analysis method

Meta-analyzing the present dataset presented multiple difficulties. The mere direction of effect sizes was more frequently reported or inferable from the information provided than the actual effect sizes. While directions cannot themselves be used as an effect size measure, they can provide a rough idea of whether the findings are in line with a null hypothesis. If the effect directions deviate strongly from those expected by chance, then it is likely that the true effect is in that direction. If the effect directions do not deviate from chance levels, then there may be an effect but sample sizes are too small to reliably detect it, or there may be no effect. These conclusions only hold given the assumption of no publication or reporting bias. For the reported directions, values were scored -1, 0, and 1 for, respectively, negative, null, and positive directions. Within and between samples the scores were summed and divided by the total number of reported directions. In this way, a sample that gave

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

consistent directions got a score of either 1 or -1, while those with mixed results got somewhere in between. For instance, a sample reporting three positive and one negative associations received a score of (3-1)/4=.5.

A random effects meta-analysis was used to analyze the effect size results. Standard errors for the correlations were calculated from the sample sizes and the reported correlations.[6] Random effects models are appropriate when the observations cannot be assumed to have been sampled from a single population (Hunter & Schmidt, 2004, p. 393). Such a model is appropriate in this case, because the dataset contains information from different sub-populations, different countries and based on different outcomes.

Weights and Multiple outcomes and Multiple ancestries x outcomes reported for a sample

To counteract the effect of sampling error in the small studies, two sets of weighted values were calculated. Scores were weighted both by the square root of the sample size and by the sample size. Means were weighted by the square-root of the sample size so that the large samples did not overwhelm the small ones. An alternative approach would have been to weight by p-values, but some studies failed to report this statistics and many did not report whether one or two-tail analyses were conducted.

Sometimes associations with multiple outcome measures were reported for a single sample and the same ancestry. Were a simple aggregation method employed, samples reporting results for multiple outcome categories would count more than those that report fewer. Two recent meta-analyses encountered this problem (Tucker-Drob & Bates, 2016; Tate & McDaniel, 2008). The method employed by the first was to use a complex weighting approach to avoid double counting. The second used a simpler approach of averaging results within samples before aggregating. An approach similar to the second was implemented; namely, median values, which are more robust than means to outliers, were taken across outcomes within each sample before meta-analyzing them. As example, Norden-Krichmar et al. (2014) reported associations between Amerindian ancestry and both SES and income of -.04 and -.10, respectively. Using a simple analysis, this would have been counted as two independent studies. Using within sample aggregation, it was counted as one datapoint with an effect size of of -.07. As Tate and McDaniel (2008) note, this method slightly throws off the standard errors, but this problem was judged to be non-substantial.

Some studies reported one or more ancestry × outcome associations for a single sample. Since results were decomposed by ancestry component this issue was deemed to not be a concern. When studies report only the correlations between outcomes and a single ancestry component, and when ancestries strongly negatively correlate, one could attempt to estimate directions/effect sizes. For instance, Bonilla (2015, extra information provided by the author) reported that European and Amerindian ancestry correlated at -.82 and -.85 in two samples (N's = 148, 164). The correlations between European ancestry and SES were .10 and .14, thus, one might infer that the Amerindian × SES correlations were -.10/-.14. In this case, however, they were -.01 and -.13; the departure from expectation resulted from the association between African BGA and SES. To avoid possible bias, results were not estimated.

Results

Directions of effects

The aggregated-within-sample directions are shown in Table 4. In general, the directions are positive for European ancestry and are in the reversed direction for the other two ancestries. The results are substantially stronger when using weighted scores, possibly reflecting the fact that smaller studies tend to give less reliable results.

6 The formula for the standard error of a correlation is (Cohen & Cohen, 2003, p. 42): $\sqrt{\frac{1-r^2}{n-2}}$

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

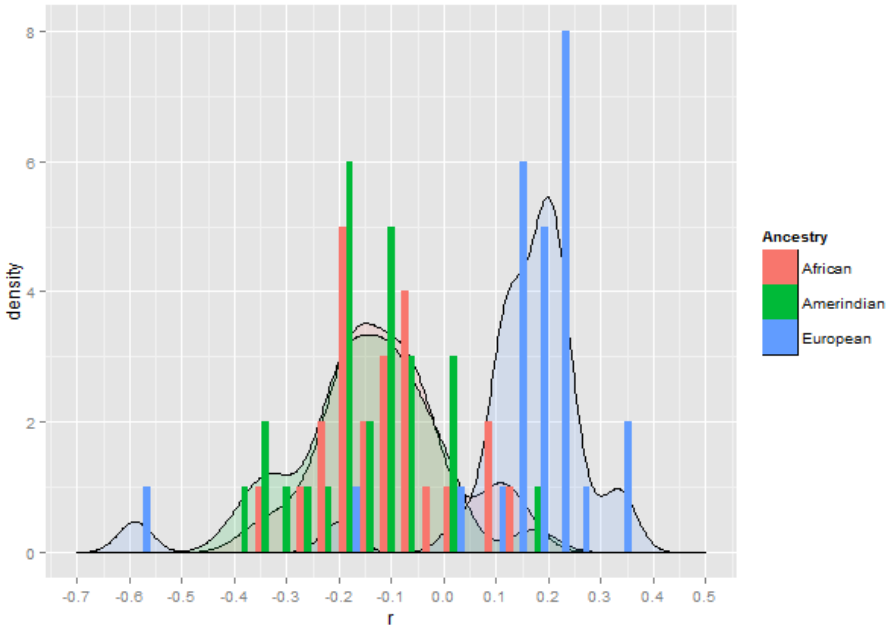
Table 4: Directions of effects by ancestry. Weighted by sample size.

Ancestry	**mean direction**	**SQRTweighted mean direction**	N-Weighted mean direction	**K**	**Total N**
African	-0.64	-0.80	-.93	37	37417.5
Amerindian	-0.80	-0.89	-.95	36	27297.5
European	0.80	0.92	.98	37	38764.5

Distributions of effects

To get an overview of the findings, a density-histogram plot of the effect sizes was made for each ancestry component. This is shown in Figure 1. There are two clear outliers for European ancestry at -.6 and -.2. The first is based on a tiny sample (N=15). The other outlier for European ancestry (Zou et al. sample 6) is also an outlier for Amerindian ancestry. The lead author (James Zou) was contacted to verify the data. He checked the code and data and reported that there were no errors. A dataset was created by excluding the outlying samples and re-running the analyses. This gave similar and slightly stronger results[7] and the between study heterogeneity (I^2) was somewhat reduced as expected (94%, 90% and 91% to 91%, 88%, 91% for European, Amerindian and African ancestry, respectively).

Figure 1: Density-histogram plot for effect sizes by ancestry.



Random effects meta-analysis

The effect sizes for each ancestry was analyzed.[8] Figures 2 to 4 show the forest plots.

7 Specifically, the results were .19 [.15 to .23], -.16 [-.20 to -.12] and -.12 [-.17 to -.07] for European, Amerindian and African ancestry, respectively.

8 The **metafor** package for R (Viechtbauer, 2015) was used.

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Figure 2: Forest plot for European ancestry results. Based on random effects model.

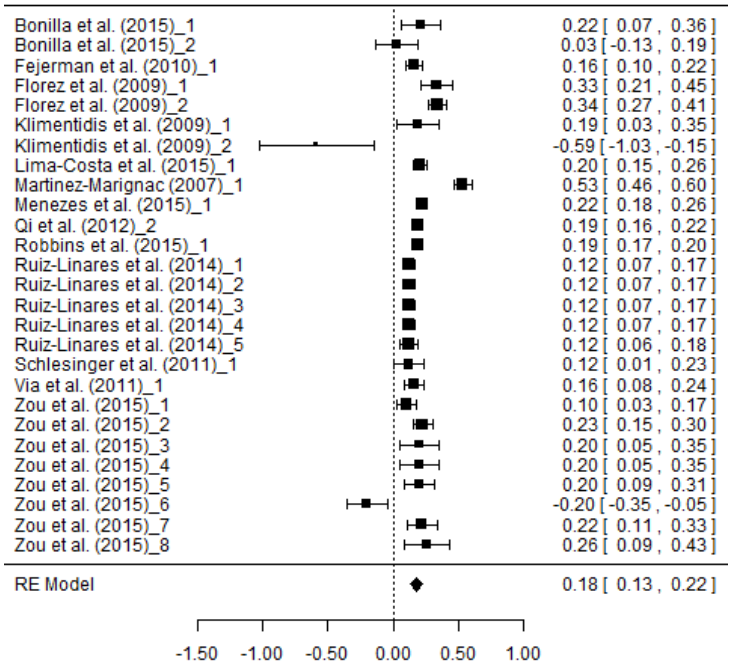


Figure 3: Forest plot for Amerindian ancestry results. Based on random effects model.

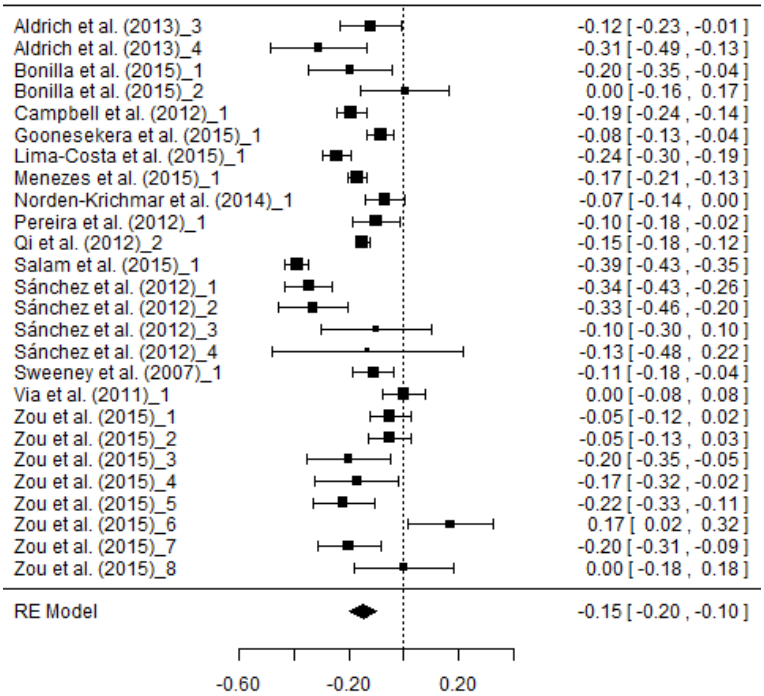
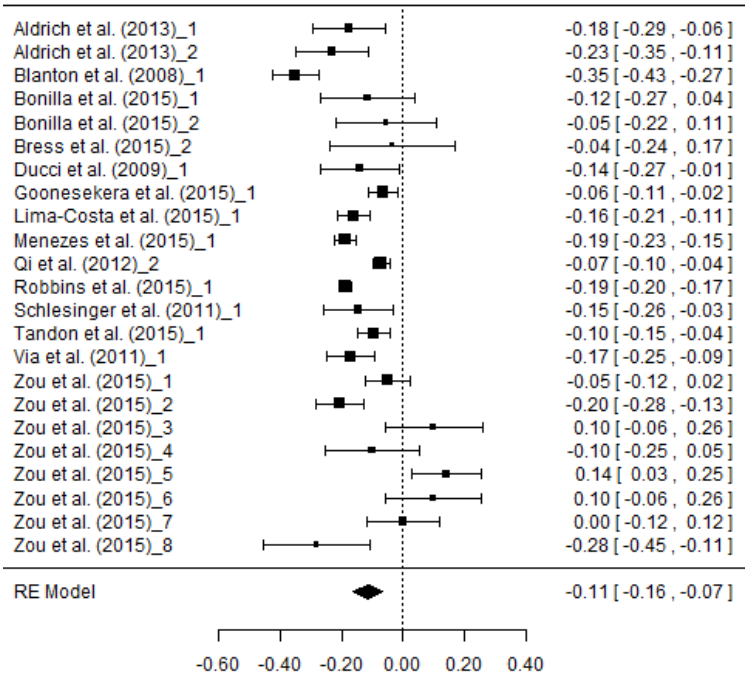


Figure 4: Forest plot for African ancestry results. Based on random effects model.

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



The meta-analytic effect sizes are .18, -.15, and -.11 for European, Amerindian and African ancestry, respectively. European ancestry showes a stronger absolute association than Amerindian and African ancestry, despite the positive European ancestry results being driven by the negative Amerindian and African ones. This is likely an artifact of publication bias, in the sense that more data points were available for the European ancestry analysis. Alternatively, the results could be due to the higher variation in the proportion of European ancestry in the subjects. The mean standard deviation of admixture was smaller for the non-European ancestries (16.9, 7.6, and 12.5 for European, Amerindian, and African, respectively). Less variation leads to smaller effect sizes owing to restriction of range (Hunter & Schmidt, 2004).

Discussion and conclusion

The results of the meta-analysis are consistent with those reported in earlier narrative reviews in that European ancestry was statistically associated with better socioeconomic outcomes relative to Amerindian and African ancestry. The effect of European ancestry was larger than the effects of Amerindian and African ancestry. A high level of between-study heterogeneity (mean I^2 = 92%) was found. Due to the limited number of datapoints, it is difficult to evaluate the cause of this pattern of results. Some possibilities are as follows:

1. Discretization: Many outcome variables were ordinal instead of continuous, even when continuous values were available (e.g., income). Correlations assume that the data are normally distributed, so the use of non-continuous data induces a downwards bias in the results. Corrections were not attempted, although one could attempt this (Hunter & Schmidt, 2004). For instance, Ruiz-Linares et al. (2014) reported a correlation of .12 between European ancestry and education in a large, multi-country sample (total N=7,342). The minimum bias for a three level measure is about 11%.[9] If corrections were made for this, the value would be about .134.

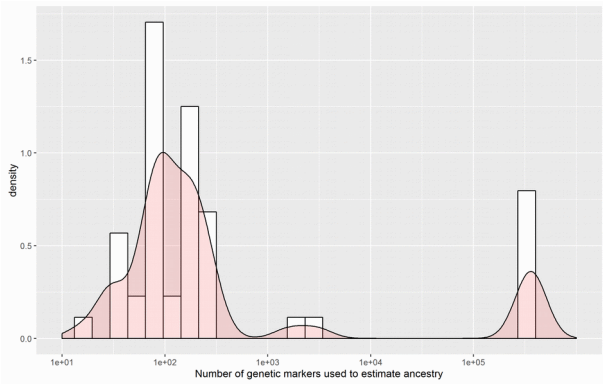
2. Number of ancestry informative markers: There were large differences in the number of genomic markers used to estimate individual BGA. Figure 5 shows a density-histogram of the distribution. Using fewer markers results in more measurement error. Ruiz-Lineras (2014) was the only study that reported correlations between

9 This is the downwards bias if one splits the a continuous variable into three bins with equal size. If the bin sizes are not equal, one can get much larger downwards biases. For instance, if the sizes are 5%, 10%, 85%, the downwards bias is about 34%.

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

admixtures estimates using different numbers of markers. They noted that a recent study (Scharf et al., 2013) had found that using 15 markers resulted in correlations of about .60 with estimates derived from 50k markers. Furthermore, using 30 and 152 makers resulted in about r = .70 and r = .85, respectively, with respect to estimated admixture based on 50k makers. It is clear that there are diminishing returns to using more markers, but also that using more reduces measurement error with respect to "true" ancestry. Ruiz-Lineras et al. themselves used only 30 markers, thus yielding a maximal observed score × true score of .70.[10] As mentioned above, they found a correlation of .12 between European ancestry and socioeconomic outcomes. Were this value corrected for unreliability in measured ancestry, it would be .171 (and .193 if also correcting for discretization). Because studies did not report the correlations needed, it would be difficult to correct for measurement error. One option would be to acquire a sufficient number of datapoints from one study to allow for the estimation of a predictive model. One could then use that model to estimate the measurement error in other studies based on the number of reported markers used. However, we failed to find a study which had sufficient datapoints, so a correction was not attempted.

Figure 5: Density-histogram of the number of genetic markers in each sample.



3. Variance in admixture: The few studies which reported the standard deviations of the ancestry estimates showed substantial variation. For instance, Bonilla et al. (2015) found a standard deviation for African ancestry of only 7.52 while Menezes et al. (2015) found one of 19.20. As mentioned earlier, this would be expected to cause differences in the observed correlations between the studies, all else being equal.

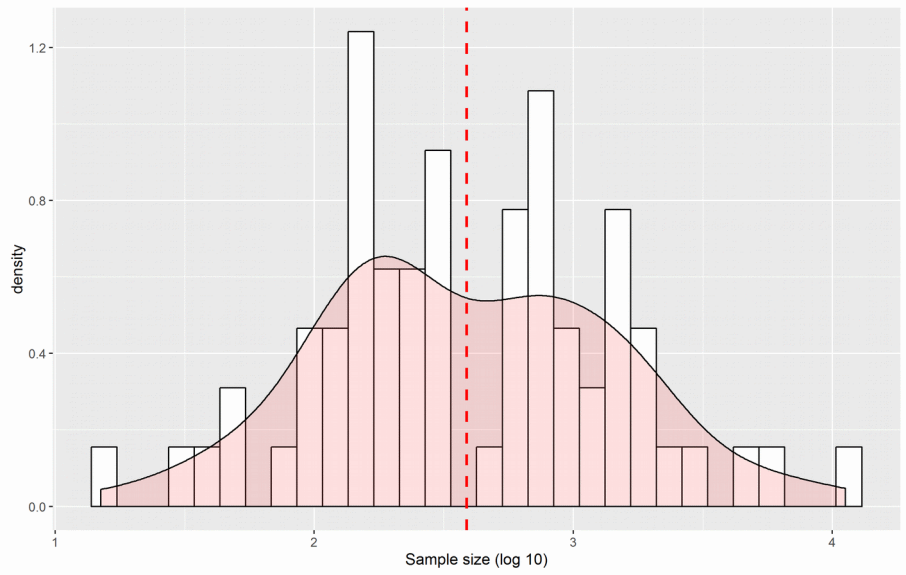
4. Heterogeneous origin: The studies in the meta-analysis came from many countries. It is probable that the effect of one's BGA depends on local cultural norms or practices that differ between countries or even regions within countries. Cross-country differences could also owe to population substructure. For instance, African Americans (in the USA) largely have Northern European ancestry, while Afro-descent groups in Latin America largely have Italian and Iberrian ancestry. Historic selection pressures could have resulted in a differential association between SES and Northern European versus Iberian and Italian BGA.

5. Sample size: The studies varied wildly in sample size. Results based on small sample sizes are expected to be less reliable. Figure 6 shows the distribution of the sample sizes.

Figure 6: Density-histogram of sample sizes (log 10).

10 *Maximally* because this is the value one gets if one assumes that 50k marker measurement has no measurement error. If it does, then comparing against it underestimates the amount of measurement error.

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.



Implications for epidemiological studies

Fairly robust associations between genomic ancestries and SES were found. Given this, to avoid spurious effects in regression analyses due to omitted variable bias, it is potentially important to include SES covariates in studies of medical outcomes. Further, it is also important to identify the factors mediating the BGA-SES associations as these could incrementally explain the BGA-medical outcome associations. Cognitive epidemiology studies have shown that measures of human capital can explain a significant portion of medical related outcomes within population (Calvin et al., 2011; Deary, 2009; Der, Batty, & Deary, 2009; Gottfredson, 2004; Wraw, Deary, Gale, & Der, 2015). Because SIRE groups are known to differ in mean levels of phenotypic cognitive ability (Roth, Bevier, Bobko, Switzer, & Tyler, 2001; Fuerst and Kirkegaard, 2016), it would be reasonable to include measures of cognitive ability in admixture analyses. It is possible that SES acts as a proxy for cognitive ability and that the latter is a more direct mediator. In this case, ideally, one would want to directly control for ability to capture its full effect. Other possible mediators include the cultural aspects of SIRE and phenotypic based discrimination, so-called colorism (e.g., M. Hunter, 2007; Telles, 2014). In principle, these factors could account for a portion of the BGA-medical outcome associations.

Untangling the effects of BGA and SIRE

In many of the studies included in this meta-analysis, individual SES outcomes are associated with BGA within SIRE groups. Hence, SIRE membership is not mediating the relationship. In other cases, particularly in Latin America, the issue is less clear and BGA may be confounded with SIRE. For example, Leite, et al. (2011) found that European ancestry was positively correlated with SES in Brasillia. This could be because it was positively correlated with ancestry net of SIRE or because it was positively correlated with SIRE but not with BGA net of SIRE. The analysis by Ruiz-Linares et al. (2014) has helped to clarify the issue. The authors looked at the association between genotype, color and SIRE in a multi-country sample from Brazil, Chile, Colombia, Mexico and Peru (mean age 20 to 25, country depending). The authors found modest correlations between genomic ancestry and SIRE (e.g., 0.48 in the case of both European/White and Amerindian). They found that wealth and educational attainment correlated with European ancestry ($r = .12$ for the full sample). However, when the effect of BGA was controlled for, education was not associated with SIRE. And wealth was only marginally so ($B = 0.00291$, $p = 6.1\times10^{-4}$) and only with regards to the European/White color group. Despite this, net of BGA, SIRE was found to be a significant predictor of racially associated phenotypes such as melanin index, hair shape, eye color and eye fold. The 1982 Pelotas Birth Cohort study showed similar results (F. Hartwig, personal communication, March 4, 2016). Table 5 below shows the regression coefficients for socioeconomic outcomes

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

with European ancestry, interviewer-rated color and self-reported color. Samples sizes for each measure are shown on the left. As seen, the association between BGA and outcomes was robust to controls for interviewer reported color and SIRE. Complete results are shown in the Supplementary File 1. Together, these results suggest that the associations between BGA and SES are not largely mediated by cultural identity. Quite possibly, cultural identity (net of ancestry) and racial phenotype based discrimination is present in some countries and absent or in the reverse direction in other ones.

Table 5. Regression coefficients (standard errors) for SES at 30-31 years of age according to European BGA and skin color.

Skin color	**Predictors**	**Household asset index**	**Income (Brazilian reais)**	**Schooling in complete years**
Interviewer-rated	**European ancestry**	$P=3.8\times10^{-48}$ 0.299 (0.036)	$P=3.8\times10^{-18}$ 0.187 (0.035)	$P=2.4\times10^{-38}$ 0.311 (0.034)
	Skin color	P=0.045	P=0.384	$P=3.8\times10^{-5}$
N=2258, 2386, 2368	White	0 (Ref.)	0 (Ref.)	0 (Ref.)
N=185, 203, 202	Brown or Mulatto	0.139 (0.088)	-0.010 (0.086)	0.052 (0.085)
N=390, 418, 412	Black	0.076 (0.100)	0.113 (0.098)	0.277 (0.097)
N=11, 11, 11	Asian (“yellow”)	-0.583 (0.291)	-0.359 (0.299)	-0.795 (0.293)
N= 10, 12, 12	Native American	-0.511 (0.306)	-0.205 (0.286)	-0.770 (0.281)
Self-reported	**European ancestry**	$P=3.5\times10^{-48}$ 0.286 (0.034)	$P=3.7\times10^{-18}$ 0.177 (0.033)	$P=2.2\times10^{-38}$ 0.287 (0.033)
	Skin color	P=0.017	P=0.169	$P=1.5\times10^{-5}$
N=2138, 2261, 2244	White	0 (Ref.)	0 (Ref.)	0 (Ref.)
N=161, 171, 170	Brown or Mulatto	-0.114 (0.088)	-0.053 (0.088)	-0.151 (0.086)
N=462, 496, 489	Black	0.077 (0.090)	0.083 (0.089)	0.213 (0.088)
N=50, 54, 54	Asian (“yellow”)	-0.362 (0.140)	-0.221 (0.139)	-0.396 (0.136)
N=43, 48, 48	Native American	-0.103 (0.149)	0.162 (0.145)	-0.140 (0.142)

Limitations and suggestions for future research

The number of effect sizes used in the present meta-analysis is limited. This is because many studies did not report effect sizes and, in some cases, the authors either did not reply to emails or were unable to provide data. In the future, it would help if scientists published their results in a manner consistent with standard scientific practices (e.g., reporting effects sizes and the specific methods used to compute these). The results significantly varied across studies (mean effect size heterogeneity = 92%), which means that there are probably effects size moderators. A moderator analyses was not conducted due to the small number of studies in the dataset. We suggest that moderator analyses be conducted as relevant data accumulates. Analyses for publication bias were also not conducted because the number of effect sizes was too small for a reliable analysis. This question should be addressed in a larger meta-analysis in the future.

Supplementary material

Supplementary Data File 1, High-quality figures and R analysis code are available at the repository at *Open Science Framework* https://osf.io/ydc3f/files/.

Conflicts of Interest

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

The authors declare no conflict of interest

References

Bonilla, C., Bertoni, B., Hidalgo, P. C., Artagaveytia, N., Ackermann, E., Barreto, I., … Kittles, R. A. (2015). Breast cancer risk and genetic ancestry: a case–control study in Uruguay. *BMC Women's Health*, *15*(1), 1–10. http://doi.org/10.1186/s12905-015-0171-8

Branigan, A. R., McCallum, K. J., & Freese, J. (2013). Variation in the Heritability of Educational Attainment: An International Meta-Analysis. *Social Forces*, *92*(1), 109–140. http://doi.org/10.1093/sf/sot076

Calvin, C. M., Deary, I. J., Fenton, C., Roberts, B. A., Der, G., Leckenby, N., & Batty, G. D. (2011). Intelligence in youth and all-cause-mortality: systematic review with meta-analysis. *International Journal of Epidemiology*, *40*(3), 626–644. http://doi.org/10.1093/ije/dyq190

Cheng, C. Y., Reich, D., Haiman, C. A., Tandon, A., Patterson, N., Elizabeth, S., ... & Altshuler, D. (2012). African ancestry and its correlation to type 2 diabetes in African Americans: a genetic admixture analysis in three US population cohorts. *PLoS One*, *7*(3), e32840.

Cohen, J., & Cohen, J. (Eds.). (2003). *Applied multiple regression/correlation analysis for the behavioral sciences* (3rd ed). Mahwah, N.J: L. Erlbaum Associates.

Deary, I. J. (2009). Introduction to the special issue on cognitive epidemiology. *Intelligence*, *37*(6), 517–519. http://doi.org/10.1016/j.intell.2009.05.001

Der, G., Batty, G. D., & Deary, I. J. (2009). The association between IQ in adolescence and a range of health outcomes at 40 in the 1979 US National Longitudinal Study of Youth. *Intelligence*, *37*(6), 573–580. http://doi.org/10.1016/j.intell.2008.12.002

Frudakis, T. N., & Shriver, M. D. (2003). Compositions and methods for inferring ancestry. U.S. Patent and Trademark Office Publication Number 20040229231. Retrieved from http://portal.uspto.gov/pair/PublicPair.

Fuerst, J.& Kirkegaard, E.O.W. The Genealogy of Differences in the Americas. Mankind Quarterly 56 (3)

González Burchard, E., Borrell, L. N., Choudhry, S., Naqvi, M., Tsai, H.-J., Rodriguez-Santana, J. R., … Risch, N. (2005). Latino populations: a unique opportunity for the study of race, genetics, and social environment in epidemiological research. *American Journal of Public Health*, *95*(12), 2161–2168. http://doi.org/10.2105/AJPH.2005.068668

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Gottfredson, L. S. (2004). Intelligence: Is It the Epidemiologists' Elusive "Fundamental Cause" of Social Class Inequalities in Health? *Journal of Personality and Social Psychology*, *86*(1), 174–199. http://doi.org/10.1037/0022-3514.86.1.174

Hill, W. D., Hagenaars, S. P., Marioni, R. E., Harris, S. E., Liewald, D. C., Davies, G., … Deary, I. J. (2016). Molecular genetic contributions to social deprivation and household income in UK Biobank (n = 112,151). *bioRxiv*, 043000. http://doi.org/10.1101/043000

Hunter, J. E., & Schmidt, F. L. (2004). *Methods of meta-analysis correcting error and bias in research findings*. Thousand Oaks, Calif.: Sage. Retrieved from http://site.ebrary.com/id/10387875

Hunter, M. (2007). The Persistent Problem of Colorism: Skin Tone, Status, and Inequality. *Sociology Compass*, *1*(1), 237–254. http://doi.org/10.1111/j.1751-9020.2007.00006.x

Leite, T. K. M., Fonseca, R. M. C., França, N. M. de, Parra, E. J., & Pereira, R. W. (2011). Genomic Ancestry, Self-Reported "Color" and Quantitative Measures of Skin Pigmentation in Brazilian Admixed Siblings. *PLoS ONE*, *6*(11), e27162. http://doi.org/10.1371/journal.pone.0027162

Marioni, R. E., Davies, G., Hayward, C., Liewald, D., Kerr, S. M., Campbell, A., … Deary, I. J. (2014). Molecular genetic contributions to socioeconomic status and intelligence. *Intelligence*, *44*, 26–32. http://doi.org/10.1016/j.intell.2014.02.006

Menezes, A. M. B., Wehrmeister, F. C., Hartwig, F. P., Perez-Padilla, R., Gigante, D. P., Barros, F. C., … Horta, B. L. (2015). African ancestry, lung function and the effect of genetics. *European Respiratory Journal*, *45*(6), 1582–1589. http://doi.org/10.1183/09031936.00112114

Norden-Krichmar, T. M., Gizer, I. R., Libiger, O., Wilhelmsen, K. C., Ehlers, C. L., & Schork, N. J. (2014). Correlation analysis of genetic admixture and social identification with body mass index in a Native American Community. *American Journal of Human Biology*, *26*(3), 347–360. http://doi.org/10.1002/ajhb.22521

Ree, M. J., Carretta, T. R., & Earles, J. A. (1998). In Top-Down Decisions, Weighting Variables does Not Matter: A Consequence of Wilks' Theorem. *Organizational Research Methods*, *1*(4), 407–420. http://doi.org/10.1177/109442819814003

Rietveld, C. A., Medland, S. E., Derringer, J., Yang, J., Esko, T., Martin, N. W., … Koellinger, P. D. (2013). GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. *Science (New York, N.Y.)*, *340*(6139), 1467–1471. http://doi.org/10.1126/science.1235488

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Roth, P. L., Bevier, C. A., Bobko, P., Switzer, F. S., & Tyler, P. (2001). Ethnic Group Differences in Cognitive Ability in Employment and Educational Settings: A Meta-Analysis. *Personnel Psychology*, *54*(2), 297–330. http://doi.org/10.1111/j.1744-6570.2001.tb00094.x

Rowe, D. C., & Rodgers, J. L. (1997). Poverty and Behavior: Are Environmental Measures Nature and Nurture? *Developmental Review*, *17*(3), 358–375. http://doi.org/10.1006/drev.1997.0434

Rowe, D. C., Vesterdal, W. J., & Rodgers, J. L. (1998). Herrnstein's syllogism: genetic and shared environmental influences on IQ, education, and income. *Intelligence*, *26*(4), 405–423. http://doi.org/10.1016/S0160-2896(99)00008-2

Ruiz-Linares, A., Adhikari, K., Acuña-Alonzo, V., Quinto-Sanchez, M., Jaramillo, C., Arias, W., … others. (2014). Admixture in Latin America: geographic structure, phenotypic diversity and self-perception of ancestry based on 7,342 individuals. *PLoS Genetics*, *10*(9), e1004572.

Salzano, F. M., & Sans, M. (2014). Interethnic admixture and the evolution of Latin American populations. *Genetics and molecular biology*, *37*(1), 151-170.

Scharf, J. M., Yu, D., Mathews, C. A., Neale, B. M., Stewart, S. E., Fagerness, J. A., … Pauls, D. L. (2013). Genome-wide association study of Tourette Syndrome. *Molecular Psychiatry*, *18*(6), 721–728. http://doi.org/10.1038/mp.2012.69

Shriver, M. D., & Kittles, R. A. (2004). Genetic ancestry and the search for personalized genetic histories. *Nature Reviews Genetics*, *5*(8), 611-618.

Shriner, D. (2013). Overview of admixture mapping. *Current Protocols in Human Genetics*, 1-23.

Tate, B. W., & McDaniel, M. A. (2008). Race Differences in Personality: An Evaluation of Moderators and Publication Bias. Retrieved from http://www.people.vcu.edu/~mamcdani/Publications/AOM_as_of_8%201%202008.pdf

Telles, E. E. (2014). *Pigmentocracies: ethnicity, race, and color in Latin America* (1 Edition). Chapel Hill, NC: University of North Carolina Press.

Tucker-Drob, E. M., & Bates, T. C. (2016). Large Cross-National Differences in Gene x Socioeconomic Status Interaction on Intelligence. *Psychological Science*, *27*(2), 138–149. http://doi.org/10.1177/0956797615612727

Viechtbauer, W. (2015). metafor: Meta-Analysis Package for R (Version 1.9-8). Retrieved from https://cran.r-project.org/web/packages/metafor/index.html

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.

Waples, R. S., & Gaggiotti, O. (2006). What is a population? An empirical evaluation of some genetic methods for identifying the number of gene pools and their degree of connectivity. *Molecular Ecology*, *15*(6), 1419–1439. http://doi.org/10.1111/j.1365-294X.2006.02890.x

Winkler, C. A., Nelson, G. W., & Smith, M. W. (2010). Admixture mapping comes of age. *Annual Review of Genomics and Human Genetics*, *11*, 65–89. http://doi.org/10.1146/annurev-genom-082509-141523

Wraw, C., Deary, I. J., Gale, C. R., & Der, G. (2015). Intelligence in youth and health at age 50. *Intelligence*, *53*, 23–32. http://doi.org/10.1016/j.intell.2015.08.001

bioRxiv preprint doi: https://doi.org/10.1101/055681; this version posted May 27, 2016. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. All rights reserved. No reuse allowed without permission.