Admixture in the Americas: Regional and National Differences

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We conducted novel analyses regarding the association between continental racial ancestry, cognitive ability and socioeconomic outcomes across 6 datasets: states of Mexico, states of the United States, states of Brazil, departments of Colombia, sovereign nations and all units together. We find that European ancestry is consistently and usually strongly positively correlated with cognitive ability and socioeconomic outcomes (mean r for cognitive ability = .708; for socioeconomic well-being = .643) (Sections 3-8). In most cases, including another ancestry component, in addition to European ancestry, did not increase predictive power (Section 9). At the national level, the association between European ancestry and outcomes was robust to controls for natural-environmental factors (Section 10). This was not always the case at the regional level (Section 18). It was found that genetic distance did not have predictive power independent of European ancestry (Section 10). Automatic modeling using best subset selection and lasso regression agreed in most cases that European ancestry was a non-redundant predictor (Section 11). Results were robust across 4 different ways of weighting the analyses (Section 12). It was found that the effect of European ancestry on socioeconomic outcomes was mostly mediated by cognitive ability (Section 13). We failed to find evidence of international colorism or culturalism (i.e., neither skin reflectance nor self-reported race/ethnicity showed incremental predictive ability once genomic ancestry had been taken into account) (Section 14). The association between European ancestry and cognitive outcomes was robust across a number of alternative measures of cognitive ability (Section 15). It was found that the general

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socioeconomic factor was not structurally different in the American sample as compared to the worldwide sample, thus justifying the use of that measure. Using Jensen's method of correlated vectors, it was found that the association between European ancestry and socioeconomic outcomes was stronger on more S factor loaded outcomes, r = .75 (Section 16). There was some evidence that tourist expenditure helped explain the relatively high socioeconomic performance of Caribbean states (Section 17).

Key words: race, admixture, ancestry, admixture mapping, cognitive ability, intelligence, IQ, academic achievement, general socioeconomic factor, Americas.

Contents

1. Introduction

The existence of large cross-national differences in both socioeconomic outcomes and measured cognitive ability is well established. Lynn & Vanhanen (2012) have shown that cognitive differences can statistically explain the socioeconomic ones to a large extent. Using a cross-lagged panel design, Rindermann (2012) found support for a model in which cognitive differences had a larger causal effect on socioeconomic ones than vice versa. Taken together the results suggest that international differences in cognitive ability are, to a significant degree, antecedent to socioeconomic ones. These cognitive differences themselves have been found to be associated with numerous historic, biological, genetic and evolutionary variables, suggesting that they have deep roots. Some of these variables are listed below in Table 1. Of particular relevance to this paper, it has been found that genetic ancestry is strongly associated with cognitive variation (e.g., Christainsen, 2013; Kodila-Tedika & Asongu, 2015). Correspondingly, Putterman & Weil (2010) found that geographic ancestry accounts for a substantial portion of the international socioeconomic variation. All

of these findings, taken together, confirm the frequent observation that, on the global level, major human biological races[2] (just "races" from now on), such as Europeans, West Africans and Amerindians, differ in their mean levels of cognitive ability (Galton, 1869; Price, 1934; Baker, 1974; Lynn, 2006, 2008). The findings are consistent with the hypothesis that differences in cognitive ability are passed on along lineages and that they explain some of the global variation in socioeconomic outcomes (Lynn, 2008). We dub this hypothesis the *racial-cognitive ability-socioeconomic* (R~CA-S) *hypothesis*.

R~CA-S hypotheses tend to be genetic ones. They typically propose that the observed associations between cognitive ability and race are mediated by genes (Lynn, 2006, 2008). According to typical R~CA-S models, over evolutionary history environmental factors led to differential selection for cognitive ability. Since cognition-related genetic differences are transmitted across generations, and since biological races are defined by ancestry, a genetic R~CA-S hypothesis predicts a robust association between racial ancestry and cognitive ability that is independent of geography. While R~CA-S hypotheses tend to be genetic ones, they need not be. Indeed, pre-Darwinian racial hypotheses were frequently epigenetic[3] (Fuerst, 2015). Apart from genes and epigenetic marks, other factors could potentially mediate a geographically dependent association between race and ability, such as cultural factors which are inter-generationally transmitted. Alternatively, the apparent association between racial ancestry and cognitive ability could be non-robust and simply a function of covarying natural-environmental factors.

Though debate about differences between races often gets bogged down on semantic issues (Fuerst, 2015), there are basic empirical facts to be explained and some which are in need of further exploration. In need of explanation is the association, on the global level, between racial ancestry and both cognitive and socioeconomic outcomes. In need of further investigation is the geographical robustness of these associations and the extent to which differences in cognitive

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[2] By "races" we mean descent-based divisions of a species (cf. Kant, 1777; Darwin, 1903; Hooton, 1946). For an adroit elaboration of the concept, see: Brues (1990). These divisions are alternatively called "geographical ancestry" groups, "genetic clusters", or genetic "populations" (Fullwiley, 2014; Kitcher, 2007; Williams, 2015).

[3] Epigenetic effects involve changes in gene function which are not due to changes in DNA sequences. Most pre-Darwinian race theorists were species realists. For them, all individuals of the same species had the same essence or structural program. For those who conceptualized races as intraspecific lineages, enduring between-group differences were typically attributed to environmentally induced changes which had become imprinted on genealogical lines. This is analogous to an epigenetic model.

ability can account for the association between racial ancestry and socioeconomic outcomes. Discussions of race differences are complicated because, owing to extensive population flows over the last 500 years, most regions of the world contain peoples of non-indigenous ancestry and because the individuals in many regions exhibit substantial racial admixture with respect to the traditionally recognized major geographic races of mankind. The Americas, for example, contain racial tribrid (three-part) populations, with individuals having varying degrees of West African, European and Amerindian biogeographic ancestry (Salzano & Sans, 2014).

Table 1. *Historic, biological, genetic and evolutionary variables associated with international differences in measured cognitive ability.*

Correlate	Reference
IQ and edu. attainment associated SNP frequencies	(Piffer, 2013, 2015a)
Cognitive functioning associated SNP frequencies	(Minkov, Blagoev, & Bond, 2015)
Immunology associated SNP frequencies	(Woodley et al., 2014)
Immunology associated SNP frequencies	(Fedderke et al., 2014)
Racial classifications (based on genetic clusters)	(Christainsen, 2013)
Genetic proximity	(Becker & Rindermann, 2014)
Genetic proximity	(Piffer & Kirkegaard, 2015)
Genetic distance from native South Africans	(León & Burga-León, 2015)
Genetic distance from the US and the UK	(Kodila-Tedika & Asongu, 2015)
Spatial proximity of nations to each other	(Gelade, 2008)
Haplogroups	(Rindermann, Woodley, & Stratford, 2012)
Haplogroups	(Rodriguez-Arana, 2010)
Cranial capacity	(Meisenberg & Woodley, 2013b)
Nasal Index	(Templer & Stephens, 2014)
Time since the origin of agriculture	(Meisenberg & Woodley, 2013b)
Technological development in 1000 B.C.	(Lynn, 2012)
Skin color	(Templer & Arikawa, 2006)
Skin reflectance	(Templer, 2008)
Temperature: annual mean	(Vanhanen, 2009)
Average winter temperature	(Meisenberg & Woodley, 2013b)
Latitude	(Dama, 2013)

Discussion of differences is also semantically complicated because "race" in the form of self/socially-identified race/ethnicity (SIRE) often does not correspond well with race in the biological sense of divisions delineated by descent (or now by ancestrally informative molecular markers). This is particularly true for

populations with long histories of admixture. For example, Ruiz-Linares et al. (2014) found a correlation of only 0.48 between European and Amerindian SIRE and European and Amerindian racial ancestry in a sample from five Latin American countries. The connection between SIRE and race is, of course, obvious. Groups such as Amerindian and European Brazilians were originally relatively unadmixed with respect to major traditionally recognized races (e.g., Amerindian and European Caucasoid). Thus they constituted separate races in the sense of "biogeographic ancestry" groups. Over time they admixed to some degree, yet the admixed groups retained some variant of the original race names, thus leading to discordance between SIRE and race in the form of "genetic ancestry."[4] This situation lends itself to semantic confusion, with the term "race" being used at times to refer to SIRE and at times to refer to biological race, even when the two do not correspond well. This situation has led a number of researchers to varyingly use terms such as "genetic ancestry", "geographic ancestry", "biogeographic ancestry", "genetic populations", "genetic structure" or "genetic clusters" to denote what historically was called, and what we call, race (e.g., Mersha & Abebe, 2015).

While the discordance between SIRE and race complicates discussions of differences, it allows for the testing of certain hypotheses concerning them (Dalliard, 2014; Rowe & Rodgers, 2005). The presence of racial admixture within SIRE groups allows one to disentangle the statistical effects of genetic ancestry from those of SIRE cultural identity (a categorical variable). Put more simply, one can see if genetically assessed racial ancestry is associated with outcomes between individuals within SIRE cultural groups. Just as admixture within SIRE groups allows one to disentangle SIRE associated cultural effects from genealogical ones, post-1500 population flows and the resultant peopling of regions with non-indigenous populations enables one, to a degree, to see if the global associations between race and outcomes transfer across environments. This allows one to better determine whether the associations are independent of the natural environment (i.e., tied to biological descent, rather than geography), as the R~CA-S model would predict.

In this paper, we take advantage of the American regional variation in European, Amerindian and West African admixture to investigate whether there is a robust association between ancestry and outcomes. Our goal is modest: we merely wish to determine if racial ancestry, with respect to three major races, is

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[4] To note, in Brazil, "color" classifications are not officially conceived racially (i.e., in terms of ancestry) but rather morphologically, in terms of phenotype. This point is often overlooked by researchers.

associated with cognitive and socioeconomic outcomes in the Americas and if the ancestry-socioeconomic association is mediated by cognitive ability as has been claimed (e.g., Lynn, 2008). We focus on the Americas because two of our ancestral lineages are not indigenous to the region. As such, for one, multicollinearity between evolutionary and contemporaneous environments is attenuated, thus allowing us to better assess the contemporaneous environmental effects on outcomes. For another, we can see if European and West African ancestry is similarly associated with outcome differences across the Americas as between the regions of origin. We focus on major racial ancestries (European, West African and Amerindian) because, for these divisions, genomic values are readily available. In Section 3, we examine state-level admixture and outcomes within Mexico. In Section 4, 5 and 6, we do the same for the US, Brazil and Colombia. In Section 7, we broaden the analysis to the pan-American national level. In Section 8, we combine our national and intranational estimates. In Section 9, we use multiple regressions to see if using more than one racial ancestry predictor improves predictive power. In Section 10, we test various theories and hypotheses, specifically the climatic and parasite load ones. In Section 11, we use automatic modeling to determine which predictors are non-redundant when predicting outcomes. Specifically, we include geographical-environmental and institutional predictors. In Section 12, we conduct robustness analyses by looking at different weighting methods. In Section 13, we test if cognitive ability mediates the association between ancestry and socioeconomic outcomes as predicted. In Section 14, we test the hypotheses of international colorism and international culturalism. In Section 15, as a robustness test, we examine whether racial ancestry is related to other measures of cognitive outcomes. In Section 16, as a robustness test, we check whether the factor structure of our primary socioeconomic outcome measure is similar to that found when analyzing all countries. Furthermore, we employ Jensen's method of correlated vectors to examine if the observed correlation between European ancestry and socioeconomic outcomes loads strongly on our general factor of socioeconomic outcomes. In Section 17, we take a closer look at the West Indies. There, we test Lynn & Vanhanen's (2012) tourist hypothesis, we attempt to validate our cognitive measure, and we re-analyze the data after including non-sovereign overseas territories. In Section 18, we take a closer look at racial ancestry and socioeconomic outcomes in the US. In Section 19, we look into the issue of spatial autocorrelation. Finally, in Section 20, we discuss the overall study findings and note study limitations.

1.1. R~CA-S model

In our analysis, the primary outcomes of interest are measured cognitive ability and a summary measure of socioeconomic outcomes, as according to the R~CA-S model the main causal route runs from cognitive ability (CA) to socioeconomic outcomes (S). Thus the *statistical* link between race and socioeconomic outcomes is proposed to run mostly through cognitive ability, though other pathways are allowed. Figure 1 shows an overview of the model. Cognitive ability and socioeconomic outcomes are modeled as having reciprocal causal effects (bidirectional arrow). Direct effects of culture and/or genes on socioeconomic outcomes are allowed. These effects could be mediated through traits such as personality, risk aversion, aggressiveness, superstitiousness, wisdom or creativity. Such causes are often posited (e.g., Sternberg, 2013), but since the proposed causal factors are not easily measured (Meisenberg, 2015), little research has been done on them. To note, we are not positing that variance in genomic ancestry (race) directly causes variance in cognitive ability and, by way of this, in socioeconomic outcomes. Rather, according to the model, ancestry covaries with causal factors (e.g., genes and/or cultural practices), which lead to differences in cognitive ability and other traits. Thus we use a tilde (~) and a dash (-) in the abbreviation of the model: the relationship between race and cognitive ability is thought to be statistical, while the relationship between cognitive ability and socioeconomic outcomes is thought to be causal.
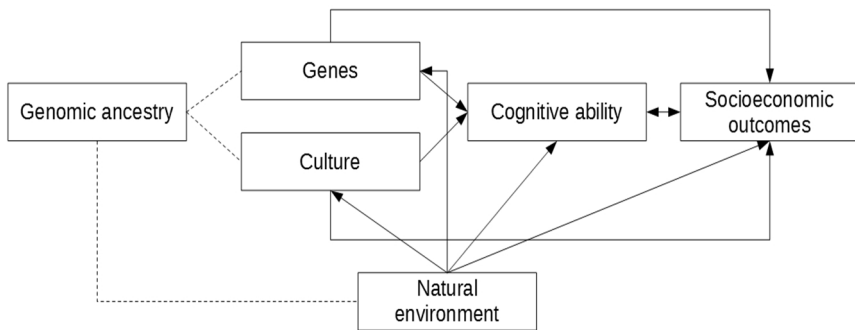

Figure 1. *R~CA-S model.*

We note that the model could easily be expanded to include more pathways. One could, for example, add a bidirectional relationship between culture and cognitive ability, e.g., having a culture of reading could increase cognitive ability (Harlaar, Hayiou-Thomas, & Plomin, 2005; Ritchie, Bates, & Plomin, 2015), which

could further stimulate the development of a reading culture, perhaps by increasing intellectual curiosity (Stumm, Hell, & Chamorro-Premuzic, 2011). However, since we are not in a position to test these pathways, we do not include them in our stylized model.

2. Methods

The general method employed for this project is as follows:

Stage 1. Compile and aggregate genomic admixture estimates. When possible validate them using other data.

Stage 2. Compile and aggregate cognitive ability, socioeconomic outcome and geographic environmental data.

Stage 3. Examine the relationship between genomic ancestry and outcomes using scatter plots, correlations, semi-partial correlations, multiple regressions and path analysis.

In selecting countries for regional analysis, to allow for reliable associations, four conditions had to be met:

Condition 1. There must be substantial inter-regional variation in admixture.

Condition 2. There must be a decent number of cases (n > 12).

Condition 3. Either genomic estimates must be available for the states/districts or SIRE admixture estimates must be available along with SIRE state/district percentages.

Condition 4. Reliable cognitive ability and socioeconomic outcome data must be available.

Regarding Stage 2, we conducted a series of studies to obtain good summary measures of socioeconomic well-being. There are many different socioeconomic outcomes that one can look at. When such socioeconomic variables are factor analyzed, though, a general socioeconomic factor (S factor) emerges such that, most of the time, desirable outcomes load positively and undesirable outcomes load negatively on it. Previous research has found S factors at the national level (Kirkegaard, 2014b), the state/region/department level (Carl, 2015; Kirkegaard, 2015b, 2015d, 2015e, 2015f, 2015g, 2015h, 2015j, 2015k, 2015l) and the city district level (Kirkegaard, 2015a). Analyses of national and state level data showed that Human Development Index (HDI) scores correlated strongly with S factor scores at typically >.9. Justified by the very strong correlation between HDI and S, when we could not obtain S scores for particular units, we employed HDI scores as reasonable proxies.

Also regarding Stage 2, humans have many cognitive abilities, yet factor analysis demonstrates the existence of a general factor – which has been called (general) intelligence, general mental ability, general cognitive ability, or simply *g*

(Kirkegaard, 2014a). This general factor has been found to be the most predictive cognitive ability for many outcomes (Carroll, 1997; Jensen, 1998; Ree, Carretta, & Green, 2003). It is measured by virtually all cognitive tests (Jensen, 1998), though not all tests measure it equally well. Large and diversified IQ batteries are good measures of it (Johnson, Nijenhuis, & Bouchard, 2008), however high-quality IQ estimates are not available for many countries, let alone for provinces within them (Rosas, 2004). For this reason, we use scholastic tests which are known to correlate strongly with IQ, especially at the group level (Condon & Revelle, 2014; Frey & Detterman, 2004; Rindermann, 2007), and for which there are high-quality data, e.g., from the OECD's PISA program. We note that it is not clear whether differences in our academic measures actually index differences in general cognitive ability.[5] Undoubtedly, though, they index differences in some type of cognitive ability. Since we are unsure about the psychometric nature of the differences being discussed, we will simply refer to them as "cognitive ability" differences, without the implication that we are necessarily dealing with variation in general intelligence.

Indeed, we think that it is implausible that the cognitive differences being discussed – see appendix A – solely represent average general intelligence. For example, given the performance of first and second generation Surinamese in the Netherlands (e.g., Lynn, 2008), individuals who were not particularly migrant selected, it is highly unlikely that Surinamese in Suriname have an average general cognitive ability score of 74 (on the standard IQ metric). Our default model would be that there are average individual-level general cognitive ability differences between nations and regions. These induce socioeconomic differences, such as differences in the quality of schooling, which in turn lead to expanded cognitive differences, broadly conceived. These latter differences are then indexed by our measures of national and subnational ability.

3. Regional racial admixture in Mexico

Mexico is a racially admixed country which exhibits substantial regional variation in mean admixture, cognitive ability and socioeconomic outcomes. There are 31 states and a federal district. Since federal districts are often outliers (Kirkegaard, 2015d, 2015e), we excluded the federal district from all analyses except the admixture plot.

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[5] Measurement invariance needs to be examined for cross-national data, or at least by proxy using Jensen's method (Jensen, 1998).

3.1. Data sources

We created regional admixture, cognitive ability and socioeconomic variables as discussed below. Data with sources and computations are available in Supplementary File 1.

3.1.1. Admixture estimates

Admixture estimates were copied from Salzano and Sans (2014), Moreno-Estrada et al. (2014) and Salazar-Flores et al. (2015). Salzano and Sans (2014) provided a review of older studies; Moreno-Estrada et al. (2014) and Salazano and Sans (2014) provided new results based on multi-state studies. The unweighted intercorrelations for the three sources were determined. For European and Amerindian ancestry the Pearson correlations were above 0.83; for African ancestry they ranged from -0.60 to 0.46. Regarding European and Amerindian ancestry, the values exhibited a high reliability, thus justifying their combination. The African ancestry values were unreliable due to the noisiness of the measures in conjunction with the limited range of African ancestry (2.04% to 11.00% in the final estimates). The minimal variance ensures that African ancestry itself will have little effect on state-level outcomes and makes it likely that any found association is spurious.

Admixture values were averaged for each state. This provided data for 18 of Mexico's 31 states. Missing data points were then estimated based on the measured admixture of adjacent regions. Details pertaining to how this was done for each region are provided in Supplementary File 1B. Figure 2 shows a ternary plot of the state racial admixture estimates (Hamilton, 2015).
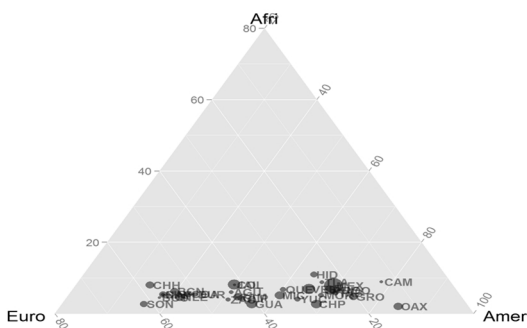

Figure 2. *Admixture estimates for Mexican states. Admixture proportions are read counterclockwise from each corner: % African on the left side, % Amerindian on the right side and % European at the base of the triangle.*

We see that Mexico is mainly European and Amerindian; the amount of African ancestry is low. This situation implies that multiple regressions, which take into account all three ancestries, should not show substantial incremental predictive power over a zero-order correlation using just European or Amerindian ancestry. We'll return to this issue in Section 9.

3.1.2. Cognitive ability estimates

PISA scores averaged across math and reading tests and across the years 2003, 2006, 2009 and 2012 were computed for each state. The original values can be found in Supplementary File 1B. State scores were highly correlated across years with an average correlation of 0.81. This justified the use of cross-year average scores. Since there were missing values for certain years and since average PISA scores varied by year, point scores could not be directly averaged. Instead, deviation scores relative to the Mexican national mean were computed for each year and then averaged. To calculate these deviation scores, we used the international average PISA standard deviations for the years and tests used. These scores were then transformed into achievement quotient scores with a standard deviation of 15 set relative to the national achievement quotient (NACHQ) score of Mexico. The Mexican NACHQ was, in turn, set relative to a UK mean of 99 following Lynn & Vanhanen's (2012) equalization of means and standard deviations method.[6] For validation of the cognitive estimates, 2002 and 2005 average state level short form Raven's Matrices scores, from the *Mexican Family Life Survey*, were also computed and correlated with the cross year average PISA scores. The original Raven's scores came from Salomón & Briseño, (n.d.). The state level Raven-PISA correlation was 0.66 (N=14). This correlation was likely attenuated by the relatively poor reliability of the Raven's scores; the correlation between the 2002 and 2005 state average Raven's scores was only .69.

3.1.3. Socioeconomic outcomes

As discussed in Section 16, when analyzing socioeconomic outcomes, a general factor tends to emerge. Since no Mexican state S factor study existed, one of us conducted a thorough study (Kirkegaard, 2015d), using outcome data from approximately 2005 to 2015. We found that year 2010 HDI correlated very strongly (r = .93) with the S scores based on 23 diverse indicators.

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[6] The UK IQ was set to 100. The ACHQ came out to one point below that. We did not adjust upwards.

3.2. Zero-order correlations and scatter plots

The zero-order correlations are shown in Table 2. Below the diagonal, weighted correlations are presented. For this and subsequent analyses, we used the square root of the regions' populations as weights. We discuss the matter of weighting in Section 12 and show results generated using alternative weighting methods.

Table 2. *Zero-order correlations for Mexican states. Weighted correlations below the diagonal. N=31 for all cases. CA, cognitive ability (PISA score); S, socioeconomic (S) factor; HDI, human development index.*

	CA	S	HDI	African%	Amerindian %	European%
CA		0.77	0.74	0.36	-0.57	0.51
S	0.80		0.93	0.21	-0.69	0.64
HDI	0.78	0.94		0.22	-0.65	0.60
African%	0.42	0.24	0.28		0.08	-0.22
Amerindian%	-0.59	-0.71	-0.65	0.03		-0.99
European%	0.52	0.67	0.60	-0.18	-0.99	

Unsurprisingly, given the ternary plot above, European% and Amerindian% were almost perfectly negatively related. To facilitate comparability across countries, we employed European% in our analyses. European%, cognitive ability scores and socioeconomic outcomes were all substantially positively related, as expected, given the R~CA-S model. Using S instead of HDI produced somewhat stronger results, but, as expected, HDI acted as an acceptable proxy for S. Regarding African%, the results were unexpected and are likely to be flukes. Figures 3 and 4 show the scatter plots for European% and cognitive ability scores and European% and S factor scores, respectively.
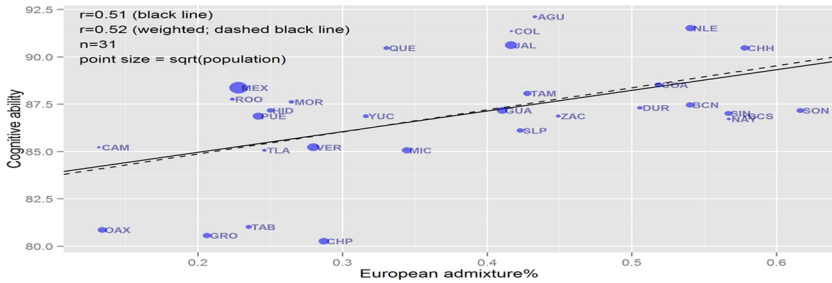
Figure 3. *European ancestry% and cognitive ability scores for Mexican states.*
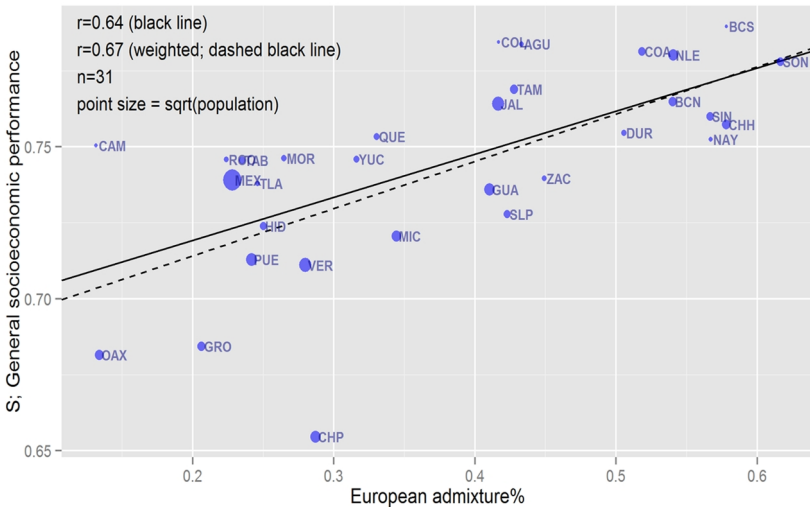
Figure 4. *European ancestry% and S factor scores for Mexican states.*

4. Regional racial admixture in the United States

We now turn to the United States. For this country, there are high-quality data concerning state-level cognitive ability scores and socioeconomic outcomes, but state-level genomic admixture data are wanting. Bryc et al. (2015) did provide some SIRE group admixture estimates by states, but data points were missing for many states and the samples (from the personal genomics company 23&Me) were not particularly representative. Thus, we estimated state-level admixture data using SIRE rates in conjunction with SIRE genomic admixture data.

4.1. Data sources

We created regional admixture, cognitive and socioeconomic variables as discussed below. The raw data are available in Supplementary File 2.

4.1.1. Admixture estimates

We computed the state racial ancestry estimates using 2010 census SIRE data, in conjunction with the SIRE admixture estimates provided by Shriver et al. (2003) and Klimentidis et al. (2009). Table 3 depicts the racial admixture for the SIRE groups.

Our state level estimates are crude, as there is regional variation in SIRE admixture. For example, Hispanics in the Northeast are more ancestrally European than are those in the Southwest (Bryc et al., 2015). Nonetheless, these estimates are reasonable approximations. The US has non-trivial Asian American, mixed ethnic and Pacific Islander populations. For three reasons this is problematic: one, no good admixture data are available for these groups, two, the Asian and Pacific Islander SIRE groups have unique cognitive and outcome profiles relative to African, White, Hispanic and Native American SIRE groups (see, for example: Fuerst, 2014) and three, the Asian and Pacific Islander SIRE groups largely belong to major races different from the three being discussed in this paper. These three problems taken together render state comparisons problematic.

Table 3. *SIRE admixture estimates.*

Ethnorace	European%	African%	Amerindian%	Source
White	96.1	3.2	0.7	Shrivers et al.
Black	18.0	82.0	0.0	Shrivers et al.
Native-American	25.3	2.9	71.8	Klimentidis et al.
Hispanic	61.6	5.7	32.7	Klimentidis et al.

We decided that the soundest method was to exclude these groups. This was done by using only White, Black, Native American and Hispanic SIRE percentages to compute state admixture percentages and by dividing the resultant admixture percentages by the White, Black, Native American and Hispanic SIRE sum percentages. Thus, the state formulas were:

European genomic% =
(White*96.1+Black*18+Native*25.3+Hispanic*61.6)/(White+Black+Native+Hispanic)

African genomic% =
(White*3.2+Black*82+Native*2.9+Hispanic*5.7)/(White+Black+Native+Hispanic)
Amerindian genomic% =
(White*0.7+Black*0+Native*71.8+Hispanic*32.7)/(White+Black+Native+
Hispanic)

By this method, outcomes are modeled as varying due only to factors related to European, African and Amerindian ancestry. We excluded Hawaii from the analyses since the majority (51%, or 68% when including individuals who reported two or more races) of Hawaiians reported East Asian and Pacific Islander ethnicity.

Figure 5 shows the ternary plot of the state admixture estimates. We see that there is substantial admixture, and unlike with Mexico, it is not solely along one axis. If African and Amerindian ancestry is associated with different levels of cognitive ability and S, then multiple regressions should give additional predictive power for this dataset.
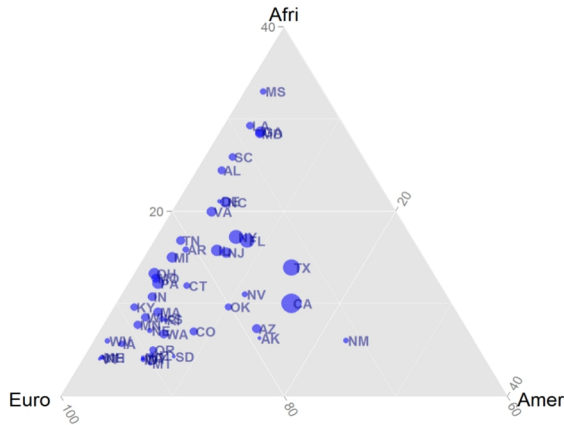

Figure 5. *Ternary plot for admixture in the US.*

4.1.2. Cognitive ability

There are no PISA scores for all states in the US. One alternative is to estimate cognitive ability scores from NAEP achievement scores. McDaniel (2006) used data from multiple years to estimate state IQs, scaled to a national mean of 100. These estimates have subsequently been employed in a number of

analyses. In addition to McDaniel's scores, we computed average 2009 and 2013 NAEP scores based on those provided by science blogger *The Audacious Epigone.*[7] The scores provided by *The Audacious Epigone* were adjusted up so as to be set relative to a national IQ of 100. The average of Audacious Epigone's scores were then averaged with McDaniel's and set relative to the national US NACHQ score.

4.1.3. Socioeconomic outcomes

There is no official set of HDI scores for the US, but there is the *American Human Development Index* (AHDI, see http://www.measureofamerica.org/). While it is not set on the same scale as the HDI values and thus is not very useful for international comparisons, we nonetheless included the 2010 AHDI scores in our US analysis. Additionally, one of us undertook an S factor study of the US (Kirkegaard, 2015e) and found an S factor using 24 diverse indicators. We excluded Washington DC in line with Kirkegaard (2015e) and the Mexican analysis in Section 3. Due to some facts which will be discussed later, one of us undertook a new and larger S factor analysis for the US (81 indicators based on 2010 data, Kirkegaard, 2015b). Between the datasets, the S factor scores correlated .961. We used the scores from the second paper as it was based on more indicators.

4.2. Zero-order correlations and scatter plots

Zero-order correlations are shown in Table 4. Regarding social outcomes, the association between European% and S scores was substantially larger than that between European% and AHDI scores, this despite the fact that our S scores correlated at .94 with AHDI scores. The discrepancy is likely due to the relative homogeneity between states in the few variables that were used to compute the AHDI scores. We also note that AHDI correlated more weakly with CA (.52) than did S (.70), which also supports the hypothesis that something is amiss with the AHDI numbers.

Table 4. *Zero-order correlations for the US. Weighted correlations below the diagonal. N=49 for ancestry variables, N=50 for cognitive ability (CA), socioeconomic (S factor) and American Human Development Index (AHDI).*

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[7] The relevant blog posts can be found here:
http://anepigone.blogspot.com/2006/07/better-state-iq-estimates.html
http://anepigone.blogspot.com/2010/05/state-iq-estimates-2009.html
http://anepigone.blogspot.co.at/2015/01/state-iq-estimates-2013.html.

	CA	S	AHDI	African %	Amerindian %	European%
CA		0.75	0.57	-0.50	-0.32	0.67
S factor	0.70		0.94	-0.39	-0.11	0.44
AHDI	0.52	0.94		-0.21	0.08	0.16
African%	-0.40	-0.37	-0.21		-0.25	-0.84
Amerindian %	-0.40	-0.06	0.15	-0.27		-0.31
European%	0.64	0.39	0.12	-0.81	-0.35	

It is notable that despite the weak correlation between racial ancestry and AHDI between states, there were substantial *intrastate* differences between SIRE groups. The AHDI differences between Africans and Hispanic Americans, on the one hand, and White Americans, on the other, were roughly three times the magnitude of the average AHDI difference between states. Moreover, the magnitude of these intrastate differences was fairly constant across states. The substantial association between SIRE and AHDI on the intrastate level lends itself to the prediction that racial ancestry will be a major predictor at the state level. However, as we have seen, this is not the case. More research is needed on this issue. We return to it briefly in Section 18.

As before, we examine the scatter plots to visualize the results. These are shown in Figures 6 and 7.
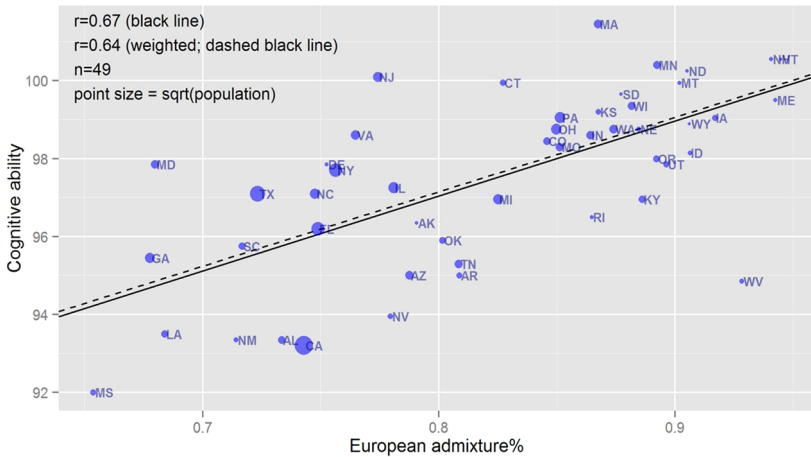
Figure 6. *Scatter plot of European% and cognitive ability scores for the US.*
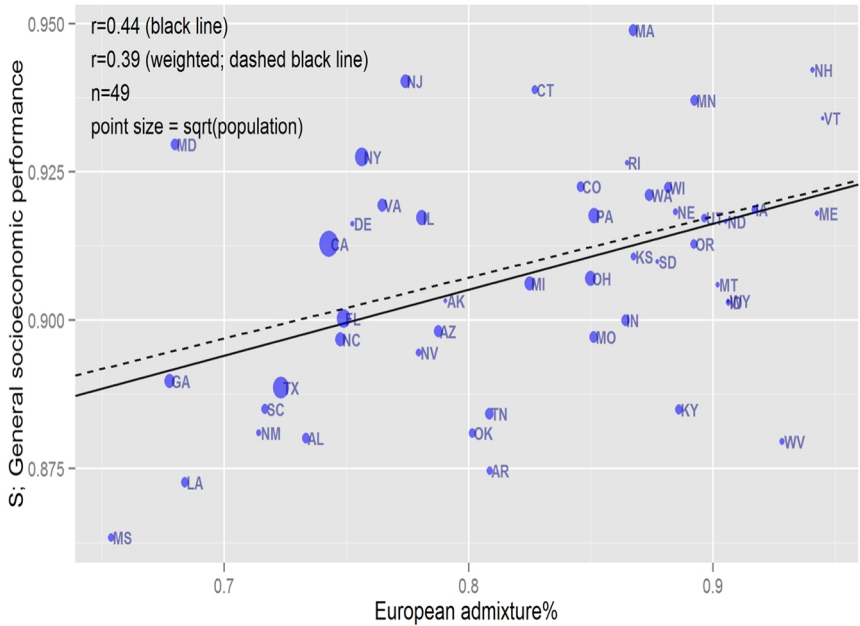
Figure 7. *Scatter plot of European% and S factor scores for the US.*

With regard to S, Maryland (MD) and West Virginia (WV) represent two major outliers. The values for these two states appear to be correct. The higher than expected S score for Maryland could be due to its proximity to the capital district, which is an enclave between Maryland and Virginia. Many affluent individuals commute from Maryland to the capital district. The weighted correlation between S scores and European ancestry without these two outliers is .50 instead of .39. Generally, it seems that state-level socioeconomic outcomes are driven largely by factors different from those correlated with the major racial lineages analyzed here. It is possible that intra-European ancestry is associated with state-level outcome differences. European ethnic groups tended to settle in different parts of the US ("American Nations Series," 2013; Fischer, 1989; Woodard, 2012) and there is some evidence that regional European ancestry is associated with regional outcome differences in the US (Fulford, Petkov, & Schiantarelli, 2015).

5. Regional racial admixture in Brazil

Brazil has 26 states and a federal district. The number of states and the amount of variation in ancestry between them is sufficient for the type of analysis which we are conducting.

5.1. Data sources

As with the other studies, we compiled data from multiple sources. The data are available in Supplementary File 3.

5.1.1. Admixture estimates

For the Brazilian estimates, we averaged the state admixture values reported in Rodriguez de Moura et al.'s (2015) meta-analysis. This provided estimates for 16 of Brazil's 26 states. The values for the 10 remaining states were filled in with the respective average values of the five major Brazilian regions (North, Northeast, Central-West, Southeast and South). This was justified because state variation in admixture clusters regionally. To validate these estimates, we correlated the European state ancestry estimates with White (Branco state SIRE%. The state SIRE percentages were obtained from the 2012 The Brazilian Institute of Geography and Statistics (IBGE) survey (http://www.sidra. ibge.gov.br/bda/tabela/listabl.asp?z=t&c=262). The correlation was 0.79 (N=26, weighted). The ternary plot is shown in Figure 8.
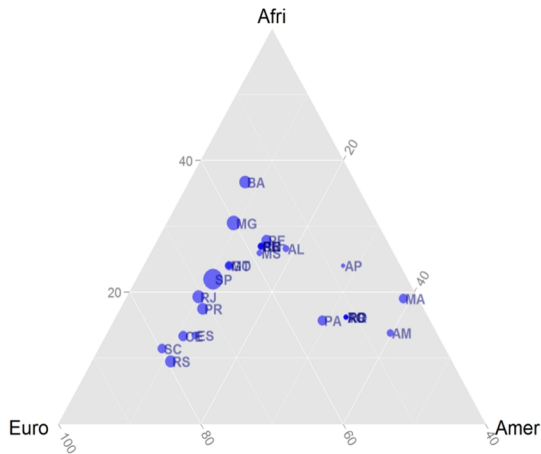
Figure 8. *Ternary plot for admixture in Brazilian states.*

5.1.2. Cognitive ability

For cognitive ability scores, we used the average of the math and reading PISA 2012 scores (OECD, 2014).

5.1.3. Socioeconomic outcomes

Both S factor and HDI scores are available for Brazilian states for the years 1991, 2000 and 2010 (Kirkegaard, 2015k). These all correlate very strongly (range .90 to .98). We used the S scores from 2010, because it was based on the largest number of indicators (26) and our socioeconomic data for our other countries came from around 2010. We also used the 2010 HDI values.

5.2. Zero-order correlations and scatter plots

The correlation matrix is shown in Table 5. The results are similar to those for Mexico, in that European ancestry is strongly related to cognitive ability scores, S scores and HDI scores. In this bivariate analysis, African ancestry was not strongly negatively associated with outcomes. As will be seen in Section 9, the negative associations become more robust when the covariance between African and Amerindian ancestry is taken into account. The scatter plots for European ancestry and cognitive scores and European ancestry and S factor scores are shown in Figures 9 and 10, respectively.

Table 5. *Zero-order correlations for Brazil. N=26 in all cases.*

	CA	S	HDI	African%	Amerindian%	European%
CA		0.81	0.71	-0.12	-0.65	0.74
S	0.84		0.95	-0.17	-0.65	0.77
HDI	0.78	0.97		-0.30	-0.47	0.67
African%	-0.17	-0.19	-0.28		-0.34	-0.31
Amerindian%	-0.65	-0.67	-0.54	-0.29		-0.79
European%	0.73	0.76	0.70	-0.44	-0.73	

It is notable that Ceará seems to be a major outlier with regards to both cognitive and socioeconomic outcomes. If it is excluded, the correlations become .72 and .80 for CA and S, respectively. As shown in Table 5, Amerindian% is more negatively associated with outcomes than is African%. This could be because provinces with high Amerindian ancestry tend to be the more remote ones.
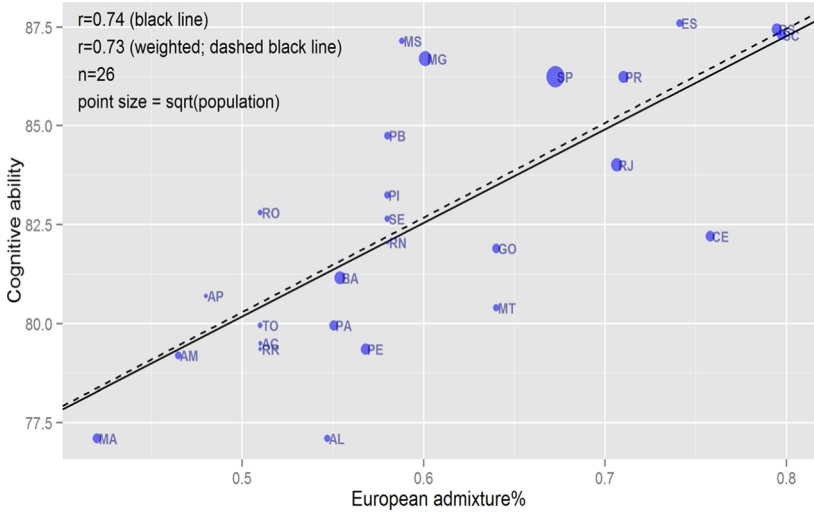
Figure 9. *Scatter plot of European% and cognitive ability scores for Brazilian states.*
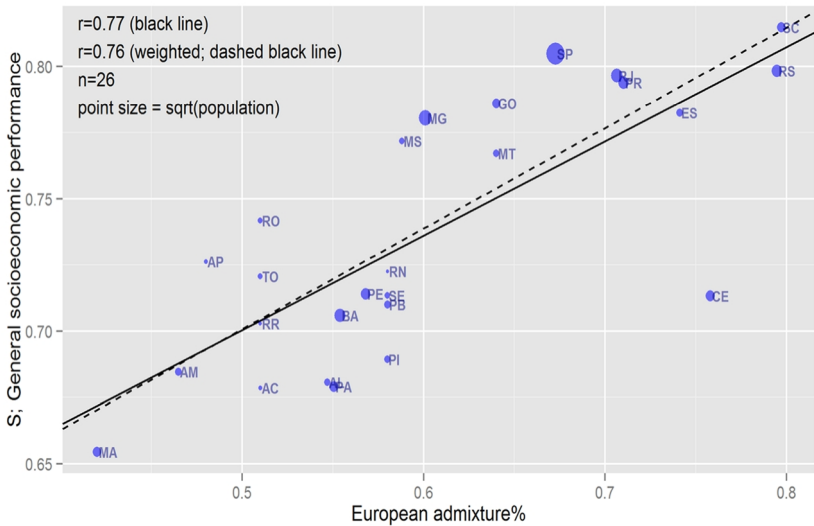
Figure 10. *Scatter plot of European% and S factor scores for Brazilian states.*

6. Regional racial admixture in Colombia

Colombia is located in the northern region of South America. It has 32 departments and a capital district with a total population of approximately 50 million. Like the three previously discussed countries, Colombia shows significant spatial variation in admixture.

6.1. Data sources

The data are available in Supplementary File 4.

6.1.1. Admixture estimates

Estimating regional admixture for Colombia's 32 departments is not without difficulty, since existent studies provide admixture data for only half of the departments. Problematically, specific estimates for the eastern and southeastern departments, which are reported to have high Amerindian components, are not available. Nonetheless, we were able to construct a set of admixture estimates. First, 18 departmental estimates were copied from Salzano and Sans' compilation (Salzano & Sans, 2014). The ancestry ratios from Salzano and Sans' two main sources correlated at 0.9, justifying the use of the combined estimates. Second, missing values were filled in based on regional values and based on Ruiz-Linares et al.'s and Rodriguez-Palau et al.'s admixture/SIRE maps (Rodriguez-Palau et al., 2007; Ruiz-Linares et al., 2014). For example, estimates for Caribbean-Pacific departments were averaged and used to fill in missing data for other departments in this region. Specific computations are provided and explained in Supplementary File 4C and 4E. To validate these estimates we computed ones using SIRE (Afro descent, Indigenous and "no ethnic" plus Roma) data from the 2005 census ("Censo Nacional," 2005), in conjunction with average SIRE admixture percentages as reported in all locatable studies. The correlations between the two estimates for African, Amerindian and European ancestry were, respectively, 0.81, 0.79 and 0.67. The relatively low correlation between our SIRE admixture derived European estimates and our district genomic ones likely relates to the imprecise nature of the SIRE categories. We ran the analysis using both sets of estimates and came up with comparable results. Below, we report results based on the genomic estimated district ancestry data (not the SIRE x admixture based estimates). Figure 11 shows the admixture plot.
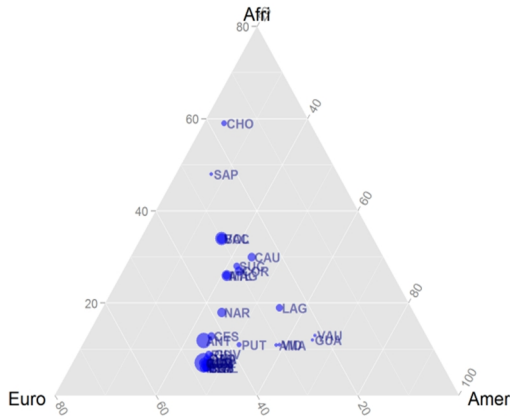
Figure 11. *Ternary plot for admixture in Colombian states.*

6.1.2. Cognitive ability

For cognitive scores, grade 5 and 8 SABER ("knowledge") math and reading exam scores were used (sources given in Supplementary File 4F). For each year, these were transformed into deviation scores. The average of the 2012 and 2014 exam scores correlated at about 0.85 with the average of the 2003 and 2005 scores. The 2012/2014 and 2003/2005 scores were on different metrics, and yearly standard deviations were not available for the 2003 and 2005 scores (given the source used), so, in the end, only the 2012 and 2014 average scores were employed. Following the previously discussed method, scores were converted to ACHQs relative to a UK mean of 99.

6.1.3. Socioeconomic outcomes

No Colombian S factor study had previously been conducted. For this reason, one of us carried out such a study (Kirkegaard, 2015j). The study extracted an S factor from 16 diverse socioeconomic variables. The variables were based on data from 2005. Results were generally in line with previous studies from other countries. In addition to S scores, we included 2010 HDI scores.

6.2. Zero-order correlations and scatter plots

Table 6 shows the zero-order correlations. As in the other countries, we see strong correlations between European% and outcomes. The cognitive ability association is driven by a strong negative relation between African% and ability. The S and HDI associations are driven by a negative association split between Amerindian% and African%. Figures 12 and 13 show the scatter plots for cognitive ability and S factor scores, respectively.

Table 6. *Zero-order correlations for Colombian departments. N=33 in all cases. CA, cognitive ability; S, socioeconomic (S) factor; HDI, Human Development Index.*

	CA	S	HDI	African %	Amerindian %	European %
CA		0.70	0.67	-0.62	0.04	0.82
S	0.65		0.83	-0.35	-0.14	0.62
HDI	0.64	0.84		-0.20	-0.25	0.51
African%	-0.70	-0.34	-0.23		-0.70	-0.76
Amerindian %	0.26	-0.05	-0.19	-0.76		0.07
European%	0.81	0.53	0.47	-0.89	0.39	
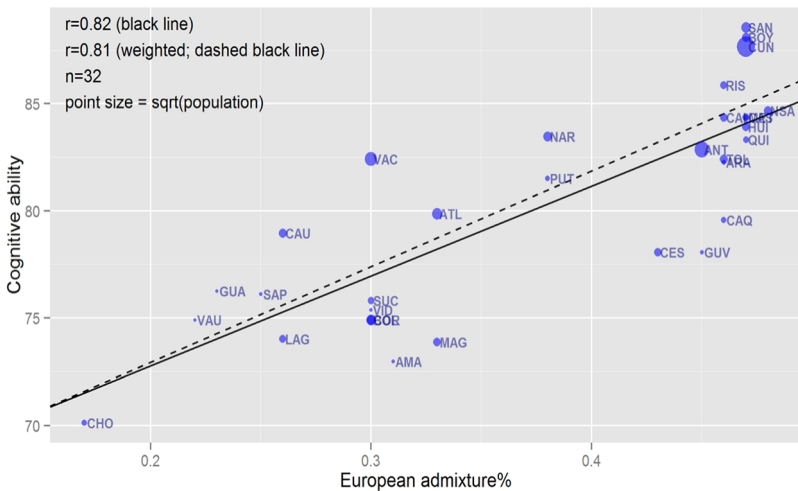
Figure 12. *Scatter plot of European% and cognitive ability scores for Colombian Departments.*
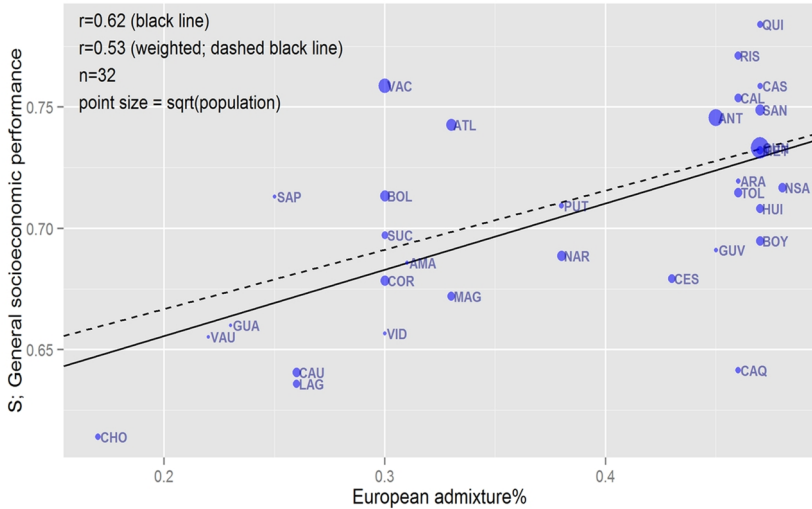
Figure 13. *Scatter plot of European% and S factor scores for Colombian departments.*

7. National racial admixture in the Americas

Previously, we used divisions within countries as units of analysis. Now it is time to zoom out and take a look at all countries in the Americas. Doing so does not drastically change the sample size because there are only 35 sovereign nations. It is worth noting upfront that many of these 35 are small island nations for which good data points are hard to come by.

7.1. Data sources
7.1.1. Admixture estimates

Estimating and validating admixture at the national level is more complex than at the intranational level, and thus, the discussion of the procedure and the results necessitates more space than used in the previous sections.

7.1.1.1. Genomic estimates

Average genomic ancestry percentages were created for the 35 sovereign American nations, based on the data available as of September 2014. Most admixture studies decomposed racial ancestry into three components: European, African and Amerindian. For some countries, a significant fraction of the population had other major ancestral components, such as South Asian, East

Asian or Oceanian. As such, an "other" category was included. Not all possible studies were used in creating the national estimates. Rather, estimates from the most methodologically sound and nationally representative studies were. To avoid problems with sex-biased dispersion and mating we used only autosomal based estimates, omitting results obtained with Y-chromosomal and mitochondrial DNA. Roughly 70 different study estimates were employed to create the 35 national ones. For some countries up to four sets of estimates were averaged, while for others only one was available. For Belize and Paraguay, no national level data were available. Estimates instead were calculated based on those of the surrounding nations and the regions within those nations. This was justified given a number of historical facts related to the peopling of these two countries. Data was also unavailable for Guyana and Antigua and Barbuda. CIA based SIRE estimates were used instead for these two countries.

For Trinidad and Tobago, values were available only for the SIRE Black population, which constitutes approximately 40% of the total. In making a Trinidad and Tobago estimate, it was assumed that SIRE South Asian Indians had a similar level of European ancestry as did SIRE Blacks. The "mixed" group was treated as one half SIRE Black and one half SIRE South Asian Indian. US national admixture estimates were created by weighing the national SIRE percentages by the admixture percentages for each SIRE group. Asians (~4.5% of the population) were treated as 100% other. Pacific Islanders and Mixed race individuals (~1.5%) were discounted. For Canada, the national estimate was made using US SIRE admixture values in conjunction with Canadian SIRE percentages. To make ancestry percentages more comparable across countries, national admixture was expressed in terms of the three main source populations: European/West Caucasian, African and Amerindian. Computations and sources are provided in Supplementary File 5B.

7.1.1.2. Self-identified race

CIA World Factbook SIRE data were used to create national racial averages, except in the case of Canada, for which the 2011 Canadian census data were used. As with genomic ancestry, European, African, Amerindian and other percentages were computed. Specific ethnic identities such as "Spanish" and "Aymara" were grouped into major regional racial identities. In regards to hybrid identities such as Mestizo and Mulatto, percentages were split by parental group (e.g., one half European and one half Amerindian). For tribrid identities such as Montubio, percentages were split three ways. Assumptions had to be made for a number of nations. For example, Costa Rica was said to be 83.6% "White and Mestizo"; this was treated as 83.6 percent Mestizo (i.e., as 41.8% European and

41.8% Amerindian). St. Lucia was said to be 85.3% Black, 3.9% White and 10.9% Mixed; it was assumed that the "mixed" group was mixed Black and White. Judgment calls such as these are noted in Supplementary File 5D.

7.1.1.3. Putterman and Weil's World Migration Matrix

Ancestry components were also computed based on Putterman and Weil's World Migration Matrix for 165 countries (Putterman & Weil, 2010). For each nation, the matrix gives the percentages of ancestors hailing from every nation in the year 1500. Putterman and Weil based their estimates on a mix of genetic studies, immigration data and other sources. The four ancestral components were created by summing the year 1500 national ancestry components into the broad categories of European, African, Amerindian and other (which includes Middle Easterner and North African). Computations are provided in Supplementary File 5C.

7.1.1.4. Skin reflectance

National skin reflectance data were provided by Gerhard Meisenberg (Personal Communication, 2014). These estimates have previously been used in a number of analyses (e.g., Meisenberg & Woodley, 2013a). For this variable, higher values correspond with brighter skin. Values are provided in Supplementary File 5A.

7.1.1.5. Results

The genomic admixture estimates, SIRE estimates, Putterman and Weil's ancestry estimates and skin reflectance scores are available in Supplementary File 5. Results are shown in Tables 7 through 9 below. Note that for this validation check, we excluded the two purely SIRE imputed genomic values (Guyana and Antigua-Barbuda) from the genomic% variable. European, African and Amerindian genomic estimates strongly correlate with estimates based on racial identification and with Putterman and Weil's World Migration Matrix. As expected, White/European ancestry is a strong positive predictor of national reflectance, while Black/African ancestry is a strong negative one.

All correlations are substantially positive. The lowest are those between the skin reflectance variable and the others. This is because skin reflectance does not discriminate well between European and Amerindian in relation to African ancestry. When we statistically control for Amerindian ancestry with a semi-partial correlation, the correlation is .73.

Table 7. *Validation correlations for European ancestry. Weighted below the diagonal. N's=25-33.*

	Genomic Euro%	CIA White%	Putterman Euro%	Skin reflectance
Genomic Euro%		0.89	0.89	0.73
CIA White	0.88		0.96	0.85
Putterman Euro	0.90	0.96		0.75
Skin reflectance	0.66	0.75	0.66	

Table 8 shows the analogous correlations for African ancestry. Again, the correlations are very strong. The skin reflectance correlations are strong because African ancestry is being contrasted with both European and Amerindian ancestry and because both of the latter are associated with relatively high reflectance levels.

Table 8. *Validation correlations for African ancestry. Weighted below the diagonal. N's=25-33.*

	Genomic Afri%	CIA Black%	Putterman Afri%	Skin reflectance
Genomic Afri%		0.96	0.96	-0.94
CIA Black%	0.95		0.93	-0.94
Putterman Afri%	0.95	0.92		-0.94
Skin reflectance	-0.89	-0.86	-0.91	

Finally, we turn to Amerindian ancestry which is shown in Table 9. As before, the ethnicity and genomic variables are very strongly correlated but, as expected for the reasons noted above, skin reflectance is not. The weighted semi-partial correlation between Amerindian genomic ancestry and skin reflectance controlling for European genomic ancestry (and thus relative to African ancestry) is .70. Figure 14 shows the admixture plot.

Table 9. *Validation correlations for Amerindian ancestry. Weighted below the diagonal. N's=25-33.*

	Genomic Amer%	CIA Amer%	Putterman Amer%	Skin reflectance
Genomic Amer%		0.87	0.9	0.48
CIA Amer%	0.88		0.94	0.49
Putterman Amer%	0.91	0.96		0.35
Skin reflectance	0.11	0.07	0.09	
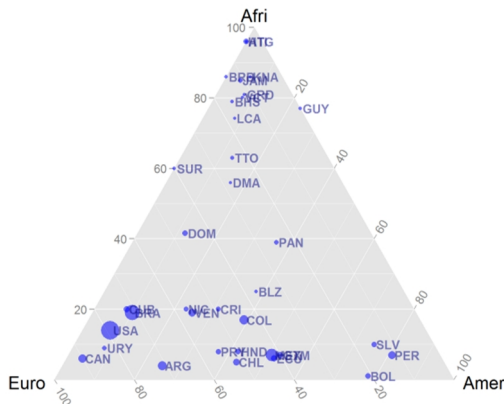
Figure 14. *Ternary plot for admixture in sovereign states.*

7.1.2. Cognitive ability

For cognitive ability scores, we used Gerhard Meisenberg's (2014/2015) achievement estimates (in preparation). These were based on international test scores, regional test scores and national GMAT/GRE scores. These scores came from tests given between 1997 and 2013. As to these, Meisenberg (personal communication, 2015) noted that:

[The strategy] was to form the averages of each TIMSS and PISA assessment first. PISA had to be adjusted for the changing standards in different assessments (published scores are based on performance in participating OECD

countries, but different OECD countries participated in different years). After adjusting TIMSS and PISA to a common metric (500/50 for countries participating in both TIMSS and PISA), the weighted average was formed. Then minor adjustments were made for % not in school. Then gaps were filled with results from several regional and older assessments (SACMEQ in Africa, SERCE in Latin America etc). Finally the last remaining gaps were filled with data from Graduate Management Admission Test, Graduate Record Exam and International Mathematics Olympiad.

These scores were transformed into achievement quotient scores relative to a UK mean of 99 following Lynn and Vanhanen's (2012) equalization of means and standard deviations method.

7.1.3. Socioeconomic outcomes
S scores were available for 142 countries from Kirkegaard (2014b), but for only 25 of the 35 sovereign American nations. These scores were based on 2012 and 2013 data. For each country there was also 2010 HDI data. As the country-level correlation between HDI2010 and the S factor scores was .96 (weighted and unweighted), we felt justified in using HDI scores as proxies when S scores were missing. We scaled the country S factor scores to the HDI2010 metric using the following formula:

S on HDI2010 metric = S score * sd(HDI2010 in all country sample) + mean(HDI2010 in American sample).

For example, the formula for Canada was:
S score Canada = 1.434 * 0.146 + 0.725 = 0.934

The HDI2010 score for Canada is 0.896, so the socioeconomic score for that country is increased somewhat by the use of the rescaled S factor score. For countries with no S factor scores (N=10), we filled in data with the countries' HDI2010 values. We refer to this variable simply as "S" in what follows.

7.2. Zero-order correlations and scatter plots
Table 10 shows the zero-order correlations between cognitive ability, S and HDI2010 scores, as well as the three ancestry variables. The results are consistent with those from the previous four analyses. Figures 15 and 16 show the scatter plots for cognitive ability and S scores.

Table 10. *Zero-order correlations for sovereign nations. Weighted correlations below the diagonal. N=35. CA, cognitive ability; S, socioeconomic (S) factor; HDI, Human Development Index.*

	CA	S	HDI	African%	Amerindian %	European %
CA		0.69	0.64	-0.60	0.06	0.74
S	0.87		0.92	-0.22	-0.21	0.48
HDI	0.89	0.96		-0.15	-0.27	0.44
African%	-0.48	-0.34	-0.36		-0.66	-0.72
Amerindian %	-0.35	-0.41	-0.40	-0.44		-0.05
European%	0.77	0.70	0.71	-0.46	-0.59	
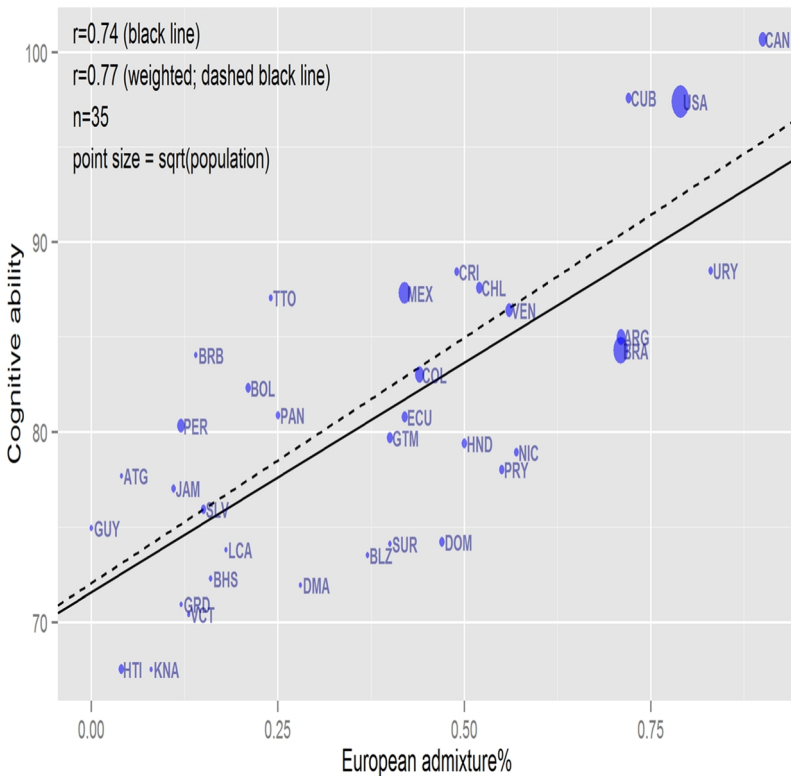
Figure 15. *Scatter plot of cognitive ability scores and European ancestry.*
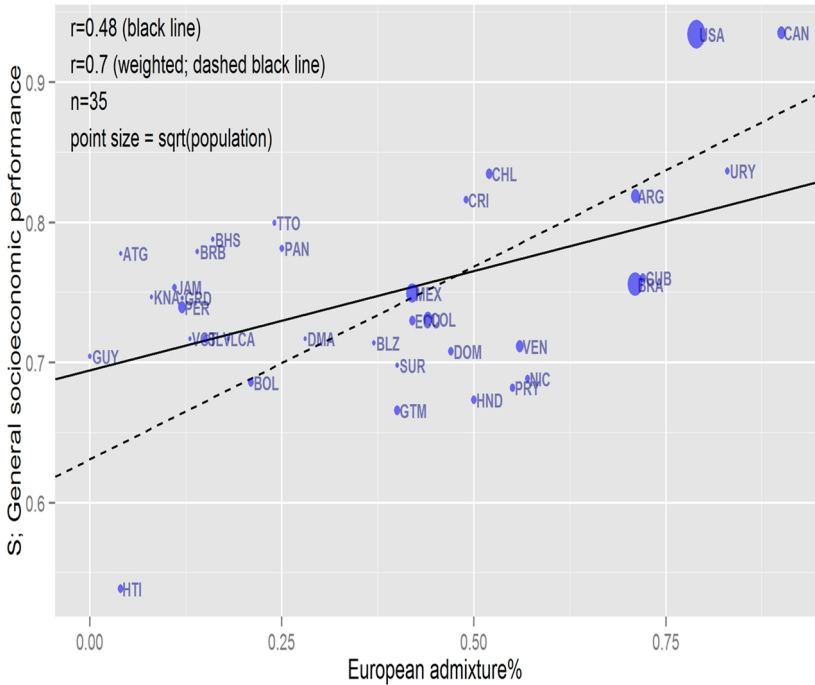
Figure 16. *Scatter plot of socioeconomic (S factor) score and European ancestry.*

Regarding cognitive ability, there are no major outliers – not even the smaller island states. Regarding S, we see a substantial difference between the results depending on whether or not we use weighted correlations. As noted prior, this is due to a number of smaller island states doing fairly well despite having very low levels of European ancestry. We will return to the question of how to explain this pattern in Section 17.

8. Sovereign nations and regional racial admixture together
We may wonder if the intranational associations more or less fall on the international regression line and if plotting all the data together greatly affects the overall association. If a racial model is correct, the result should hold when analyzed together. Statistically this is not necessary; it is possible to obtain a

negative correlation when combining several datasets each of which contains data with a positive correlation. This situation is visualized in Figure 17.
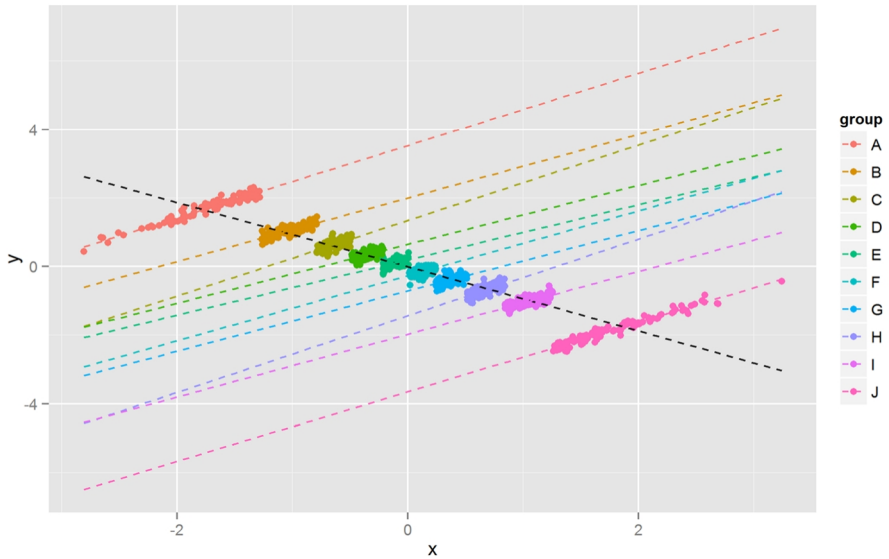
Figure 17. *Simpson's paradox for continuous data.*
From http://emilkirkegaard.dk/understanding_statistics/?app=Simpson_paradox

The general phenomenon is called *Simpson's paradox*. This situation may seem strange, but it has in fact happened in important cases in medicine and higher education (Kievit et al., 2013). When it happens, we have evidence that the relationship between x and y is either not causal or at least is not simple. With respect to the present analyses, Simpson's paradox would suggest that the ancestry-outcome relations do not scale up in a simple fashion.

8.1.1. Admixture estimates
The admixture estimates from the above analyses were used without modifications. Figure 18 shows the admixture plot.

8.1.2. Cognitive ability
The state-level ACHQ deviations, which were already scaled on the international metric, were added to the sovereign nation NACHQs, which were computed as discussed previously.
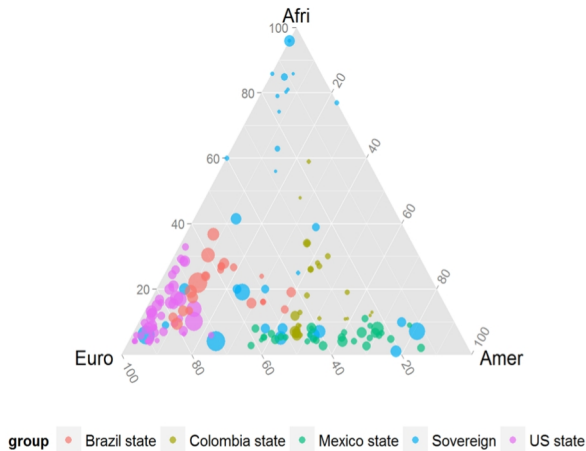
Figure 18. *Ternary plot for admixture in countries and states/districts.*

8.1.3. Socioeconomic outcomes

When extracting an S factor, the scores will be standardized in the dataset (i.e., with a mean of 0 and SD of 1). This however means that one cannot directly combine data when dealing with countries with different mean levels of the construct. To overcome this problem, we rescaled the state/district level S scores using the within country HDI score standard deviations and the countries' mean S scores (Kirkegaard, 2014b).

8.2. Zero-order correlations and scatter plots

Table 11 shows the zero-order correlations. Note that for these we have, as before, excluded capitals. Additionally, we excluded countries which had intranational units (Mexico, US, Brazil and Colombia), as otherwise we would be double-counting them.

The results are comparable to those which we found before. European% is strongly associated with better outcomes, while both Amerindian% and African% is negatively associated with them. Weighting had little effect on these results. Figures 19 and 20 show the scatter plots.

Table 11. *Zero-order correlations. Weighted correlations below the diagonal. N = 169-170. CA, cognitive ability; S, socioeconomic (S) factor; HDI, Human Development Index.*

	CA	S	HDI	African %	Amerindian %	European %
CA		0.89	0.76	-0.50	-0.43	0.82
S	0.91		0.84	-0.24	-0.63	0.79
HDI	0.85	0.90		-0.27	-0.46	0.66
African %	-0.40	-0.25	-0.28		-0.37	-0.47
Amerindian %	-0.51	-0.63	-0.49	-0.35		-0.65
European %	0.78	0.80	0.70	-0.30	-0.78	
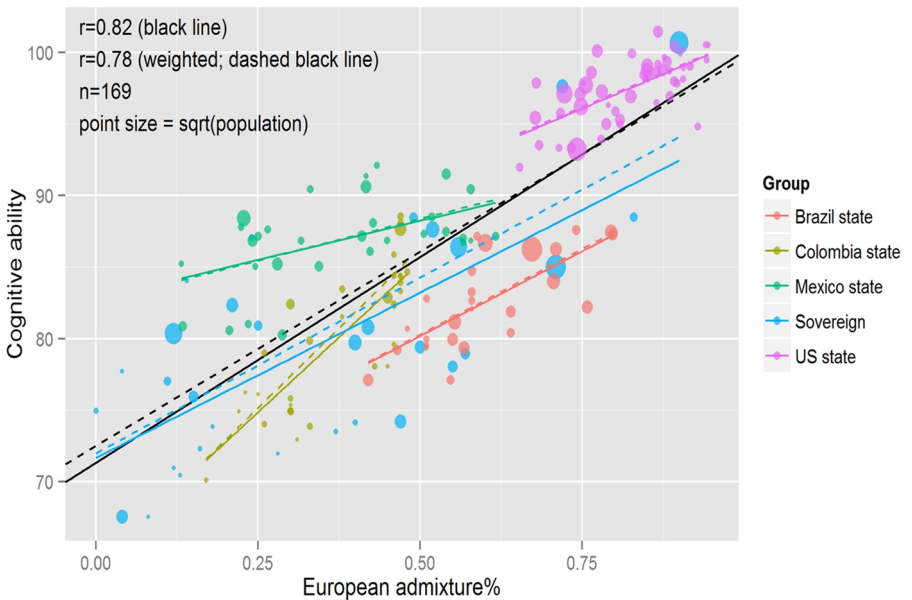
Figure 19. *Scatter plot of European ancestry and cognitive ability scores for countries and states/districts.*
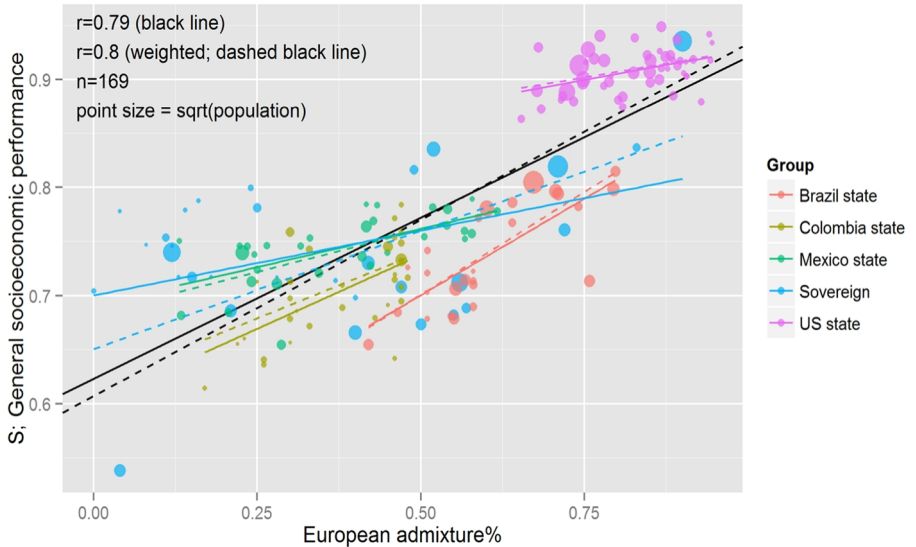
Figure 20. *Scatter plot for European ancestry and S factor scores for countries and states/districts.*

In general, we find that results hold when countries and states/districts are analyzed together. Moreover, the intranational regression lines are not very divergent from the international one.

9. Taking into account all ancestry: multiple regression

In the previous sections, we simply looked at the correlations between ancestries and outcomes. However, it is possible that combining two ancestries in multiple regression would improve the predictive power. In this section we present standardized betas for all three components. Since the three ancestry values add up to 1, it is not possible to insert all three at once into a regression model (perfect multicollinearity). As such, the betas for two at a time are presented. We have retained models with one predictor for comparison. We also report adjusted R as a measure of model fit, a metric akin to correlation that is calculated as the square root of adjusted R^2. We caution that standardized betas, especially when weighted in multiple regression models, are not as easy to interpret as correlations. We will see examples of this below. For these analyses, the federal districts are excluded.

9.1. Mexico

Tables 12 and 13 show the beta matrix, generated using the method presented in Kirkegaard (2015c), for the regression results.

Table 12. *Multiple regression results for cognitive ability in Mexico. Each row represents one model.*

African%	Amerindian%	European%	adj. R
0.42			0.38
	-0.61		0.57
		0.54	0.50
0.44	-0.62		0.71
0.53		0.64	0.71
	-3.51	-2.95	0.71

Table 13. *Multiple regression results for S factor scores in Mexico.*

African%	Amerindian%	European%	adj. R
0.24			0.16
	-0.75		0.70
		0.70	0.65
0.26	-0.76		0.74
0.38		0.77	0.74
	-2.50	-1.78	0.74

For cognitive ability, the results show that we can improve our prediction slightly by adding a second ancestry variable: from .57 (Amerindian) to .71. However, for the S factor scores, there seems to be little gain from using more than one predictor, as the gain is a mere .04. It is notable that African ancestry is positively associated with outcomes, meaning that the strong positive associations between European ancestry and outcomes are driven solely by the strong negative ones between Amerindian ancestry and outcomes. As noted in Section 3, not much can be concluded from these results as the African ancestry estimates were unreliable and as the range and variance in African ancestry was small.

The results in the last row of both tables seem strange: how can all predictors be negative, and why is European ancestry negative when it is positive in the other models? This is something that can happen when there is very little variation in the predictor not included in the model (in this case African ancestry); refer

back to Figure 2. Note that one can compare the relative value of the betas across the three 1-predictor models and within the three 2-predictor models. From this, one can note their relative order. With regards to positive associations between outcomes and ancestry, the order is consistently: European > African > Amerindian. Not much should be made out of the finding that African ancestry is associated with better outcomes than is Amerindian because of the unreliability of the African ancestry estimates.

9.2. The US

Now we repeat the same procedure as before for the US. Tables 14 and 15 show the beta matrices.

Table 14. *Multiple regression results for cognitive ability in the US.*

African%	Amerindian%	European%	adj. R
-0.42			0.38
	-0.37		0.37
		0.65	0.63
-0.57	-0.50		0.64
0.32		0.91	0.64
	-0.18	0.58	0.64

Table 15. Multiple regression results for S factor scores in the US.

African%	Amerindian%	European%	adj. R
-0.38			0.34
	-0.06		
		0.41	0.37
-0.43	-0.16		0.35
-0.15		0.29	0.35
	0.08	0.44	0.35

The apparent missing value in the second row of Table 15 is because the adjusted R^2 is negative and one cannot take a square root of a negative number (without using imaginary numbers). Both with regards to cognitive ability and S scores, there seems to be no gain from using more than just European ancestry

as a predictor. With regards to positive associations between outcomes and ancestry, the order is consistently: European > Amerindian > African.

9.3. Brazil

We repeat the same procedure for Brazilian states. Tables 16 and 17 show the beta matrices. As above, the results show that using multiple ancestry variables provides no incremental predictive power. Using European ancestry alone is sufficient. As in the Mexican analysis, the order in terms of positive associations is consistently European > African > Amerindian.

Table 16. *Multiple regression results for cognitive ability in Brazil.*

African%	Amerindian%	European%	adj. R
-0.16			
	-0.70		0.63
		0.74	0.72
-0.37	-0.83		0.72
0.17		0.82	0.72
	-0.27	0.56	0.72

Table 17. Multiple regression results for S factor scores in Brazil.

African%	Amerindian%	European%	adj. R
-0.19			
	-0.76		0.65
		0.82	0.75
-0.42	-0.90		0.76
0.17		0.90	0.76
	-0.27	0.63	0.76

9.4. Colombia

Again, we repeat the same procedure for Colombian states. Tables 18 and 19 show the beta matrices. As in the other analyses, using two ancestry predictors

does not seem to give additional predictive power. It is notable that the order is not consistent: European > Amerindian > African is the norm, but one model has African > Amerindian, though only by .08 (Model 4, S regression).

Table 18. *Multiple regression results for cognitive ability in Colombia.*

African%	Amerindian%	European%	adj. R
-0.74			0.69
	0.36		0.19
		0.88	0.80
-1.28	-0.93		0.80
0.12		0.98	0.80
	-0.10	0.91	0.80

Table 19. *Multiple regression results for S factor scores in Colombia.*

African%	Amerindian%	European%	adj. R
-0.35			0.30
	-0.07		
		0.55	0.51
-0.93	-1.01		0.56
0.64		1.14	0.57
	-0.41	0.67	0.56

9.5. Sovereign states

We repeat the same procedure for sovereign states. Tables 20 and 21 show the beta matrices. Again, we see that using European ancestry alone is as good as using two predictors. Also, the order is consistently European > Amerindian > African.

Table 20. *Multiple regression results for cognitive ability in Sovereign nations.*

African%	Amerindian%	European%	adj. R
-0.73			0.45
	-0.34		0.31
		0.79	0.76
-1.19	-0.67		0.77
-0.23		0.72	0.77
	0.16	0.90	0.77

Table 21. *Multiple regression results for S factor scores in sovereign nations.*

African%	Amerindian%	European%	adj. R
-0.67			0.30
	-0.52		0.37
		0.94	0.69
-1.27	-0.87		0.68
-0.03		0.93	0.68
	0.02	0.95	0.68

9.6. Sovereign nations and regions

Tables 22 and 23 show the beta matrices for the combined samples of states/districts and sovereign countries. This final analysis shows no surprises. Using European ancestry alone is sufficient for predicting the outcomes. Here, though, we see that the order, in terms of positive associations, is not consistent. In Table 22, we see that it is European > Amerindian > African, but in Table 23, it is either European > African > Amerindian or European > Amerindian > African. However, the differences between the actual betas are small.

Table 22. *Multiple regression results for cognitive ability for countries and states/districts.*

African%	Amerindian%	European%	adj. R
-0.48			0.39
	-0.47		0.51
		0.77	0.78
-0.81	-0.68		0.80
-0.22		0.72	0.80
	0.25	0.98	0.80

Table 23. *Multiple regression results for S factor scores for countries and states/districts.*

African%	Amerindian%	European%	adj. R
-0.33			0.24
	-0.63		0.62
		0.87	0.80
-0.72	-0.82		0.80
-0.01		0.86	0.80
	0.01	0.88	0.80

10. Adding non-admixture predictors: theory-driven approach

We now come to the issue of modeling outcomes using a combination of admixture variables and non-admixture ones. There are a very large number of ways to do this. Perhaps the most commonly used approach is the theory-driven one: researchers select variables for the models based on prior beliefs they have about causal relationships. They may either add them all into the model at once, or in a stepwise fashion showing that some particular variable retains predictive power while controlling for other variables. There are some problems with this approach. First, researchers commonly select predictors that are causally related to each other and try to have the model treat them as independent variables. Second, researchers only try some possible models and may also not report all

the models they tried. This makes it possible for them to bias the results, perhaps inadvertently (Kirkegaard, 2015c; Zigerell, 2015).

Due to these problems, we include another approach: automatic modeling. This approach is not without its own problems. For one, there are a number of methods to pick from: forward selection, backward, best subset, Bayes Factor selection (Etz, 2015), ridge/lasso regression and more. For another, there is no consensus as to which model fit criteria one should use: AIC, BIC, adjusted R^2 and so on. Applying all of these approaches to every modeling question would result in hundreds of tables which could not be presented succinctly. Our solution to the aforementioned problems is to use both general approaches. We will fit some theory driven models and report some automatic modeling results, leaving the curious reader to explore the data for himself. In this section, we report some theory-driven results; in the next, we will report automatic modeling results.

10.1. What sort of predictors are we looking for?

A large set of potential predictors for cognitive and socioeconomic outcomes exist. Due to the nature of the S factor, a great number of these would actually be part of the S factor and so would have a part-whole relationship with one of our dependent variables. Given this, we will focus on what might be called geographic variables: those related to geospatially specific climatic and ecological factors that are under minimal human control. We will apply these method driven analyses only to sovereign nations. Specifically, we will look at the independent effects of cold weather ("cold demand") and parasite load on outcomes. Previous research has centered on these geographical variables in predicting cognitive ability scores and has shown that these variables are robustly associated with national-level outcomes (Kanazawa, 2008; Lynn, 2006; Templer & Arikawa, 2006). We will also include a measure of institutional effects ("Anglo") in the form of historic British versus Iberian colonial rule (where British rule is operationalized by English as an official language and Iberian rule is indexed by Spanish or Portuguese as an official language).

Proponents of genetic models have interpreted such associations from an evolutionary perspective. The association of cognitive ability with both latitude and temperature, for example, has been interpreted in line with cold winters theory (e.g., Hart, 2007; Kanazawa, 2012; Lynn, 2006; Templer & Rushton, 2011). According to this theory, as humans spread across the globe, some populations ended up in cold climate regions in which survival was more difficult than in warm climates. This led to increased selection for cognitive ability, which accounts for some of the correlation between national ability, climate and latitude. Similar models have been proposed to explain the association between parasite

load and outcomes (e.g., Woodley et al., 2014). In this case, increased parasite load is said to be associated with an investment in immune defenses at the expense of cognitive development. Over evolutionary time, this situation is said to have depressed selection for cognitive ability in high parasite load regions. In line with this model, Fedderke et al. (2014) found that ACP1 alleles associated with immunological function predicted national outcomes independent of contemporaneous disease/parasite burden. Regarding institutions, a genetic explanation would point to intra-European genetic differences. One recent paper showed that regional outcomes across the US are associated with European regional ancestry (Fulford, Petkov & Schiantarelli, 2015). The same logic could apply across countries.

It is not clear to what extent geographic variables index evolutionary effects and to what extent they index the effects of contemporaneous environmental factors. It might be thought that our analysis could disentangle causality, as two of our geographic lineages (Africans and Europeans) hail from outside of the Americas and, as such, could not be evolutionarily adapted to American environments. Unfortunately, this is only partially the case, as our ancestry variables are correlated with our geographic ones. This is the result of various historical contingencies. For example, owing to their genetic adaptation to parasite-ridden environments, West Africans were disproportionately imported into American regions with high parasite and disease loads. Thus African% correlates with parasite load, which in turn correlates with latitude and warm weather. To some extent this tangled causality can be demonstrated. If we assume that the association between European ancestry and skin reflectance owes predominately to genes, then the degree to which geographic variables mediate the ancestry-skin reflectance association indicates the degree to which they covary with genetic effects. Regression results are shown in Table 24. As can be seen in Model 2, parasite load and cold demand explain some of the ancestry-reflectance association. Our measure of institutions also explains some of the association.

To note, the cold demand variable comes from Van de Vliert (2013), who argued that climate is a key determinant of outcomes. Canada was a major outlier, so the Canadian value was reduced to 3 SD above the pan-American average, in line with the recommendation of Field (2013). The parasite load values come from the World Health Organizations's (2004) *The Global Burden of Disease* (Mathers, Fat & Boerma, 2008). To create the values, we used the average of the parasite disease rates: numbers 8 (malaria) to 14 (intestinal nematode infections) in Table 6 of "Age-standardized DALYs per 100,000 by cause, and member state" (DALY = disability-adjusted life years). The

Anglophone variable was dichotomously coded 1 for English, as an official language, and 0 for otherwise. For all analyses in this section, N=35.

Table 24. *Regression results for skin reflectance. Standardized betas presented.*

Model #	Euro%	Parasites	Cold demand	Anglo	adj. R²
1	0.475				0.410
2		-0.212			0.061
3			0.377		0.353
4				0.060	-0.031
5	0.465	-0.023			0.391
6	0.330		0.219		0.481
7	0.530			-0.344	0.434
8		0.116	0.443		0.348
9		-0.335		-0.426	0.075
10			0.540	-0.731	0.485
11	0.341	0.146	0.296		0.491
12	0.490	-0.178		-0.572	0.453
13	0.344		0.382	-0.762	0.636
14		-0.049	0.523	-0.776	0.470
15	0.342	-0.020	0.376	-0.780	0.623

10.2. Parasites, cold weather and Anglo institutions

In this analysis (Table 25), we look at the independent effect of European genomic ancestry on cognitive ability scores. Model 1 includes just European ancestry, while Model 15 includes all of the predictors. It can be seen that European ancestry remains a robust predictor (Model 15). Parasite load is the most significant other predictor. Table 26 shows the same models predicting S factor scores. Again, European origin remains a robust predictor.

Table 25. *Regression results for cognitive ability scores. Standardized betas are presented.*

Model #	Euro%	Parasites	Cold demand	Anglo	adj. R²
1	0.794				0.581
2		-0.759			0.554
3			0.676		0.576
4				1.246	0.285
5	0.574	-0.532			0.815
6	0.509		0.429		0.738
7	0.680			0.756	0.675
8		-0.448	0.426		0.687
9		-0.686		0.251	0.548
10			0.586	0.413	0.588
11	0.483	-0.415	0.210		0.839
12	0.570	-0.502		0.107	0.811
13	0.505		0.345	0.391	0.753
14		-0.451	0.427	-0.015	0.677
15	0.483	-0.415	0.210	-0.002	0.834

Table 26. *Regression results for S scores. Standardized betas are presented.*

Model #	Euro%	Parasites	Cold demand	Anglo	adj. R²
1	0.939				0.477
2		-1.035			0.614
3			0.885		0.586
4				2.115	0.509
5	0.611	-0.793			0.787
6	0.518		0.633		0.681
7	0.695			1.614	0.749
8		-0.655	0.519		0.731
9		-0.726		1.063	0.683
10			0.615	1.241	0.706
11	0.479	-0.622	0.304		0.817
12	0.577	-0.540		0.917	0.842
13	0.507		0.373	1.219	0.803
14		-0.481	0.445	0.785	0.765
15	0.483	-0.444	0.228	0.799	0.857

10.3. Parasites, HIV and cognitive ability

Parasite load is a particularly problematic "geographic environmental" factor because it significantly correlates with STD and HIV rates (at 0.47 for our 35 nations). Yet the spread of HIV throughout the Americas, in the 1970s and 1980s, was subsequent to the origin of cognitive ability differences. Thus we can infer that, if anything, HIV rate differences are a consequence of cognitive ability differences. The correlation between HIV rates and parasite load suggests that this may also be the case for some of the parasite load differences. To put the point in simpler terms, countries with smarter populations might just do a better job of controlling parasites. We can attempt to control for this reverse causation if we allow for some assumptions. If we grant that cognitive ability protects against HIV and parasite load to the same extent, we can regress out the effect of HIV from parasite load to gain an estimate of parasite load without the causal influence of cognitive ability on it. Finally, we can enter this corrected parasite load measure into our regression model above. Table 27 shows the results.

Table 27. *Parasite regression models for cognitive ability. Parasites cor is parasite load, corrected for reverse effects of cognitive ability on parasite load.*

Model #	Euro%	Parasites	Parasites cor	adj. R^2
1	0.794			0.581
2		-0.759		0.554
3			-0.530	0.211
4	0.574	-0.532		0.815
5	0.745		-0.435	0.734
6		-1.317	0.702	0.653
7	0.520	-0.720	0.210	0.817

Alone, European ancestry and the original parasite load measure are about equally good predictors (Models 1-2). The corrected parasite measure is still a good predictor, but somewhat weaker than the original version (Model 2 vs. 3). The predictive ability of European ancestry and the original parasite measure overlap to some extent because their combined adj. R^2 is less than the sum of their individual adj. R^2's (Models 1 + 2 vs. 4). Interestingly, there is little overlap between European ancestry and the corrected parasite measure, as their adj. R^2 is nearly equal to the sum of the parts (.734 vs. .792). The results are consistent with a model in which both European ancestry has an effect on parasite load by

way of cognitive ability and in which parasite load has a direct effect on cognitive ability. Of course, proponents of a strict parasite model would argue that parasite prevalence is antecedent to differences in cognitive ability, which are, in turn, antecedent to differences in HIV rates. We cannot rule out this possibility; we can merely show that causality is tangled.

10.4. Genetic distance controlling for European ancestry

Recent research has shown that measures of genetic distance from Africa correlate with cognitive and socioeconomic outcomes at the global level (León & Burga-León, 2015). We might wonder if such an index better explains outcomes than our racial ancestry categories. Table 28 shows the results for cognitive ability, using semi-partial correlations to control for the effect of European ancestry on genetic distance. For comparison, we also did the same for cold demand and parasite load.

Table 28. *Weighted zero-order correlations and semi-partial correlations (European ancestry controlled) of non-ancestry variables with cognitive ability. Genetic distance is the extent of genetic differences from South Africans. N=35 countries. Correlation of European ancestry with cognitive ability is .77.*

Secondary variable	Orig. cor	Semi-partial cor
Cold	0.767	0.517
Parasite	-0.753	-0.692
Genetic distance	0.322	0.113

We see that genetic distance from South Africans is a much worse predictor than European ancestry, and that once European ancestry is taken into account, the correlation between cognitive ability scores and genetic distance is strongly reduced. In contrast, our geographic environmental variables do show sizable correlations after European ancestry has been taken into account. This could mean that they truly have independent effects. Table 29 shows the same as the above, but for S. The results for S mirror those for cognitive ability.

Table 29. *Weighted zero-order correlations and semi-partial correlations (European ancestry controlled) of non-ancestry variables with the socioeconomic factor (S). Genetic distance is the extent of genetic differences from South Africans. N=35. Correlation of European ancestry with S is .70.*

Secondary variable	Orig. cor	Semi-partial cor
Cold	0.774	0.526
Parasite	-0.791	-0.711
Genetic distance	0.240	0.017

10.5. Path diagram

In Figure 21 below, we depict a weighted path analysis for the sovereign national analysis. This is our proposed model. Since we lacked cross-temporal data, we were unable to test causal pathways. Standardized path coefficients are shown. For parasite load, we use our corrected value from Section 10.3. In the model, European Ancestry has a strong direct effect on cognitive ability ($\beta EU{\rightarrow}CA$ = .55) and a smaller effect on S ($\beta EU{\rightarrow}S$ = .22). Cognitive ability has a modest effect on S ($\beta CA{\rightarrow}S$ = .33) and strong effect on HIV ($\beta CA{\rightarrow}HIV$ = -.66). Parasite load (corrected) has direct effects on cognitive ability ($\beta ParCor{\rightarrow}CA$ = -.28) and S ($\beta ParCor{\rightarrow}S$ = -.15). Likewise, cold stress had direct effects on cognitive ability ($\beta ParCor{\rightarrow}CA$ = .34) and S ($\beta ParCor{\rightarrow}S$ = .15). Tourist expenditure had a negligible effect on S ($\beta Tourist{\rightarrow}S$ = .05). Anglo had no effect on cognitive ability ($\beta Anglo{\rightarrow}CA$ = -.02) but a modest one on S ($\beta Anglo{\rightarrow}S$ = .31). To keep the figure readable, we excluded residuals. More detailed results are shown in Appendix B. Regarding the relative effects of the geographic and ancestry variables, it is worth keeping in mind that the former are measured much more precisely than the latter. In this situation, regression and path models will assign independent effects to the more precisely measured variables even if they have no causal effects, because these geographic variables capture some of the variance that is not captured by the ancestry variable owing to measurement error.
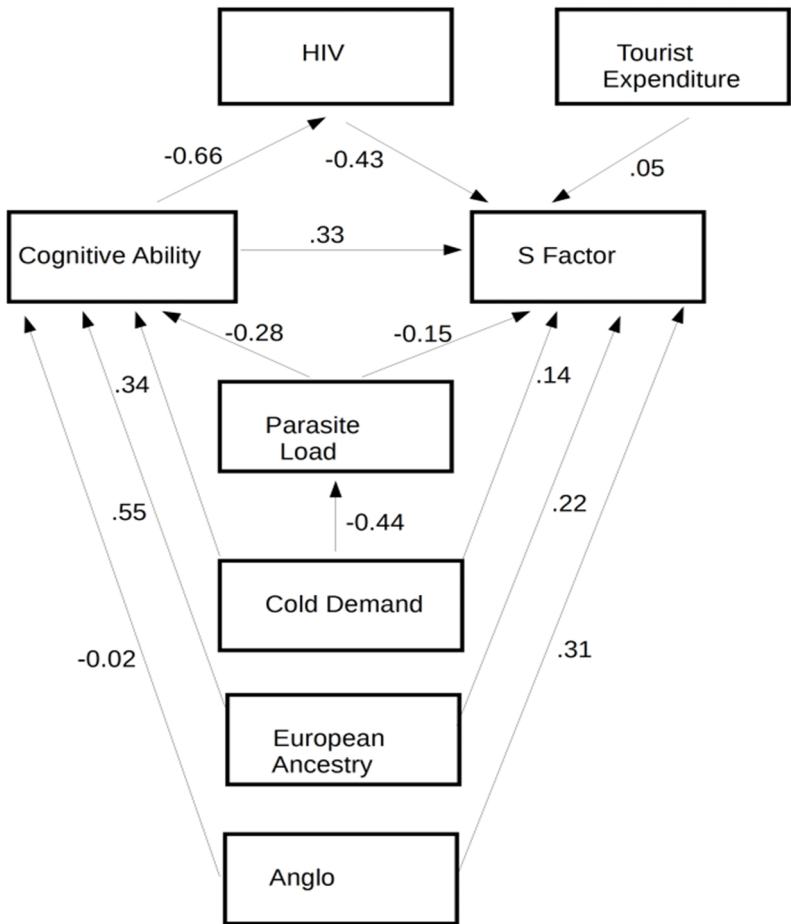
Figure 21. *Path diagram for European Ancestry. N=35. Fit measures: CFI .93, GFI .935, SRMR .077, indicating acceptable fit.*

11. Adding non-admixture predictors: automatic approach

We now turn to automatic selection methods. They are called s*election* methods because they select which variables to include in the model. Since many readers are probably unfamiliar with these methods, we will describe them first (James et al., 2013). The simplest idea is *best subset selection*. Here we simply fit every possible model and then assess them by some model fitting criteria. R^2 adjusted is a common choice, but alternatives include AIC, BIC and many others. The reason for the *adjusted* is that R^2 increases monotonically when adding variables, even if they have no real predictive power aside from that which happens by chance from sampling error (overfitting). The adjusted version penalizes models by the number of variables they include to avoid overfitting. AIC and BIC also include a penalty for the number of predictors (James et al., 2013). We use R^2 adj. as our primary model fit measure because it is the one readers are most familiar with and because it has a natural interpretation (percent variance accounted for).

Results were very similar using the two alternatives. One of the problems with best subset selection is that it is computationally demanding. This is because the number of possible models is 2^p, where p is the number of variables. So, for example, if we have 10 predictor variables, we have to fit 1024 models. Another problem is that it tends to overfit the models, capitalizing on random patterns in the dataset. Lasso regression is similar to best subset selection in that it involves all the predictors initially. It differs in that it assigns a penalty for the sizes of the betas, which results in the betas estimated being generally smaller. Due to the way the penalizing works, many predictors are shrunken to exactly zero, which means that they have been excluded from the model entirely (James et al., 2013). The shrinkage parameter is found through cross-validation (i.e., through splitting the dataset into parts and using one part to fit the model and using the other part to test it). Because the cross-validation procedure is based on resampling methods, the results are not deterministic and will vary somewhat each time the algorithm is run. To stabilize the results, we ran the lasso regression 500 times and calculated summary statistics for the results. For these analyses, the cognitive ability and S factor variables were the same as those used earlier.

11.1. Mexico
11.1.1. Cognitive ability

A recent analysis (Cabeza de Baca & Figueredo, 2014) found that cold weather (estimated based on latitude, altitude and temperate zone) predicted regional cognitive ability in Mexico. We obtained the data from this study. We used best subset selection by testing all possible models and selecting among

them based on the R^2 adj. R^2 fit measurement. It is easy to run all the regressions using a function developed by one of us (Kirkegaard, 2015c). Standardized betas and adjusted R^2s are shown in Table 30 for all 31 models (5 predictors, 2^5=32, and then we skip the null model).

Table 30. *Beta coefficients for models predicting cognitive ability scores of Mexican states.*

Model #	Euro%	Temperature	Latitude	Temperate	Altitude	adj. R^2
1	0.544					0.247
2		-0.484				0.172
3			0.476			0.190
4				-0.018		-0.034
5					0.134	-0.018
6	*0.497*	*-0.425*				*0.383*
7	0.519		0.028			0.220
8	0.629			0.195		0.262
9	0.634				0.318	0.310
10		-0.416	0.416			0.316
11		-0.731		-0.369		0.260
12		-0.909			-0.542	0.261
13			0.538	0.156		0.189
14			0.563		0.305	0.244
15				-0.136	0.227	-0.039
16	0.558	-0.429	-0.068			0.362
17	0.438	-0.508		-0.113		0.369
18	0.446	-0.539			-0.137	0.366
19	0.586		0.048	0.196		0.235
20	0.558		0.086		0.322	0.286
21	0.648			0.053	0.285	0.286
22		-0.549	0.326	-0.176		0.311
23		-0.588	0.333		-0.202	0.301
24		-0.998		-0.282	-0.414	0.298
25			0.565	0.009	0.300	0.216
26	0.524	-0.521	-0.101	-0.124		0.347
27	0.550	-0.582	-0.135		-0.180	0.345
28	0.385	-0.626		-0.115	-0.140	0.350
29	0.572		0.086	0.053	0.290	0.261
30		-0.746	0.230	-0.186	-0.223	0.297
31	0.513	-0.696	-0.177	-0.133	-0.197	0.331

The best model according to adj. R^2 is Model 6, marked in italics above. This is the model with just two predictors: European% and temperature. Generally, when presenting the results, we will not present the entire beta matrix, as it is too lengthy. We present it above for illustrative purposes. It is worth noting that the top 8 models (by R^2 adjusted) include European% as a predictor (Models 6, 17, 18, 16, 28, 26, 27 and 31).

For lasso regression, we included all of the predictors and used cross validation, as recommended by James et al. (2013) to select the most appropriate shrinkage parameter value. Table 31 shows the mean beta for each predictor, as well as how often lasso regression thought that it was identical to 0 (not a useful predictor at all).

Table 31. *Lasso regression results for cognitive ability scores and Mexican states. 500 runs.*

Statistic	Euro%	Temperature	Latitude	Temperate	Altitude
mean	0.199	-0.118	0	0	0
median	0.218	-0.135	0	0	0
sd	0.048	0.040	0	0	0
fraction zero	0.028	0.030	1	1	1

We see that of the geographic environmental predictors, only temperature was non-redundant. European% was about twice as important a predictor as was temperature. Both predictors failed to be identified as non-redundant in about 3% of the runs.

11.1.2. S factor scores

As before, we attempt to predict general socioeconomic performance using our set of predictors. Table 32 shows the top 5 models.

Table 32. *Top 5 models from best subset selection for predicting Mexican socioeconomic (S factor) scores.*

Model #	Euro%	Temperature	Latitude	Temperate	Altitude	adj. R^2
18	0.534	-0.436			-0.434	0.442
28	0.469	-0.528		-0.122	-0.437	0.430
1	0.705					0.428
27	0.495	-0.420	0.050		-0.418	0.421
7	0.507		0.219			0.418

We see that all 5 have European% as a strong positive predictor. In fact, all top 14 models do. The inclusion of the other predictors was inconsistent across the top 5 models.

Results for lasso regression predicting S factor scores are shown in Table 33. Lasso regression wants to only keep European% and to do so only in about 90% of the runs.

Table 33. *Lasso regression results for prediction of socioeconomic (S factor) scores of Mexican states. 500 runs.*

Statistic	Euro%	Temperature	Latitude	Temperate	Altitude
mean	0.123	0	0	0	0
median	0.120	0	0	0	0
sd	0.058	0	0	0	0
fraction zero	0.108	1	1	1	1

11.2. The US
11.2.1. Data sources

We collected a dataset of climatic and parasite variables from, respectively, the website Currentresults.com and Thornhill & Fincher (2014, p. 164).

11.2.2. Cognitive ability

Results for best subset selection are shown in Table 34. European% has a negative beta in one of the models and is absent from the others, which is odd. A finding of this sort suggests multicollinearity or model misspecification. Lasso regression results are shown in Table 35.

Table 34. *Top 5 models from best subset selection for predicting US cognitive ability scores. Hum mor. = morning humidity, Hum. after. = afternoon humidity, Para. = parasites.*

Temp	Rain	Hum. mor.	Hum. after.	Sun %	Sun hours	Clear days	Para.	Euro %	adj. R²	Model #
-0.302	0.320	0.239	-0.450		-0.395		-0.745		0.634	387
-0.328	0.251	0.299	-0.471	0.685	-1.067		-0.743		0.634	467
-0.248	0.375		-0.347		-0.448		-0.710		0.627	276
-0.367	0.260	0.329	-0.507	0.781	-1.183		-0.841	-0.119	0.627	504
-0.300	0.220	0.283	-0.465	0.737	-1.042	-0.109	-0.728		0.626	502

Table 35. *Lasso regression results for models predicting cognitive ability scores of states in the US. 500 runs.*

Statistic	Temp	Rain	Hum. mor.	Hum. after	Sun %	Sun hours	Clear days	Para.	Euro %
mean	-0.047	0	0	0	0	0	-0.028	-0.006	0.248
median	-0.055	0	0	0	0	0	-0.016	0	0.257
sd	0.025	0	0	0	0	0	0.034	0.019	0.043
fraction zero	0.110	1	1	1	1	1	0.426	0.888	0

The lasso results contrast strongly with those from best subset selection. Only two environmental predictors are found to be non-redundant; for one of them, it is found so in only 57% of the runs. Parasite load, the strongest predictor in best subset selection, was considered redundant in 89% of the runs, while European% was redundant in 0 out of 500. The nearly opposite results, with regards to parasite load and European%, suggest that there is something going on with these two variables and that further analysis is needed.

11.2.3. The sun factor

To see if we could identify the cause of the problem, we inspected the predictor intercorrelations. These revealed that some variables had very strong correlations:

Sun% and Sun hours r=.99.
Clear.days and the Sun variables r=.93 and .92.
Euro% and Para r=-.87.

The first three arguably measure the same construct: the amount of time the sun is shining, whether this is measured in days, hours, or days without precipitation. Thus, a new variable was created by factor analyzing the sun variables (all loadings >.92). This approach is somewhat akin to principal component regression (James et al., 2013, p. 230). We reran the best subset selection analysis for cognitive ability scores. Table 36 shows the results.

Table 36. *Top 5 models from best subset selection for predicting US cognitive ability scores. Sun factor introduced.*

Temp.	Rain	Hum. mor.	Hum .after	Sun	Para.	Euro %	adj.R²	Model #
-0.307	0.339	0.226	-0.430	-0.373	-0.739		0.630	120
-0.247	0.388		-0.339	-0.437	-0.708		0.625	105
-0.321	0.347	0.234	-0.442	-0.380	-0.776	-0.045	0.621	127
-0.246	0.387		-0.339	-0.436	-0.704	0.005	0.616	124
	0.269		-0.419	-0.648	-0.796		0.615	90

The results are substantially the same with regards to parasite load and European%. Table 37 shows the lasso results. The lasso results are also substantially the same as before. Both the new sun factor and parasite load are found to be redundant in nearly all runs (89% and 96%), while European% is found to be non-redundant in almost all runs (499 of 500). This matter requires further analysis.

Table 37. *Lasso regression results for cognitive ability scores and the US. 500 runs. Sun factor introduced.*

Statistic	Temp.	Rain	Hum. mor.	Hum. after.	Sun	Para.	Euro %
mean	-0.039	0	0	0	-0.004	-0.002	0.224
median	-0.040	0	0	0	0	0	0.234
sd	0.035	0	0	0	0.018	0.017	0.053
fraction zero	0.246	1	1	1	0.884	0.964	0.002

11.2.4. S factor

For the S factor analyses, we used the same sun factor as mentioned before. Results for best subset selection are shown in Table 38. The results for European% are stranger yet. Surely, no plausible model of state differences in socioeconomic well-being posits European ancestry as a strong *negative* determinant. Lasso regression results are shown in Table 39.

Table 38. *Top 5 models from best subset selection for predicting socioeconomic (S factor) scores for the states of the US.*

Temp	Rain	Hum. mor.	Hum. after.	Sun	Para.	Euro %	adj. R²	Model #
-0.647	0.450	-0.251	0.284		-1.032	-0.739	0.662	122
-0.708	0.481	-0.231	0.330	0.107	-1.008	-0.724	0.656	127
-0.696	0.386		0.140		-1.128	-0.804	0.653	107
-0.782	0.441		0.228	0.161	-1.079	-0.773	0.651	124
-0.751	0.488				-1.173	-0.840	0.647	73

Table 39. *Lasso regression results for socioeconomic (S factor) scores among the states of the US. 500 runs. Sun factor introduced.*

Statistic	Temp.	Rain	Hum. mor.	Hum. after.	Sun	Para.	Euro %
mean	-0.434	0.136	-0.061	0.215	0	-0.612	-0.268
median	-0.448	0.148	-0.066	0.222	0	-0.639	-0.293
sd	0.056	0.064	0.034	0.027	0	0.110	0.112
fraction zero	0	0.104	0.108	0	1	0	0.102

In contrast to the analysis for cognitive ability, lasso regression did not show that parasite load was a redundant predictor. In fact, the only predictor found to be consistently redundant was the sun factor. Strangely, European% still had a negative beta. The unexpected results, with regards to European ancestry, in this section are the reason why we undertook a second study of the S factor across the US. This, however, did nothing to change the results. Since the reliability of the S factor across datasets is so high (r=.961), the strange results are unlikely to be due to measurement error with respect to the S factor. More likely, the results have to do with the strong relationship between European% and parasite load (r=-.87). This matter will be discussed further in a later part of this paper.

11.3. Sovereign nations

We repeat the sovereign national analyses from Section 10 using automatic modeling.

11.3.1. Data sources

The variables were explained in Section 10.

11.3.2. Cognitive ability

Table 40 shows the best subset results for cognitive ability scores. Both European% and parasite load were found to be consistently important predictors. In fact, the top 1-124 of 511 models included both European% and parasite load. The adjusted R^2 values are very high, suggesting that the distribution of cognitive ability is well predicted by these variables. Lasso regression results are shown in Table 41.

Table 40. *Automatic modeling results for cognitive ability scores and sovereign nations. Top 5 models. Cold dem. = cold demand, hot dem. = hot demand, Infec. dis. = infectious diseases.*

Cold dem.	Hot dem.	Infec. dis.	Para.	Tourism	Anglo	Tax haven	Euro %	Gen. dist. SA	adj R²	Model #
0.167			-0.472			-0.578	0.455		0.845	173
0.189			-0.477	-0.249			0.464		0.844	168
0.160		-0.105	-0.416			-0.562	0.423		0.844	298
0.168			-0.492	-0.154			0.453		0.842	314
0.129		-0.165	-0.345		0.214		0.401		0.842	423

Table 41. *Lasso regression results for cognitive ability scores and sovereign nations. 500 runs.*

Statistic	Cold dem.	Hot dem.	Infec. Dis.	Para.	Tourism	Anglo	Tax haven	Euro %	Gen. dist.
mean	0.153	0	-0.090	-0.258	0	0	0	0.336	0
median	0.154	0	-0.090	-0.258	0	0	0	0.336	0
sd	0.008	0	0.004	0.016	0	0	0.003	0.018	0
fraction zero	0	1	0	0	1	1	0.996	0	1

The results for lasso regression are similar to those for best subset, at least with respect to European ancestry. A fairly large number of predictors were found to be non-redundant for most analyses. For tax haven status, the methods did produce substantially divergent results. Best subset selection thinks that it is a strong negative predictor, while lasso finds that it is redundant in 99.6% of the runs.

11.3.3. Socioeconomic (S factor) scores

Table 42 shows the best subset results for S. In contrast to the results for cognitive ability, genetic distance from South Africa seems to be a useful predictor. Likewise, Anglo seems to be associated with higher S, while strangely, tourism is not. Both European% and parasite load were useful predictors as before. Lasso regression results are shown in Table 43.

Table 42. *Automatic modeling results for socioeconomic (S factor) scores and sovereign nations. Top 5 models according to R² adj.*

Cold dem.	Hot dem.	Infec. Dis.	Para.	Tourism	Anglo	Tax haven	Euro %	Gen. dist. SA	adj. R²	Model #
0.173	0.228		-0.528		0.990		0.320	0.450	0.888	410
0.186	0.228		-0.508	0.147	0.930		0.329	0.465	0.885	483
0.179	0.228	-0.079	-0.472		1.012		0.299	0.407	0.884	474
	0.193		-0.558		1.203		0.372	0.555	0.884	354
0.182	0.226		-0.519		0.977	0.107	0.326	0.446	0.884	485

Table 43. *Lasso regression results for socioeconomic (S factor) scores and sovereign nations. 500 runs.*

Statistic	Cold dem.	Hot dem.	Infec. Dis.	Para.	Tourism	Anglo	Tax haven	Euro %	Gen. dist. SA
mean	0.190	0.028	-0.140	-0.317	0.003	0.788	0	0.348	0.037
median	0.187	0	-0.141	-0.304	0	0.788	0	0.350	0
sd	0.007	0.045	0.017	0.029	0.011	0.060	0	0.012	0.073
fraction zero	0	0.528	0	0	0.936	0	1	0	0.682

The lasso results show a stark contrast for the genetic distance predictor, which had a mean beta of only .04 and was found to be redundant in about 70% of runs. Tourism was not found to be a useful predictor for S using lasso

regression, while Anglo was. Both infectious disease and parasite load were useful predictors, which is not too surprising as these variables have a part whole relation with respect to the S factor. Cold demand had positive but somewhat weak predictive power. European% continued to be a useful predictor in all runs.

12. Units of unequal size: using weights

So far, we have used weighted correlations/regressions whenever possible. The rationale is that countries/states/departments with populations of, let's say, 500,000 should not be treated as equally important as ones with populations ten times the size (Hunt & Sternberg, 2006). However, there is a question of which weighting method should be utilized. Clearly, it should be based on either population or some transformation of population. We have used the square root of population so far in this paper, but one could also use a logarithmic transformation or no transformation at all. Since only the relative size matters, one can rescale the weights using each method to have a mean of 1. Figure 22 shows density curves of the relative weights using three methods for assigning weights in the dataset of sovereign nations. Similarly, Table 44 shows some descriptive statistics for the weights by method.
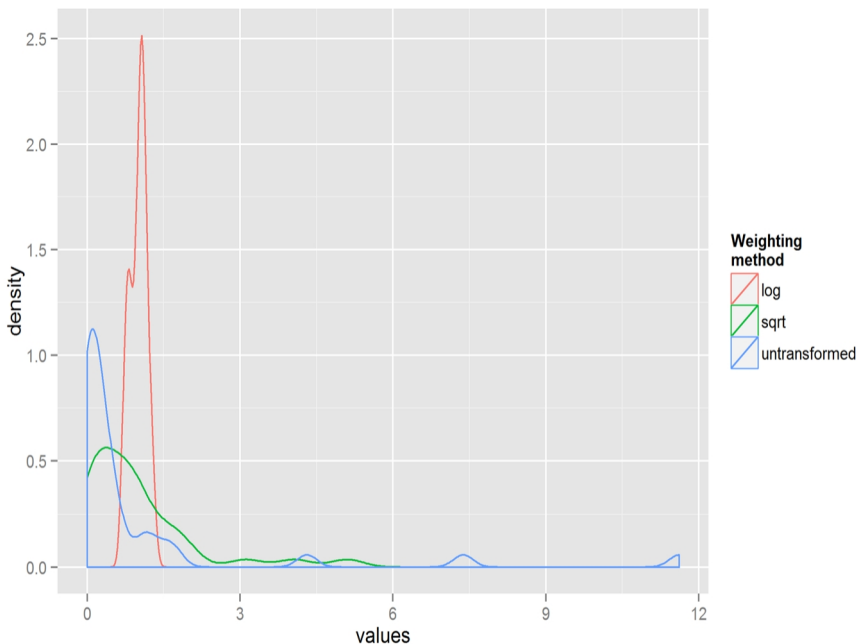

Figure 22. *Density plot of relative weights by method.*

315

Table 44. *Descriptive statistics of weighing methods by population size.*

method	mean	median	sd	min	max	range	skew	kurtosis	max/min
no weights	1	1	0	1	1	0			1
log	1	1.04	0.16	0.72	1.29	0.58	3.34	-1.03	1.80
sqrt	1	0.72	1.13	0.06	5.10	5.04	-0.20	3.99	78.67
untransformed	1	0.23	2.33	0.00	11.61	11.61	2.01	11.08	6189

In short, using log transformed values makes the weights relatively egalitarian: the ratio of largest to smallest value is only 1.80. Using untransformed weights makes the weights extremely unequal: a max-min ratio of over 6,000. The largest country is the United States, with a population of about 320 million, and the smallest is Saint Kitts and Nevis with a population of about 50,000. Square root weighting produces intermediate results with a max-min ratio of about 80. We decided to use this latter method as our primary one, since it strikes a reasonable balance between taking the effect of population size into account and not obscuring the effects of individual units, and because it is similar to the standard error often used in meta-analysis. Nonetheless, in Tables 45 and 46 we present the main results – the correlations with European ancestry – for cognitive ability and S respectively for each method of weighing.

Table 45. *Correlations between European ancestry and cognitive ability scores by different methods of weighing.*

Method	Mexico	USA	Brazil	Colombia	Sovereign	All units	Mean
(no weights)	0.510	0.668	0.736	0.824	0.742	0.819	0.716
log	0.514	0.663	0.736	0.822	0.750	0.813	0.716
sqrt	0.522	0.635	0.729	0.808	0.770	0.781	0.708
untransformed	0.491	0.610	0.701	0.795	0.736	0.759	0.682

Table 46. *Correlations between European ancestry and S by different methods of weighing.*

Method	Mexico	USA	Brazil	Colombia	Sovereign	All units	Mean
(no weights)	0.642	0.437	0.767	0.615	0.485	0.794	0.623
log	0.647	0.431	0.768	0.605	0.525	0.797	0.629
sqrt	0.669	0.393	0.763	0.531	0.702	0.803	0.643
untransformed	0.666	0.367	0.739	0.425	0.743	0.795	0.623

As can be seen, the exact method chosen does not matter much except for the S analysis in regards to sovereign nations. The reason for this was discussed earlier.

13. Race~Cognitive ability-S: does cognitive ability mediate the relationship between racial ancestry and S?

As mentioned in Section 2, according to the R~CA-S model, the primary route of statistical relationship between racial ancestry and socioeconomic outcomes runs through cognitive ability. Stated in simpler language, according to this model, there is nothing special about Europeans compared to Africans and Amerindians with regards to building better societies, except that the former are smarter on average. One can test this model with our dataset by checking if there is a relationship between S and ancestry, controlling for cognitive ability. According to the R~CA-S model, this relationship should be small or nonexistent. Is it?

Technically, there are various ways one could try to determine this. One could enter both cognitive ability and European ancestry into multiple regressions, with S as the dependent variable, but because the predictors correlate so highly and are causally related, doing so would not produce readily interpretable results. Another option is to use partial correlations. However, using partial correlations would regress out the effect of cognitive ability on S *and* on European ancestry. Doing the latter does not make sense. A third option is to use semi-partial correlations. Here, one regresses out the effect of the controlling variable only on one variable of a pair and then correlates the residuals of the one variable with the other variable. In our case, we want to regress out the effect of cognitive ability

on S and then see if European ancestry can predict the remaining variance in S. This is the method we will use. Table 47 shows the results.

Table 47. *Weighted (semi-partial) correlations of European ancestry (Euro%) and socioeconomic development (S), without and with controlling for cognitive ability scores (CA). The capital districts were excluded from all datasets. 95% confidence intervals in brackets. Confidence intervals generated by bootstrapping with 1000 replications.*

Dataset	*r* Euro%-S	*r* Euro%-S, CA controlled	Sample size
US	.39	-.09 [-.36; .21]	49
Mexico	.67	.42 [.13; .69]	31
Brazil	.76	.28 [.05; .51]	26
Colombia	.53	.01 [-.28; .31]	32
Sovereign nations	.70	.07 [-.14; .28]	35
Countries and states/districts	.80	.22 [.11; .34]	169

The correlations in the left column merely recapitulate those presented in earlier sections. As shown in the center column, except in the case of Mexico, cognitive ability scores explain the major portion of the positive association between European ancestry and S.

14. International colorism?

Within countries, it has often been found that cognitive ability, income and other socioeconomic measures correlate positively with lighter skin color (M. Hunter, 2007), which our measure of skin reflectance indexes. The usual explanation offered for this state of affairs is color based discrimination: the colorism hypothesis. Kinship studies have disconfirmed a strong version of this explanation. The predominant portion of outcome variance, in mixed populations, has been found to be between families. Little variance has been found between biological siblings within families, even though such siblings differ substantially in color (e.g., Mill & Stein, 2012). This indicates that family background is the major cause of the color-outcome association. An alternative test of colorism would be to look at the semi-partial correlations between color or skin reflectance and outcomes, controlling for genomic ancestry. While this has been done on the individual level in conjunction with Ruiz-Linares et al. (2014), results have yet to be published (K. Adhikari, personal communications, November 04, 2014).

One might wonder if color or skin reflectance is associated with outcomes net of genomic ancestry on the national level. Our data for sovereign countries have the three necessary components to test this hypothesis: skin reflectance, genomic ancestry, and some relevant dependent variable (in our case S and cognitive ability). The correlations are shown in Table 48. We used semi-partial correlations to control for European ancestry. As can be seen, regional-level genomic ancestry mediates most of the association between reflectance and outcomes.

Table 48. *Results for international colorism hypothesis: correlation of skin reflectance (light skin) with outcome variables. N=35 sovereign countries.*

Variable	Skin reflectance	Skin reflectance controlling for European ancestry
Cognitive ability	.62	.18
S	.60	.19

We might likewise ask if the associations of self-identified race and ethnicity (SIRE) with outcomes are also mediated by genomic ancestry. Individual level results, with respect to socioeconomic outcomes, have been reported (Ruiz-Linares et al., 2014) for five Latin American countries. They indicate that independent of genomic ancestry SIRE is only weakly associated with outcomes. Results for the national level analysis are shown below in Table 49.

Table 49. *Results for international culturalism hypothesis: correlations of self-identified ethnic European identity with outcome variables. N=35 sovereign countries.*

Variable	European identity	European identity controlling for European ancestry
Cognitive ability	.70	.08
S	.52	.08

Generally, genomic ancestry statistically explains most of the associations between skin reflectance and outcomes and between SIRE and outcomes.

15. Other measures of cognitive ability and human capital

We have high confidence in our socioeconomic variable since it is based on solid sources and numerous variables. This is not the case for our cognitive index

on the national level. While many of the scores were based on well-vetted international achievement tests, others, particularly for the small Caribbean nations, were based on less reliable indexes, such as results from US university exams. As a robustness check, we examine whether the previously documented positive relationship between European ancestry and cognitive ability scores holds when using other measures. This section is concerned with sovereign countries only as these other measures are not available for states or districts within countries.

15.1. Measures
A wide variety of measures were sought, to preclude claims that we employed only narrow measures of cognitive ability and skills:

15.1.1. Academic achievement (ACH)
This is the same as that used throughout the paper. See 7.1.2 for more details.

15.1.2. Lynn and Meisenberg's (2015) IQ dataset (IQ_L15)
This is an early version of Lynn and Meisenberg's (2015) IQ dataset (G. Meisenberg, personal communications, April, 06, 2015). Three points are worth noting: First, Richard Lynn has rejected some of the values calculated by Gerhard Meisenberg for various reasons, so some of the scores presented in Lynn and Meisenberg's future compendium may be different from the ones we use here. Second, we altered several of G. Meisenberg's (April, 06, 2015) values. These were Peru (94 to 90, added new data and removed some scores calculated based on a Mexican sample), Cuba (84 to 86; removed a mentally disabled sample), El Salvador (deleted, sample size below 100), Bolivia (deleted, sample size below 100), Barbados (93 to 87, removed a redundant source), Dominican Republic (deleted, sample size below 100). Third, this dataset is still under construction. Supplementary File 7 contains the national IQs provided to us along with our final 2015 national IQs.

15.1.3. Average achievement and IQ (ACH+IQ)
This is the average of the academic achievement scores and Lynn and Meisenberg's (2015) IQ scores (i.e., the previous two variables).

15.1.4. Lynn and Vanhanen's (2012) IQ dataset (IQ_LV12)
This is the widely used and latest published list of national IQs by Richard Lynn (Lynn & Vanhanen, 2012).

15.1.5. Altinok's educational quality dataset (Altinok)

This is an alternative international achievement dataset calculated using a different method than that employed by Lynn and Meisenberg (2015). Data from (Altinok, Diebolt, & Demeulemeester, 2014)

15.1.6. GRE scores (GRE_Total)

These were the GRE (Graduate Record Examination) by citizenship scores from ETS's report, *Snapshot of the Individuals Who Took the GRE® revised General Test (2011-2012; 2012-2013; 2014-2015)*. We used the sum of quantitative and verbal scores.

15.1.7. GMAT scores (GMAT)

These were the GMAT (Graduate Management Admission Test) by citizenship scores from GMAC's 2001 to 2012 *Profile of GMAT Candidate Executive Summary* reports. We computed n-weighted average GMAT scores. Note that the GMAT is used by 5,900 business programs at 2,100 universities worldwide. While the test is given in English, it is designed to be as minimally English dependent as necessary to predict successful completion of Business programs taught in English.

15.1.8. Mean years of schooling in 2013 (YearsofSchool13)

This is the average number of years of education which individuals aged ≥ 25 years are estimated to have. The data came from the Human Development Index dataset (http://hdr.undp.org/en/content/mean-years-schooling-adults-years).

15.1.9. Scientific papers per capita (SciPapers)

This is based on the World Bank's reported number of scientific papers published per country, between 2005 and 2014. We divided the numbers by the national populations to derive a per capita estimate. The data were extremely skewed and some countries had 0. To get a more normal distribution, we changed the 0 values to the smallest value and took the log which gave a satisfactory result. The original dataset is available at: http://data.worldbank.org/indicator/IP.JRN.ARTC.SC/countries.

15.1.10. Fraction of GDP spent on research and development (R&D)

This is the fraction of each country's GDP that is spent on research and development (R&D). The data are from the Democracy Ranking dataset (http://democracyranking.org/).

15.1.11. Math Olympics (MathOlympiad)

These are the average rankings based on International Math Olympiads. 2000 to 2014 national rankings were averaged. Because a smaller ranking is better, we reversed this variable (multiplying by -1).

15.2. Factor analysis (G)

A country-level general cognitive factor (Rindermann, 2007) was extracted from the non-overlapping variables. The factor was extracted using the least squares method and scored using Bartlett's method. Figure 23 shows the loadings plot.
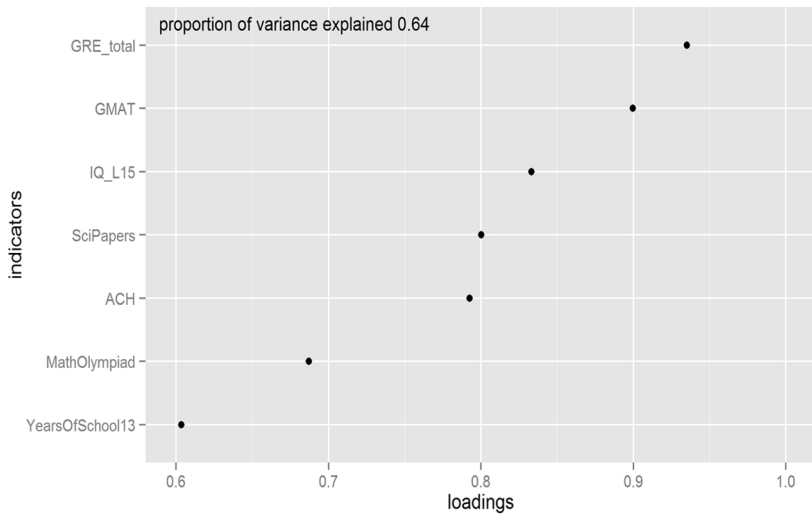
Figure 23. *International general cognitive factor, G.*

15.3. Correlations

Table 50 shows the correlations among the cognitive measures. They all show medium to strong intercorrelations, which forms the basis of the international G factor (Rindermann, 2007)**,** and all cognitive measures have substantial correlations with European%. One of the weakest correlates, with regards to both European% and the other cognitive measures, is R&D as a fraction of GDP. This is probably because this variable is influenced more by national policy than by mean cognitive ability. Generally, the results seem to be robust across measures of cognitive ability.

Table 50. *European ancestry and cognitive outcomes. ACH, school achievement scores; R&D, R&D expenditure as % of GDP; Euro%, genomic European ancestry. Weighted correlations below the diagonal. N ranges from 16 (G) to 35.*

	ACH	ACH+IQ	IQ_LVl2	IQ_L15	Altinok	GMAT	GRE	Years in School	Sci papers	Math Olympiad	R&D	Euro %	G
ACH		0.92	0.77	0.65	0.96	0.75	0.69	0.54	0.70	0.56	0.30	0.74	0.61
ACH+IQ	0.93		0.84	0.93	0.89	0.81	0.82	0.61	0.70	0.66	0.18	0.70	0.86
IQ_LVl2	0.86	0.92		0.81	0.80	0.73	0.74	0.46	0.57	0.66	0.21	0.72	0.84
IQ_L15	0.73	0.94	0.86		0.63	0.71	0.79	0.69	0.62	0.60	0.12	0.52	0.86
Altinok	0.97	0.92	0.87	0.73		0.48	0.56	0.75	0.83	0.57	0.35	0.65	0.65
GMAT	0.59	0.73	0.71	0.74	0.41		0.91	0.34	0.65	0.59	0.13	0.68	0.89
GRE	0.66	0.80	0.81	0.81	0.56	0.90		0.51	0.73	0.56	0.13	0.56	0.94
Years in School	0.82	0.84	0.80	0.78	0.88	0.48	0.64		0.66	0.52	0.38	0.21	0.77
Sci papers	0.86	0.89	0.82	0.80	0.88	0.73	0.75	0.81		0.71	0.29	0.53	0.88
Math Olympiad	0.65	0.74	0.71	0.70	0.68	0.62	0.56	0.62	0.82		0.58	0.44	0.67
R&D	0.60	0.51	0.53	0.40	0.64	0.32	0.34	0.68	0.56	0.66		0.29	0.35
Euro%	0.77	0.73	0.77	0.60	0.71	0.64	0.63	0.51	0.74	0.56	0.49		0.51
G	0.69	0.88	0.87	0.88	0.72	0.85	0.93	0.78	0.89	0.72	0.54	0.64	

16. The S factor in the American sample

As a robustness check, we examined whether the S factor previously extracted from samples of N=132 and N=115 countries was structurally similar in the American sample (N=35). We did this by extracting the first factor from three different datasets: the combined Social Progress Index and Democracy Ranking datasets (96 indicators in total, N=18 with complete data), the Social Progress Index dataset (54 indicators, N=18 with complete data) and the Democracy Ranking dataset (42 indicators, N=23 with complete data). Analysis showed that results were unstable across scoring methods (using the *FA_all_methods()* function from the *kirkegaard* package).[8] Since a previous study had shown that Bartlett's method works even when there are many more indicators than cases (Kirkegaard, 2015d), we used this method in all analyses. Table 51 shows the intercorrelations of the factor scores.

Table 51. *Intercorrelations between S factor scores. Soc Progr, score from 54 variables in Social Progress dataset; Democracy, score from 42 variables in Democracy dataset; SP + D, SocProgr and Democracy combined, 96 variables. Weighted correlations below the diagonal. N's = 18-23 sovereign countries.*

	S_rescaled	SP + D	SocProgr	Democracy
S_rescaled		0.98	0.96	0.99
SP + D	0.97		0.98	0.99
SocProgr	0.94	0.98		0.95
Democracy	0.99	0.98	0.93	

The correlations were very strong, especially for the unweighted results. There was a slight difference between weighted and unweighted results. This could have been due to the factor analysis process which does not use weights to derive the covariance/correlation matrix. Regardless, there was no evidence that the S factor structure was substantially different in the American sample as compared to the worldwide sample.

Comparing factor scores is a more indirect method of comparing factor structure similarity. Different sets of loadings can theoretically lead to the same scores. Thus, we also investigated the factor loadings across samples. We extracted the S factors using the full dataset for this purpose. The correlations between loadings across datasets were .91, .93 and .84 for the 96, 56 and 42 indicator datasets respectively. It is often said that the most appropriate method for comparing loadings is to use the factor congruence coefficient (Jensen, 1998,

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[8] The package is on Github: https://github.com/Deleetdk/kirkegaard

p. 99; Lorenzo-Seva & Ten Berge, 2006). For the same datasets, in all cases, the coefficient was .93. A common rule of thumb for factor identity is ≥.95, which is not quite met here. However, the samples were fairly small, so it is probable that sampling error decreased the congruence coefficients (and the correlations) somewhat.

16.1. Jensen's method applied to the European ancestry x S factor correlation

Our results show medium to strong correlations between European ancestry and S scores at the international level. It is possible, however, that European ancestry is not related to the latent S factor, but is solely related to one or more group factors found in the data or to indicator specific (unique) variance. One can use Jensen's method of correlated vectors (Jensen, 1998) to examine whether European ancestry correlates more strongly with more S loaded variables. If so, this would suggest that general factor differences explain the association. The Jensen coefficients (MCV correlations) were .75, .69 and .85 across the three datasets. The strength of these associations suggests that European ancestry is substantially related to the underlying S factor. Figure 24 shows the scatter plot for the analysis with all 96 S indicators.
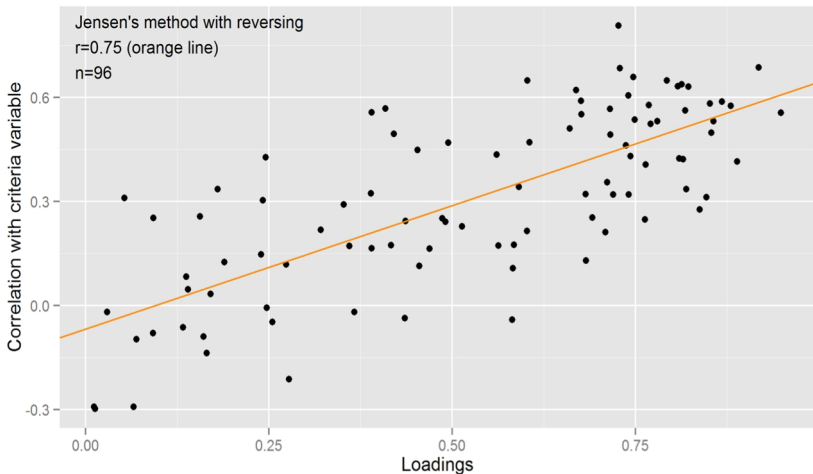

Figure 24. *Jensen's method scatter plot for 96 socioeconomic indicators and European ancestry as criteria variable. Reversing is used. Variables with higher loadings on the general socioeconomic factor tend to have higher correlations with European ancestry.*

17. The West Indies

In Section 7 we saw that West Indian countries were outliers when it came to the association between S and European ancestry. Lynn and Vanhanen (2012) had previously found similar results with respect to the association between National IQ and various socioeconomic indicators. They attributed the large positive residuals of West Indian countries to wealth gained from tourism. We test this explanation by including a measure of per capita tourist spending in our regression analysis. This measure was calculated using World Bank values for tourist expenditure in 2010. We divided the expenditure values by the national populations to compute per capita estimates. Because the island states in question have small populations, we ran the regression analyses both with and without weights. We also included a dichotomously coded European Union classified tax haven variable. Table 52 shows the unweighted and Table 53 the weighted results. In line with Lynn and Vanhanen's conjecture, we find that when adding per capita tourist expenditure and tax haven status, the model improves.

Table 52. *Regression results for sovereign nations: tourism, tax haven and European ancestry. N=35.*

Model #	Euro%	Tax Haven	Tourist spending	adj. R^2
1	0.48			0.212
2		0.16		-0.026
3			0.19	0.007
4	0.66	0.88		0.303
5	0.64		0.43	0.355
6		-0.23	0.25	-0.018
7	0.69	0.40	0.33	0.350

Table 53. *Weighted regression results for sovereign nations: tourism, tax haven and European ancestry. N=35.*

Model #	Euro%	Tax_Haven	Tourist spending	adj. R^2
1	0.939			0.477
2		-0.157		-0.030
3			0.775	0.040
4	1.006	1.196		0.493
5	0.965		0.911	0.560
6		-1.890	1.293	0.065
7	0.959	-0.138	0.948	0.546

17.1. West Indies territories

So far we have only presented results for sovereign nations and states. However, the Caribbean is host to over a dozen tiny island territories.[9] These territories do not have official HDI values, but more or less reliable estimates can be constructed. For these territories, we used Avakov's (2012) HDI 2010 estimates, except for Puerto Rico, in which case we used Fuentes-Ramírez's (2014) HDI 2012 estimate. Most of these territories lack genomic admixture data, yet it was possible to create crude ancestry estimates using CIA Factbook SIRE and ancillary data. More problematic was the poor quality of the cognitive data. Estimates based on a combination of (1986 to 2014) GMAT[10] scores, CXC scores (discussed below), Lynn's (2012/2015) IQ scores and other sources are shown in Table 54.[11] Detailed computations are provided in Supplementary File 6. The same file provides alternative estimates for the Caribbean nation states. It needs to be emphasized again that, except in the case of the US Virgin Islands and Puerto Rico, the quality of data is very poor. This was one of the reasons why these territories were not included in the previous analyses – another being that the populations are often minute.

Table 54. *ACHQ scores for West Indian territories.*

Nation	ACHQ	Data sources
Anguilla	74.3	CXCQ
British Virgin Islands	76.1	GMATQadj + CXCQ
Cayman Islands	85.7	GMATQadj + IQ + GCSE/CXCQ
Montserrat	79.9	CXCQ
Netherlands Antilles	84.4	GMATQadj + Lynn + OtherQ (Cito) + CXCQ
Turks & Caicos	79.3	Lynn + CXCQ
US Virgin Islands	72.3	GMATQadj + LYNN + Other (SAT+NAEP)
Bermuda	87.3	GMATQadj + LYNN + OtherQ (TerraNova+GED scores)
Martinique	84.9	GMATQadj+ OtherQ (French Literacy exam)
Guadeloupe	83.7	GMATQadj+ OtherQ (French Literacy exam)
French Guiana	86.6	OtherQ (Based on French Literacy exam)
Aruba	76.8	GMATQadj
Puerto Rico	78.9	ACHQ

---

[9] The non-sovereign Caribbean islands usually have the status of "overseas territory" or something similar. Sometimes they constitute departments or comparable entities.

[10] For several of the territories, we had to use older GMAT scores since they ceased to be listed in later Profile reports.

[11] For Puerto Rico, the ACHQ value was 78.9 and the ACHQ+IQ value was 81.4. We used the former value since it was already in our dataset.

To get an idea of where these territories are located in the American context, we show the scatter plots for European% and cognitive ability scores (as operationalized above) and European% and S scores (Figs. 25 and 26). For cognitive ability, the weighted correlation became negative. This result is mainly driven by Puerto Rico, which has a relatively large population as compared to the other territories, a relatively low cognitive score, and yet a relatively high percentage of European admixture (64%).
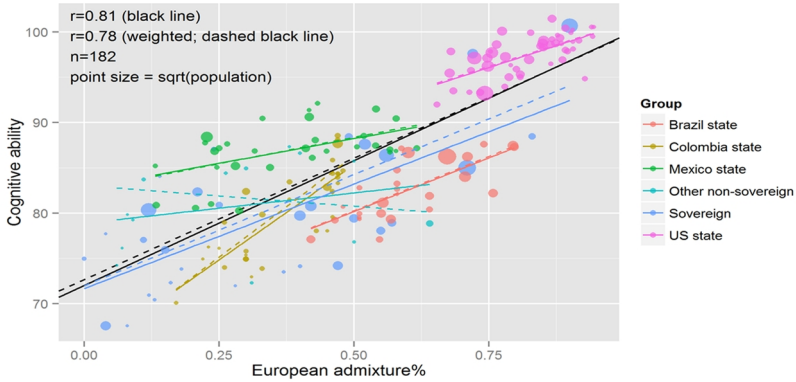

Figure 25. *European ancestry and cognitive ability scores for countries and states/districts. Most of the "other non-sovereign" territories are Caribbean islands.*
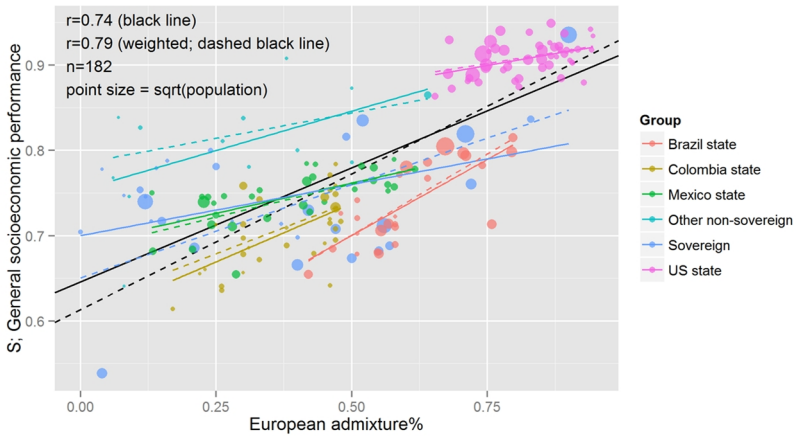

Figure 26. *European ancestry and socioeconomic (S factor) scores for countries and states/districts.*

Clearly, the territories have higher S scores than expected from a simple R~CA-S model. We might wonder if including per capita tourist expenditure and tax haven status can, as before, salvage the model. Thus we repeat the analyses above for the combined sample of territories and sovereign nations. Table 55 shows the beta matrix for results without weights. Table 56 shows the same but with weighted results.

Table 55. *Regression models for European ancestry, Tax haven status and tourist spending for sovereign nations and territories. Dependent: socioeconomic (S-factor) scores.*

Model	Euro%	Tax Haven	Tourist spending	adj. R^2	N
1	0.394			0.140	48
2		0.201		-0.013	48
3			0.311	0.052	47
4	0.559	0.764		0.226	48
5	0.492		0.459	0.273	47
6		-0.164	0.362	0.034	47
7	0.557	0.408	0.352	0.278	47

Table 56. *Weighted regression models for European ancestry, Tax haven status and tourist spending for sovereign nations and territories. Dependent: socioeconomic (S-factor) scores.*

Model	Euro%	Tax Haven	Tourist spending	adj. R^2	N
1	0.808			0.440	48
2		-0.035		-0.022	48
3			0.641	0.002	47
4	0.878	1.159		0.467	48
5	0.846		1.001	0.489	47
6		-0.775	0.955	-0.007	47
7	0.870	0.535	0.795	0.483	47

We see that for the unweighted results, adding tax haven status and tourist expenditure substantially improves the proportion of variance (.140 vs. .278) accounted for, compared to European ancestry alone. In the weighted analysis, we see the same but to a much smaller degree. This is, of course, because the populations of the territories are tiny and so they barely affect the estimates.

17.2. Alternative measures of cognitive ability for the West Indies

An alternative explanation to the tourism/tax haven hypothesis is simply that West Indian countries have higher national cognitive abilities than estimated (i.e., that our cognitive measures are biased). This is a plausible hypothesis; it is difficult to find alternative measures to test it, though. The Caribbean specific Caribbean Exam Council's (CXC) math and reading tests are possible measures. Unfortunately, we were unable to obtain data from the CXC. However, pass rates for math and reading tests are often reported in the economic literature (e.g., Thomas, 2014). It is possible to transform these pass rate differences into deviation scores with respect to the Caribbean average. Since both international achievement and CXC scores are available for Trinidad and Tobago, Belize and the Dominican Republic, one can compute crude CXC quotient (national CXCQ) scores to get a rough idea if any Caribbean nations deviate much from the Caribbean average. It needs to be noted that pass rates represent non-linear effects of mean ability and, therefore, are less than ideal to use (La Griffe du Lion, 2001, 2007). Moreover, the CXC tests are similar to the UK GCSE exams, which have shown extensive malleability over time and across groups. For these two reasons, CXC pass rates can only be taken as a crude indirect measure of ability. Nonetheless, they provide some, albeit limited, information.

We computed the national CXCQ scores using 1991-1997 math scores and 2000, 2001, 2003, 2008 and 2011 math and reading scores reported in the literature. For a specific year, not all countries were represented. As such, for each year we calculated deviation scores with respect to the average for Dominica, St. Lucia, Trinidad and Tobago and Guyana. For these countries, there were pass rates for each year thus giving us a baseline for a cross country comparison. We computed deviation scores from this baseline and averaged them. These were then transformed into national CXCQ scores, using the previously discussed method. Specifically, we used the international achievement test scores of Dominican Republic, Trinidad and Tobago and Belize as anchors, since CXC tests were more comparable with international achievement ones than with, for example, IQ tests. In line with Lynn and Vanhanen (2012), we applied a conservative correction for enrollment rates. For the enrollment rates, we used the 2000, 2003, 2004, 2005, 2009, 2010, 2011 World Bank estimates. Barbados, Dominica, St. Kitts and Nevis and Trinidad and Tobago had enrollment rates for each year. For a baseline, we used the average rates for these countries and then calculated the percentage difference from this for each year and country. These percentage differences were averaged across years for each country and then multiplied by 0.5 SD on the assumption that non-enrolled individuals perform about one half of a standard deviation in ability below those in school. This value

was added to the original CXCQ for an enrollment corrected CXCQ. For example, our baseline average enrollment rate was 82%. The average enrollment rate for the Dominican Republic was about 54%. The 28% difference was multiplied by 7.5 quotient points, giving us a value of 2 points below the baseline mean. This negative two points was then added to the Dominican Republic mean. The sources and specific computation are shown in Supplementary File 6. Table 57 shows the estimates.

Table 57. *School achievement scores based on pass rates on the Caribbean Examination Council (CXC) exams. Correction of CXC achievement quotients (CXCAQ) is for incomplete school enrollment.*

Country	Deviation Score	ACHQ	CXCAQ	CXCAQ corrected	NACHQ
Antigua and Barbuda	0.13		80.25	80.00	77.73
Barbados	0.47		85.32	85.82	84.06
St. Kitts and Nevis	0.21		81.48	81.73	67.57
Dominica	0.39		84.12	84.23	71.98
Dominican Republic	-0.34	74.23	73.10	70.99	74.23
Trinidad and Tobago	0.13	87.07	80.27	79.69	87.07
St. Lucia	0.11		79.90	79.17	73.84
Belize	0.26	73.52	82.17	81.00	73.52
Grenada	-0.18		75.59	75.32	70.96
Jamaica	-0.14		76.10	75.95	77.04
St. Vincent and the G.	-0.02		77.94	77.53	70.44
Guyana	-0.51		70.66	71.20	74.96
Average	0.04	78.27	78.91	78.55	75.28

Generally speaking, the results suggest that none of the Caribbean countries score far above the Caribbean mean on CXC exams. St. Kitts and Nevis and Dominica did substantially better than our NACHQ results would have predicted, and as a result, the correlation between CXCAQ and NACHQ was near zero. Nonetheless, these countries' CXCAQ scores are similar enough to our NACHQ scores that using them would not substantively change our previous results. In the future, better data will need to be found for the Caribbean.

18. Parasite prevalence and European ancestry in the US

In Section 11, we saw some fairly odd findings for European ancestry in the United States. It seems that parasite load is so correlated with European ancestry (r = -.88, weighted r = -.82) that multiple regressions cannot disentangle the effects. Two variables that correlate at .88 share 77% ($.88^2$) of their variance, which of course means that 23% is not shared. One can check if the remaining variance has predictive power for both dependent variables. We did this by calculating the semi-partial correlations where we first regress out either European ancestry or parasite load and then correlate the residuals with the remaining variable. Table 58 shows the results.

Table 58. *Semi-partial correlations for cognitive ability and S scores. Weighted correlations.*

Analysis	Correlation
Cognitive ability scores	
Parasite load	-.56
Parasite load, European ancestry controlled	-.05
European ancestry	.64
European ancestry, parasite load controlled	.22
S factor scores	
Parasite load	-.55
Parasite load, European ancestry controlled	-.25
European ancestry	.39
European ancestry, parasite load controlled	-.07

What we see is that for cognitive ability scores, European ancestry seems to have a small amount of validity controlling for parasite load (.22), while the opposite case did not hold (-.05). For S we see the opposite pattern, parasite prevalence seems to have some validity controlling for European ancestry (-.25), while European ancestry has none controlling for parasite prevalence (-.07; wrong direction!). The confidence intervals include 0 for all cases, however. The results are curious because state-level parasite load does not actually explain away either SIRE associated cognitive ability or socioeconomic differences in the US. The SIRE differences can be found within each state and they are actually *smaller* in the more parasite loaded states than in parasite light ones (results not shown). This is a topic that deserves further investigation; however it falls outside the scope of this paper.

19. Spatial autocorrelation

Autocorrelation concerns the similarity or dissimilarity of cases that are located close to each other, which can be in time (*temporal autocorrelation),* space (*spatial autocorrelation* (SAC)) or any other dimension (e.g., phylogenetic distance) (Corey & Waite, 2008). Figure 27 illustrates the concept.
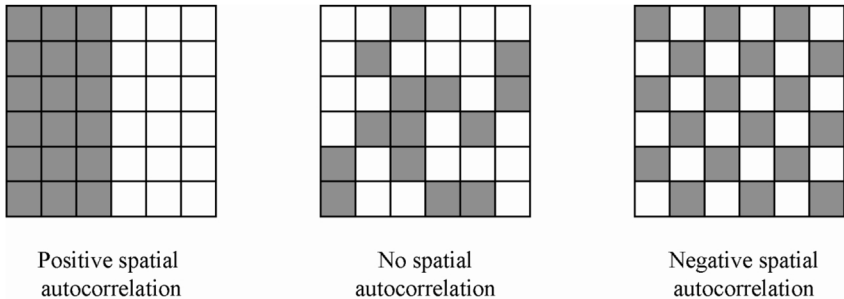

| Positive spatial | No spatial | Negative spatial |
| autocorrelation | autocorrelation | autocorrelation |

Figure 27. *Illustration of spatial autocorrelation. Copied from Radil (2011).*

Most social science research concerns units that have a location (persons live somewhere, companies have their buildings somewhere, schools are located somewhere, etc.). However, most social scientists do not take SAC into account, perhaps because they are unfamiliar with the issue or the statistics needed to examine it. This is also true for research on cognitive and socioeconomic differences between administrative divisions such as countries or states, or between regionally delineated divisions such as geographic races. There are a few notable exceptions to this tendency (Gelade, 2008; Hassall & Sherratt, 2011; Piffer, 2015a). Gelade (2008) pointed out the problem and provided measures of SAC for IQ, temperature and precipitation and showed that SAC was higher for national IQs than for the climate variables. Hassall and Sherratt (2011) provided a fairly comprehensive analysis of the relationships between national IQs and other variables both with and without corrections for SAC. Piffer (2015a) examined genomic autocorrelation in context to a polygenic score based on SNPs linked to cognitive ability (Rietveld et al., 2013) and national IQs. He then developed his own method (correlation of distances; CD) for controlling for SAC and found that national IQs were still highly correlated with the polygenic score, after SAC was controlled for.

We sought to find methods to measure the amount of SAC in our variables and to analyze their relationships when SAC was controlled for. The method used by Hassall and Sherratt (2011) could not be used because it relied upon a third

party program, and the method used by Piffer was untested. For these reasons, one of us developed another method for measuring SAC and two more for controlling for it. The same author conducted a simulation study to examine the inter-method agreement in measuring SAC and to determine how well the SAC controlling method could distinguish between true and spurious causes of SAC (Kirkegaard, 2015i). The spatial statistics methods used are explained below.

19.1. Brief explanation of the spatial autocorrelation methods
19.1.1. Moran's I

Moran's I is probably the most widely used measure of spatial autocorrelation (10,600 mentions on Google Scholar as of 2015-11-11). Mathematically, it is very similar to the commonly used Pearson correlation, as shown in Equations 1 and 2.

$$r_{xy} = \frac{\sum_{i=1}^{n} z_{i,x} z_{i,y}}{S_x S_y}$$

Equation 1. One formula for Pearson's r.

where S_x and S_y are the sample standard deviations of x and y, and $z_{i,x}$ and $z_{i,y}$ are the deviation scores for case i and variables x and y. Deviation scores are scores from which the sample means have been subtracted.

$$I = \frac{n \sum_{i=1}^{n} \sum_{j=1}^{n} w_{i,j} z_i z_j}{S_0 \sum_{i=1}^{n} z_i^2}$$

Equation 2. One formula for Moran's I (ArcGIS Resource Center, 2015). where $w_{i,j}$ is the spatial weight for cases i and j, S_0 is the sum of all spatial weights and the other symbols are as above.

With Pearson's correlation, the deviation scores for each variable are multiplied and summed to get the dot product, then divided by the product of the standard deviation of x and of y. The intuitive explanation is that when a given case deviates in the same direction for both x and y, the product will be positive, no matter the deviation direction (the product of two negative numbers is positive). However, when the case deviates in different directions, the product is negative.

When we then sum the products and standardize the sum, we get a standardized (values between -1 and 1) measure of how cases that are higher in x are also higher in y – a measure of a linear co-relationship: co-(r)relation (Galton, 1888; Stigler, 1989).

With Moran's I, we calculate the product of the deviation scores for each pair of cases and multiply that by the spatial weight (usually the inverse of distance). We then divide the sum of squared deviations by the sum of all spatial weights times. The intuitive explanation is that we simply calculate the Pearson correlation but weigh the cases by their distance and standardize the result, which means that Moran's I is always between -1 and 1.

19.1.2. k nearest spatial neighbor regression

In k nearest spatial neighbor regression (KNSNR), we find each case's k nearest spatial neighbors and calculate their mean on the variable of interest.[12] This gives us a predicted value for each case, based solely on its neighbors' values. One can then correlate the predicted with the actual values to get a standardized measure of how well the actual values can be predicted from the neighbors'. Alternatively, one can use the predicted values with standard methods such as multiple regression or (semi-)partial correlations to control for SAC. Thus, KNSNR can be used both as a measure and as a control method. For a longer explanation see Kirkegaard (2015i).

One problem with KNSNR is that one has to choose a reasonable k value; k controls the locality or zoom-level of the regression. This choice, however, can also provide more information because SAC can be more or less local as shown in Figure 28.
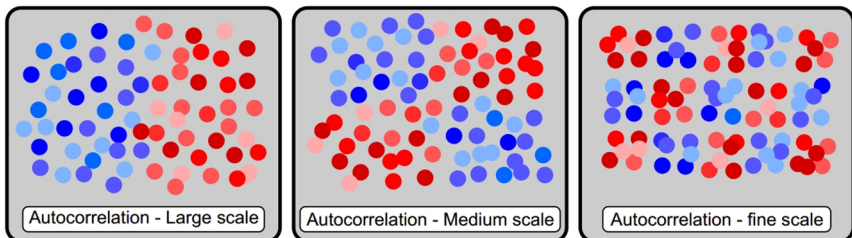

Figure 28. *Locality of spatial autocorrelation.*

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[12] The arithmetic mean has been used so far, but it is possible that other more robust measures such as the median or winzored mean would perform better on noisy data.

19.1.3. Correlation of distances

In correlation of distances, one calculates the pairwise distances for each pair on all variables of interest. For non-spatial variables, the absolute difference is used. This creates a new dataset, with (n*(n-1))/2 cases on which one can use standard methods. With KNSNR, CD can be used both as a measure and as a control method like KNSNR. While simulations seem to show that this method is a fine measure of SAC, they also seem to show that this method poorly controls for SAC (Kirkegaard, 2015i). Simulations also show that one needs to take the square root of the CD results for them to be on a correlation-like scale and thus comparable with the results generated by other methods. This procedure is done in the following analyses without further notice.

19.1.4. Spatial local regression

In spatial local regression (SLR), one conducts a regression for each case and its k-1 neighbors.[13] When k is small (3 is the minimum possible), it means that one is using cases from only a small region of the total space, thus reducing SAC. Each individual regression has N=k, so sampling error is very strong. However, one can aggregate the results by calculating a summary value for each beta (a kind of meta-analysis). This method makes it possible to reduce SAC confounders, but it does not provide a measure of SAC. SLR makes it possible to reduce SAC, but it does not provide a measure of it. As with KNSNR, one must choose a value of k for SLR. Kirkegaard (2015i) showed that using the smallest possible value of 3 gives the best results.

With SLR, there is a question of when to implement weights in the analysis. One could do this at the level of each cluster or at the aggregation/meta-analysis level. The implementation procedure used in this analysis weights at the cluster-level and not at the meta-level. Further research is needed to determine if this is the preferable method. Lastly, there is the question of how to summarize the beta values. The simplest solution is to use the (arithmetic) mean of the betas, but because the sample size is so small for each cluster, betas can vary substantially.

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[13] In the original implementation discussed in Kirkegaard (2015i) the method was implemented by using each case's k neighbors, but not the case itself. This was an oversight on my (Emil's) part, but it does result in two slightly different methods. It seems more theoretically sensible to include the case as well as the k-1 nearest neighbors in each cluster, but this issue has not been extensively tested. When one uses the case itself as well one cannot use the inverse weighting method discussed in the paper because this would result in an infinite/undefined weight for the 'home' case (its distance to itself is 0, and 1/0 is either ∞ or undefined). Both methods are available in the function and the default is to include the home case.

This situation can result in outliers having strong influences. One can avoid this problem by using the median or trimmed/winzored means instead. The default setting (as of 2015-11-11) is to use a 10% trimmed mean. More research is needed on this issue.

19.2. Spatial autocorrelation in the main variables of interest

How spatially correlated are our main variables of interest (cognitive ability, S factor score and Euro%)? Before we compare results from the three methods, we need to take a look at all the results from one method, KNSNR. This is because one must choose a k value. One could try all the reasonable k values (e.g., 1-20) on each dataset and simply go with the one that generates the highest SAC value. This would mean, however, that we would potentially be measuring SAC in different ways in each dataset, making it difficult to interpret results across datasets. Instead of this method, we opted to choose the k value which, on average, gave the highest SAC values. Figures 29-31 show, for each dataset, correlations between neighbor-based predictions of values and the actual values for k 1-20, as well as an unweighted mean across datasets.
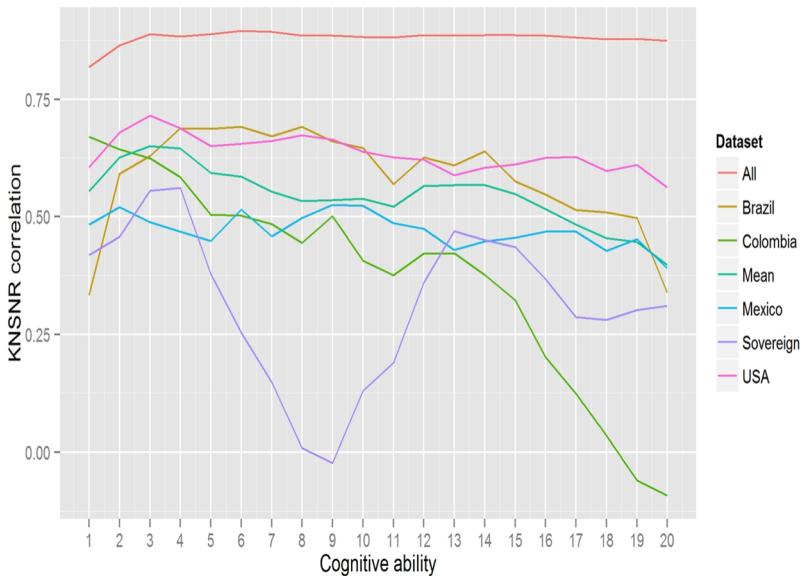

Figure 29. *k nearest spatial neighbor correlation of SAC for cognitive ability in each dataset for k 1-20.*
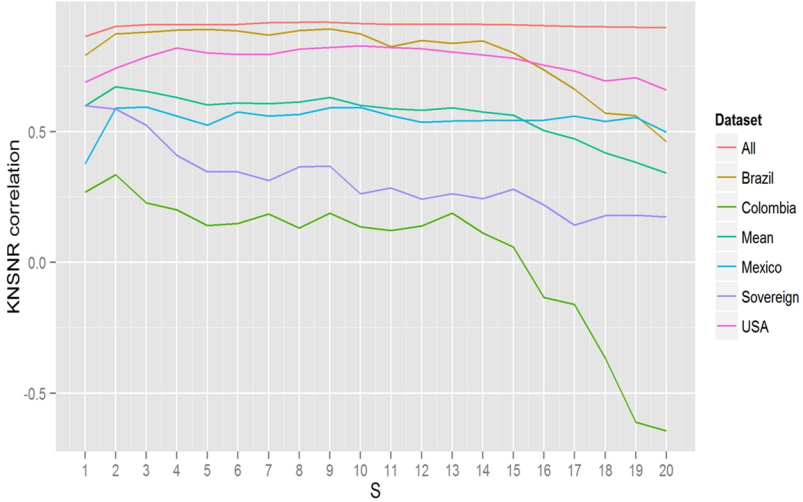
Figure 30. *k nearest spatial neighbor correlation of SAC for S in each dataset for k 1-20.*
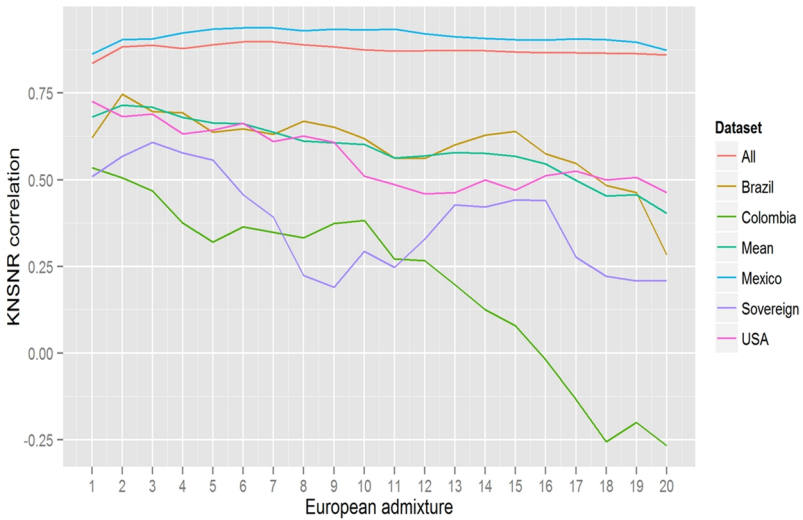
Figure 31. *k nearest spatial neighbor correlation of SAC for European admixture in each dataset for k 1-20.*

Overall, we see strong positive SAC in each dataset for each measure, as expected from prior studies (Gelade, 2008; Hassall & Sherratt, 2011). The values of k yielding the strongest SAC results were 3, 2, 2, respectively, for cognitive ability, S and European admixture. Thus, we use k=2 for KNSNR in the following analyses. The drop in SAC for cognitive ability for k 5-12 is odd, but this drop is also seen in a weaker form for European admixture. It is not seen for S. Future research should examine the locality of SAC in the national and regional data. Table 59 shows the SAC results for each dataset and for each of the main variables.

Table 59. *Measures of spatial autocorrelation in each dataset and for each main variable of interest.[14]*

Dataset	Moran's I	CD	KNSNR2
Cognitive ability			
Mexico	0.114	0.161	0.520
USA	0.163	0.339	0.679
Brazil	0.184	0.567	0.592
Colombia	0.135	0.320	0.643
Sovereign	0.090	0.401	0.457
All	0.381	0.543	0.865
S factor score			
Mexico	0.121	0.379	0.590
USA	0.262	0.258	0.742
Brazil	0.322	0.688	0.875
Colombia	0.061	0	0.336
Sovereign	0.074	0.479	0.587
All	0.398	0.551	0.902
European admixture			
Mexico	0.304	0.776	0.904
USA	0.134	0.231	0.682
Brazil	0.193	0.616	0.747
Colombia	0.086	0.382	0.505
Sovereign	0.177	0.518	0.568
All	0.348	0.405	0.883

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[14] Note that the value of 0 for CD is imputed because the real value could not be calculated. This is because the CD correlation is sometimes negative when SAC is absent/very low, and one cannot take a square root of a negative number without the use of imaginary numbers.

Generally, there is moderate to strong agreement across methods. Moran's I and KNSNR results correlated highly with each other and the CD results correlated less strongly with both of these. Intercorrelations are shown in Table 60. However, it is clear that CD is the outlier.

Table 60. *Intercorrelations among spatial autocorrelation measures across datasets and models.*

	Moran's I	**CD**	**KNSNR**
Moran's I	1	0.566	0.911
CD	0.566	1	0.651
KNSNR	0.911	0.651	1

Note that while all measures range from either -1 to 1 or 0 to 1, they are not on the same scale (i.e., if KNSNR is .90, the expected value for Moran's I is not .90 but much lower). We were unable to find interpretation guidelines for values of Moran's I (similar to Cohen's guidelines for effect sizes of other measures), so we cannot contextualize the magnitude of SAC found in terms of general standards. Finally, it should be noted that while both Moran's I and CD are global measures of SAC, KNSNR is a local measure.

19.2.1. Accounting for the variance in SAC

Table 59 shows that the degree of SAC varies across regions and variables. Figures 32 and 33 show Moran's I by variable and by dataset. One can see clearly that variation in the data is associated more with the dataset analyzed than with the variables examined. One can quantify this by performing a two-way analysis of variance (ANOVA)[15] and calculating eta squared, which is the proportion of variance associated with each variable. Table 61 shows the results.

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[15] Note that ANOVA relies upon the assumption of equality of variances/homoscedasticity, which does not seem to be true. However, because the sample size is so small, the differences in variances could be due to chance. Furthermore, the effect of heteroscedasticity is to decrease power, not bias effect size estimates (Gung, 2013).
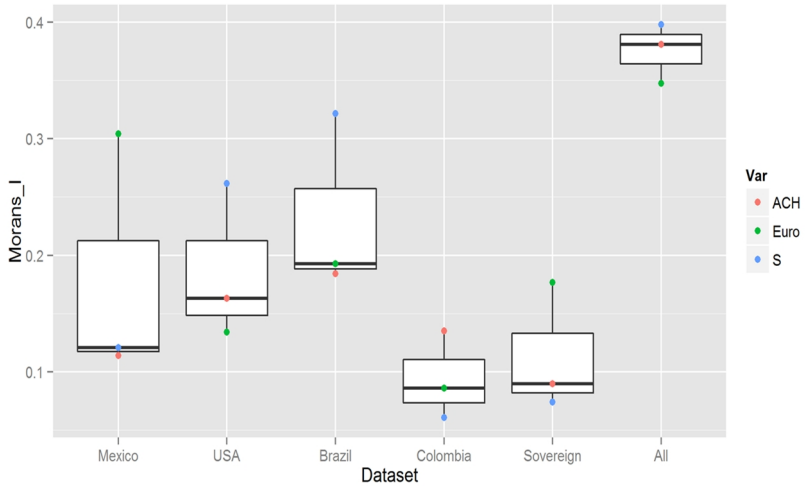
Figure 32. *Moran's I across 6 datasets (x-axis) and 3 variables (colors). ACH, achievement (cognitive ability) scores; Euro, % European ancestry; S, S factor score.*
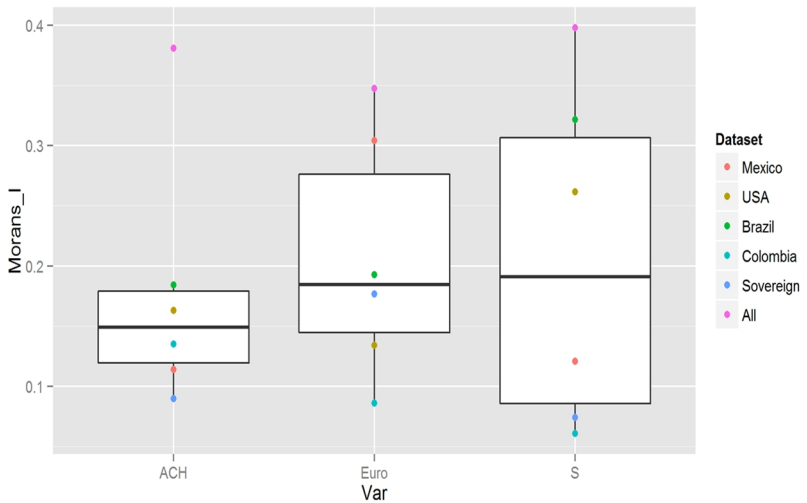
Figure 33. *Moran's I across 3 variables (x-axis) and 6 datasets (colors).*

Table 61. *Effect sizes (eta squared) for 2-way ANOVAs of SAC measures of key variables.*

SAC measure	Variable	Dataset
Moran's I	0.016	0.738
CD	0.060	0.503
KNSNR	0.049	0.618

The results in Table 61 match with what we saw in Figures 32 and 33, namely that the variance in SAC magnitude is driven mostly by differences in dataset, not variable. Note that one could examine the interaction of the two categorical variables. This was not done because it would reduce the sample size to 1 per group.

19.3. Controlling for spatial autocorrelation

It is one thing to measure SAC in variables, but quite another to decide how to handle the problem. Hassall and Sheratt (2011) employed a dual approach. First, they examined model fits without accounting for SAC and showed that the residuals contained SAC, meaning that the predictors did not jointly explain all the SAC in the outcome variable. Second, they used spatial eigenvector mapping to control for SAC. Unfortunately, their method was employed in a third-party program and was not explained in detail. We attempted to find a way to implement their method in R, but the existing R packages were not user-friendly, and so we could not use this approach.

This left us with two working, but experimental approaches, to control for SAC: KNSNR and SLR. If one uses the KNSNR predicted values in a residualization approach, as opposed to a multiple regression approach, one faces the question of which variables one should control for SAC: the predictor(s), the outcome, or both. This question was examined by Kirkegaard (2015i) but not in detail. What the limited analysis showed was that controlling both seemed to produce the best results. Still, because the (semi-)partial correlation approach would not enable us to use multiple predictors, we instead opted to use a multiple regression approach. This approach can get into problems when the KNSNR neighbor-predicted values correlate very strongly with the other predictors (multicollinearity). One could examine this using the variance inflation factor (Field, Miles & Field, 2012, sec. 7.7.2.4), although this was not done.

19.3.1. SAC in the model residuals

Before presenting the controlled results, we first want to examine whether the model residuals contain SAC, as Hassall and Sheratt did. Which models should we examine? In most of this paper, we have only been concerned with cognitive ability, S and European admixture variables, and because it would take too much space to cover other models, we confine ourselves to models which include only these variables. Since we share all the data and code, other researchers can perform more detailed analyses. For each dataset, we fit 4 main models and aggregated the data. As before, we plot the results for Moran's I, which are shown in Figures 34 and 35. Models are written in standard R formula syntax, namely "outcome ~ predictor". More predictors can be added and they are separated by "+".
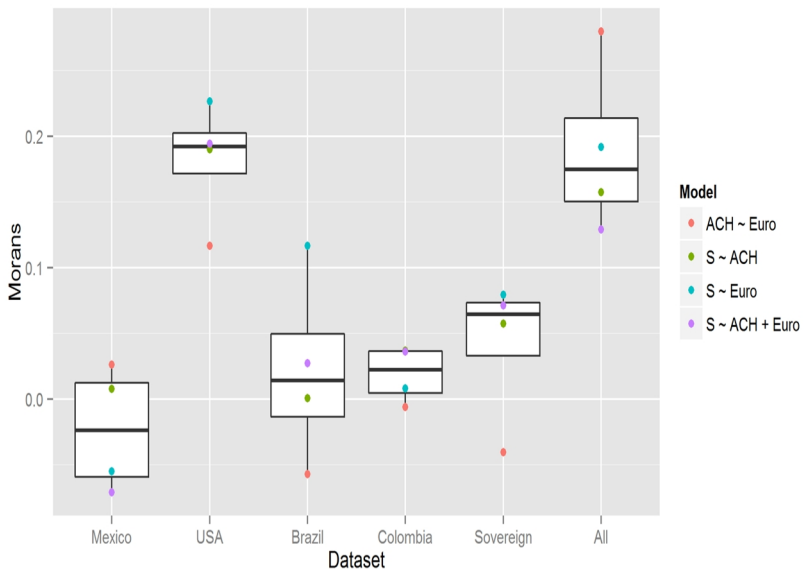
Figure 34. *Moran's I by dataset (x-axis) and model (colors).*
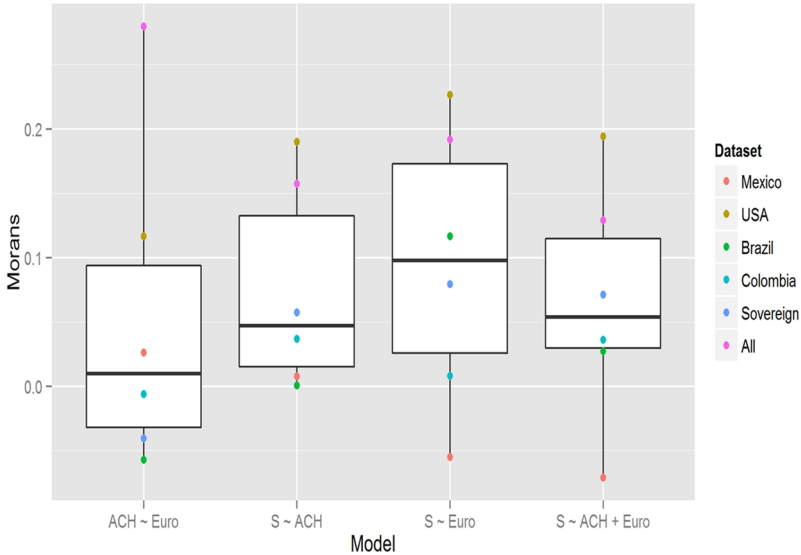
Figure 35. *Moran's I by model (x-axis) and dataset (colors).*

One can clearly see that variation in the data is associated with the dataset analyzed and not so much with the model fitted. One can quantify this by performing a two-way ANOVA and calculating eta squared which is the proportion of variance associated with each variable. Table 62 shows the results.

Table 62. *Effect sizes (eta squared) for 2-way ANOVAs of SAC measures of residuals.*

SAC measure	Model	Dataset
Moran's I	0.026	0.759
CD	0.034	0.429
KNSNR	0.035	0.615

All three measures tell a consistent story: differences in SAC are mostly driven by differences between datasets, not the type of model fit. Furthermore, as shown by the figures above, SAC is fairly weak in the residuals. Table 63 shows

the unweighted mean values of each SAC measure in the key variables and in the model residuals.

Table 63. *Mean spatial autocorrelation in key variables and model residuals.*

Group	Moran's I	CD	KNSNR
Key variables	0.197	0.448	0.671
Residuals	0.072	0.161	0.271

This shows that the SAC pattern in the key variables are generally explained by the SAC patterns in the other variables.

19.3.2. Controlling for SAC with KNSNR and SLR

Finally, one can try to outright control for SAC using the methods described above. The simplest approach using KNSNR is to add a spatial neighbor variable, which is the predicted variable for each case based on its 2 closest neighbors (2 because we found, in Section 19.2, that this was the value at which neighbor values best predicted home values). Even using only the simplest method, the results are not easy to present in written form. Instead, we present them in tabular form in Table 64. Each of the four parts of the table contains the results for the 6 datasets for a particular model.

Interpreting the results is difficult for a variety of reasons. First, we are dealing with novel statistical methods which may have unexpected properties. Second, because the samples are fairly small, large standard errors are expected and this situation is made worse by the introduction of a control procedure. Third, and most importantly, causal interpretations of spatial autocorrelation are not straightforward. While it is clear that the SAC-control methods employed here can distinguish between a true and a spurious cause in simple scenarios, it is not clear how well they work in a scenario where the causal network is much more complex as it likely is with our data. Thus, it is not clear to what extent controlling for SAC controls for spurious associations and to what extent doing so (over)controls for true causal relation. Also, because we are using weighted regressions, standardized betas can act strangely. They do not correspond to correlations even when the model has only one predictor. We see this, for instance, with the Sovereign dataset where the beta is 1.128 for S ~ CA, whereas the weighted correlation is .87 (Table 10). One could use the weighted correlation for comparison instead of the regression, but this would not work for the models with

more than one predictor. As such, we are left with the problematic standardized betas. Still, we might wonder how much smaller the SAC-controlled betas are. A simple approach is dividing them by the original values to get their fractional size. These values are shown in Table 64.

Table 64. *Spatial autocorrelation controlled results across 4 models and 6 datasets. Weighted analysis with standardized betas. KNSNR = standardized betas using k nearest spatial neighbor regression to control for SAC; SLR = standardized betas using spatial local regression to control for SAC; KNSNR_frac and SLR_frac = the fraction the SAC corrected betas are of the SAC uncorrected betas.*

Dataset	Uncorr.	KNSNR	SLR	Predictor	KNSNR_frac	SLR_frac	SLR_frac_cor
Cognitive ability and European admixture							
Mexico	0.544	0.341	-0.050	Euro	0.627	-0.091	-0.091
Mexico		0.423		spatial			
USA	0.662	0.397	0.454	Euro	0.600	0.686	0.686
USA		0.413		spatial			
Brazil	0.744	0.544	0.754	Euro	0.731	1.013	
Brazil		0.257		spatial			
Colombia	0.877	0.703	0.512	Euro	0.802	0.584	0.584
Colombia		0.294		spatial			
Sovereign	0.794	0.503	0.429	Euro	0.633	0.540	0.540
Sovereign		0.374		spatial			
All	0.773	0.264	0.418	Euro	0.342	0.541	0.541
All		0.664		spatial			
S and cognitive ability							
Mexico	0.809	0.665	0.477	CA	0.822	0.590	0.590
Mexico		0.216		spatial			
USA	0.713	0.439	0.652	CA	0.616	0.915	0.915
USA		0.465		spatial			
Brazil	0.88	0.325	0.449	CA	0.369	0.510	0.510
Brazil		0.701		spatial			
Colombia	0.619	0.611	0.617	CA	0.986	0.996	0.996
Colombia		0.039		spatial			
Sovereign	1.128	0.826	0.472	CA	0.733	0.418	0.418
Sovereign		0.273		spatial			
All	0.997	0.554	0.576	CA	0.556	0.578	0.578
All		0.473		spatial			

Dataset	Uncorr.	KNS NR	SLR	Predictor	KNSNR_ frac	SLR_ frac	SLR_frac_ cor
S and European admixture							
Mexico	0.705	0.438	0.252	Euro	0.621	0.357	0.357
Mexico		0.345		spatial			
USA	0.405	0.056	-0.032	Euro	0.138	-0.080	-0.080
USA		0.690		spatial			
Brazil	0.817	0.267	0.689	Euro	0.327	0.844	0.844
Brazil		0.772		spatial			
Colombia	0.55	0.544	0.417	Euro	0.990	0.758	0.758
Colombia		0.017		spatial			
Sovereign	0.939	0.489	0.009	Euro	0.521	0.010	0.010
Sovereign		0.512		spatial			
All	0.870	0.238	0.185	Euro	0.273	0.213	0.213
All		0.736		spatial			
S, cognitive ability and European admixture							
Mexico	0.626	0.642	0.187	CA	1.025	0.299	0.299
Mexico	0.364	0.388	0.275	Euro	1.064	0.756	0.756
Mexico		-0.042		spatial			
USA	0.782	0.548	0.706	CA	0.700	0.902	0.902
USA	-0.113	-0.209	-0.496	Euro	1.848	4.376	
USA		0.497		spatial			
Brazil	0.634	0.238	0.510	CA	0.376	0.804	0.804
Brazil	0.345	0.175	0.226	Euro	0.509	0.655	0.655
Brazil		0.652		spatial			
Colombia	0.605	0.608	0.178	CA	1.005	0.295	0.295
Colombia	0.020	0.005	0.544	Euro	0.229	27.532	
Colombia		0.038		spatial			
Sovereign	1.047	0.748	0.529	CA	0.714	0.505	0.505
Sovereign	0.108	0.105	-0.427	Euro	0.974	-3.958	
Sovereign		0.273		spatial			
All	0.794	0.515	0.418	CA	0.648	0.526	0.526
All	0.256	0.109	0.044	Euro	0.426	0.173	0.173
All		0.423		spatial			

As can be seen, most values were below 1, meaning that some reduction in the predictive validity was found once SAC was statistically controlled for. There are some oddities. For example, some predictors had negative values after

adjusting for SAC, making their fractions negative as well. SLR gave some peculiar results with betas >|1|.[16] If these are removed, however, the methods agree to some degree on the SAC-corrected values, r=.48 [CI95: .09 to .74; N=24]. Figure 36 shows a scatter plot of the fractions across methods.[17]
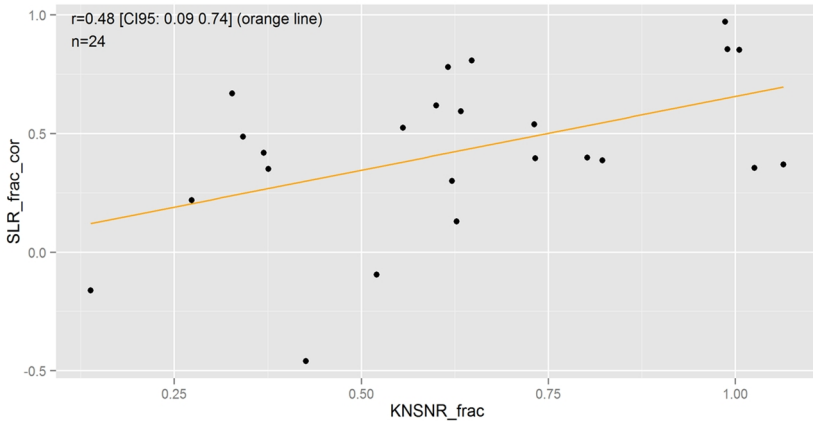
Figure 36. *Fractions of original betas after SAC control by k nearest spatial neighbor regression and spatial local regression. Outliers removed for SLR.*

The mean fraction was .67 for KNSNR and .43 for SLR. Some of the reduction is likely due to a downward bias of the method, which was observed in the simulation study (Kirkegaard, 2015i). In the simulation with the most realistic dataset (dataset 6), the true betas were reduced from .662 to .501 (24%) with SLR and to .548 (17%) with KNSNR.[18] However, the first result was calculated using an older implementation of SLR with different default settings. Using the new implementation, the SAC-corrected value is .605, a 9% reduction. The reason this overcorrection occurs is presumably because there is a random component to the SAC pattern which overlaps with the true cause(s). The SAC-

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[16] We tried a number of other parameter settings to see if we could avoid the peculiar results, including not including the home case, using more cases per cluster and using means or medians as summary measures. None of these produced more stable results. Clearly, more research is needed.

[17] The correlation when the outliers were retained was .02.

[18] This result is not found in the paper because the multiple regression approach to KNSNR was not examined, but it was calculated using the source code for the paper.

control then corrects for the overlapping variance, reducing the estimated betas beyond what controlling for only spurious effects would.

If we use the values based on the simulation results to correct our estimates, in accordance with Hunter and Schmidt's (2004) procedures, the corrected estimates of the true betas would be .81 and .47. We note that there is substantial uncertainty about these estimates, due to the experimental nature of the methods and the number of parameters used in the analysis. With that said, we can average the results across methods and see if any patterns emerge. The reason to average across methods is to reduce the method variance. Note, however, that because we excluded some odd values, the combination of results isn't balanced, a situation which can bias results. Box plots of the results grouped either by model or by dataset are shown in Figures 37 and 38.
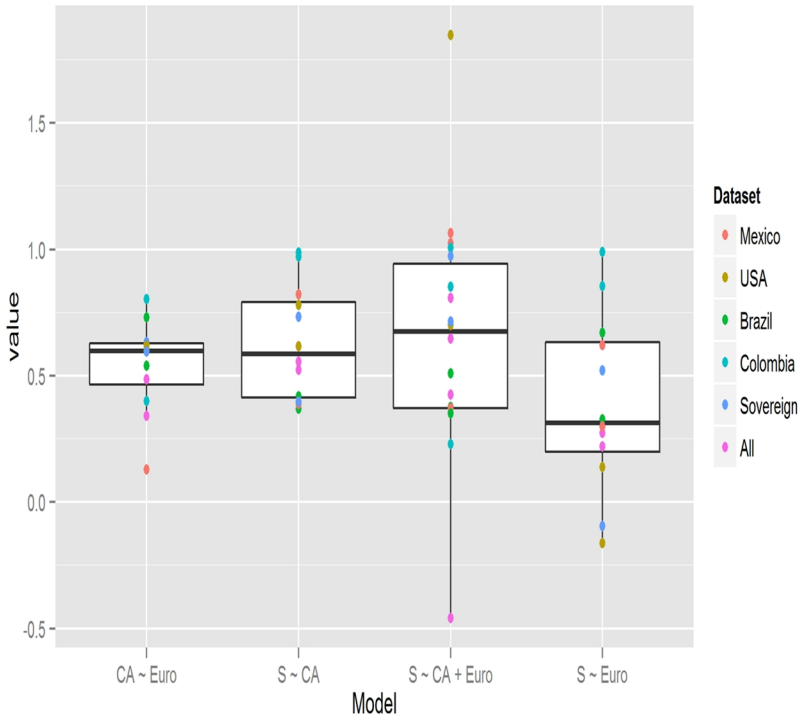
Figure 37. *Box plot of fractional betas by model (x-axis) and dataset (colors).*
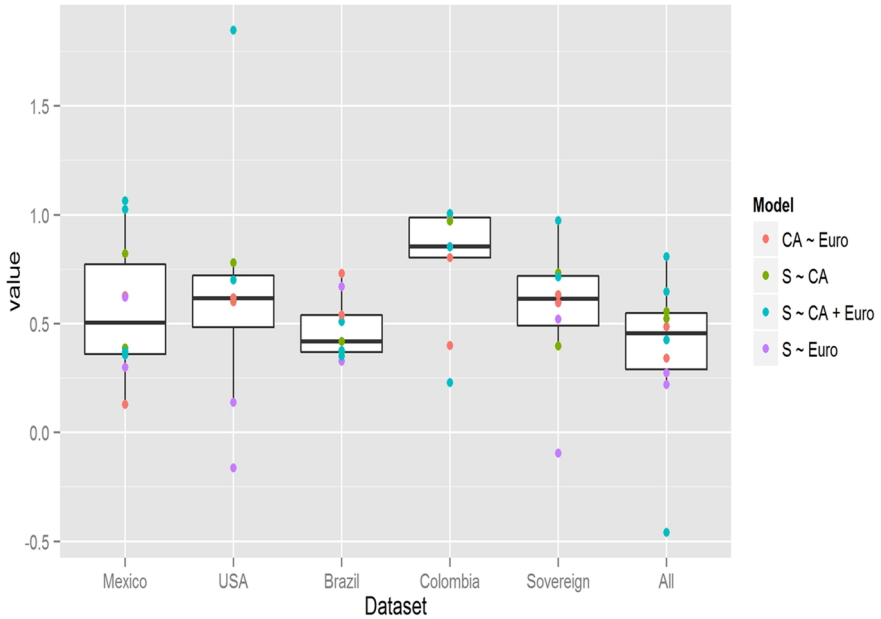
Figure 38. *Box plot of fractional betas by dataset (x-axis) and model (colors).*

Visual inspection shows that there are no strong, consistent patterns in the data. We carried out an ANOVA as well, with results shown in Table 65.

Table 65. *ANOVA results for fractional betas. df, degrees of freedom; CI, confidence interval.*

Predictor	df	Eta²	CI_lower	CI_upper
Model	3	0.094	0	0.220
Dataset	5	0.141	0	0.259
Residuals	45			

The results match the visual inspection, in that both predictors had large confidence intervals that included 0. To sum up, our analysis found that the primary variables – cognitive ability, S and European admixture – showed moderate to strong SAC. Nonetheless, the general relationships between the primary variables were not entirely explainable in terms of SAC.

20. Discussion and conclusion

We set out to determine whether there was a fairly consistent, positive relationship of racial ancestry with both cognitive and socioeconomic outcomes in the Americas and, if so, to determine if measured cognitive ability statistically mediated the association between ancestry and socioeconomic outcomes. 12 zero-order correlational analyses found a substantial positive relationship of European ancestry with both cognitive ability and general socioeconomic well-being. Multiple regression results generally found that European ancestry remained a non-redundant positive predictor when including natural-environmental predictors in the models. Socioeconomic (S factor) scores in the United States were the sole exception. More research is needed on the relationship between socioeconomic outcomes and racial ancestry in that country.

In line with the R~CA-S model, our path analysis and semi-partial analyses indicated that cognitive ability scores can largely statistically explain the association between ancestry and socioeconomic outcomes. We were unable to conduct strong tests of causal pathways, however, as our values were roughly co-temporal. As noted in the text, our S scores were based on 2005 to 2015 data and our cognitive scores were based on measures mostly taken between 1997 and 2013. Also, our ancestry data was based on studies conducted mostly between 2000 and 2015.

The association between racial ancestry and outcomes could be mediated by genetic, cultural or other factors (Rindermann, 2015). As it has been demonstrated that indices of genetic ancestry track an array of inter-generationally transmitted cultural traits (Spolaore & Wacziarg, 2015), the results are consistent with a cultural mediation model. While the association between racial ancestry and outcomes is also consistent with an evolutionary genetic model, to obtain decisive evidence in support of such a model, one would need to identify specific alleles that vary between ancestral groups which are directly (e.g., Piffer, 2015b) or (plausibly) indirectly (e.g., Fedderke et al., 2014) associated with cognitive and/or socioeconomic outcomes at the individual level (Rindermann, 2015).

As noted, the R~CA-S model does not entail a genetic one. As such, it can be investigated while remaining agnostic about the cause of the association between racial ancestry and outcomes. This hypothesis can be further tested by examining the associations between racial ancestry and inter-state outcomes within other countries. The analysis can be improved by including better measures of manifest national/state cognitive ability and by adding, if obtainable, measures of latent general cognitive ability (refer back to the discussion at the

end of Section 2). It can also be improved by obtaining cross-temporal cognitive and socioeconomic data, which would allow one to robustly test causal models.

The R~CA-S model can further be tested by examining the intranational association between ancestry, cognitive ability and socioeconomic outcomes (income, education and other SES indexes) between individuals within SIRE groups. Based on a review of dozens of studies, Fuerst and Kirkegaard (2015) found that racial ancestry was associated with inter-individual socioeconomic outcome differences within admixed populations (e.g., Black Trinidadian and Toboggans) throughout the Americas (e.g., in Brazil, Chile, Colombia, Mexico, Peru, Puerto Rico, Trinidad and Tobago and the United States). Across studies, African and Amerindian ancestry was negatively and European ancestry was positively associated with socioeconomic outcomes. It is an open question, however, as to whether, on this same level of analysis, cognitive ability is robustly associated with racial ancestry and as to whether cognitive ability mediates the biogeographic ancestry-socioeconomic outcome association. There are, at present, a number of datasets which allow for the testing of these hypothesis, such as the US based *Pediatric Imaging, Neurocognition and Genetics* (PING) survey and *The National Longitudinal Study of Adolescent to Adult Health* (Add Health) survey.

As for limitations, we wish to emphasize that our national level cognitive measures were suboptimal. Our intranational level indexes of ancestry were often likewise. Also, measurement error can give problems with multiple regression-type approaches resulting in false positives (Westfall & Yarkoni, under review), and it is unknown how measurement error and the SAC measure and control methods interact. We suspect that better measures will not substantively alter the results, as they generally were robust across different analyses and different measures. Nonetheless, replicating the analyses using better and more fine-grained measures would be worthwhile.

Supplementary material
All data files, source code and figures are available at the Open Science Framework repository: https://osf.io/78nvf/

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21. Appendix A – Main data table

To avoid cluttering the figures with the full names of countries, states and territories, we have used commonly used abbreviated names. For countries we use the ISO-3 standard with some additions for missing values. For intra-country regions, we use common abbreviations. Table 66 lists all the full names and their abbreviations.

Table 66. *List of data abbreviations, full names and groups. ONS = Other non-sovereign countries; Ability = cognitive ability score; S = socioeconomic (S factor) score.*

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
AIA	Anguilla	ONS	0.06	0.94	0.00	74.25	0.768
ABW	Aruba	ONS	0.50	0.00	0.50	76.82	0.786
BES	Bonaire	ONS					
ANT	Netherlands Antilles	ONS	0.15	0.77	0.08	84.4	0.811
ARG	Argentina	Sovereign	0.71	0.04	0.25	85.001	0.819
ATG	Antigua and Barbuda	Sovereign	0.04	0.96	0.00	77.729	0.778
BHS	Bahamas The	Sovereign	0.16	0.79	0.05	72.301	0.788
BLZ	Belize	Sovereign	0.37	0.25	0.38	73.518	0.714
BMU	Bermuda	ONS	0.38	0.58	0.04	87.32	0.908
BOL	Bolivia	Sovereign	0.21	0.01	0.78	82.324	0.686
BRA	Brazil	Sovereign	0.71	0.19	0.10	84.298	0.756
BRB	Barbados	Sovereign	0.14	0.86	0.00	84.065	0.779
CHL	Chile	Sovereign	0.52	0.05	0.43	87.614	0.835
COL	Colombia	Sovereign	0.44	0.17	0.39	83.02	0.731
CRI	Costa Rica	Sovereign	0.49	0.20	0.31	88.438	0.816
CUB	Cuba	Sovereign	0.72	0.20	0.08	97.608	0.761
CUW	Curacao	ONS	0.15	0.77	0.08		
CYM	Cayman Islands	ONS	0.50	0.50	0.00	85.72	0.873
DMA	Dominica	Sovereign	0.28	0.56	0.16	71.98	0.717
DOM	Dominican Republic	Sovereign	0.47	0.42	0.12	74.229	0.708
ECU	Ecuador	Sovereign	0.42	0.06	0.52	80.785	0.73
GLP	Guadeloupe (France)	ONS	0.11	0.89	0.00	83.72	0.827
GTM	Guatemala	Sovereign	0.40	0.07	0.53	79.704	0.666
GUF	French Guiana	ONS	0.40	0.60	0.00	86.6	0.8

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
GUY	Guyana	Sovereign	0.00	0.77	0.23	74.956	0.704
GRD	Grenada	Sovereign	0.12	0.81	0.07	70.96	0.746
HND	Honduras	Sovereign	0.50	0.08	0.42	79.401	0.674
HTI	Haiti	Sovereign	0.04	0.96	0.00	67.554	0.539
JAM	Jamaica	Sovereign	0.11	0.85	0.04	77.035	0.754
KNA	St. Kitts and Nevis	Sovereign	0.08	0.86	0.06	67.572	0.747
LCA	St. Lucia	Sovereign	0.18	0.75	0.08	73.841	0.717
MAF	St. Martin (French)	ONS					
MEX	Mexico	Sovereign	0.42	0.07	0.51	87.317	0.75
MTQ	Martinique (France)	ONS	0.30	0.70	0.00	84.95	0.838
MSR	Montserrat	ONS	0.08	0.92	0.00	79.85	0.641
NIC	Nicaragua	Sovereign	0.57	0.20	0.23	78.941	0.688
PAN	Panama	Sovereign	0.25	0.39	0.36	80.898	0.781
PER	Peru	Sovereign	0.12	0.07	0.81	80.337	0.74
PRI	Puerto Rico	ONS	0.64	0.21	0.15	78.862	0.865
PRY	Paraguay	Sovereign	0.55	0.08	0.37	78.053	0.682
SLV	El Salvador	Sovereign	0.15	0.10	0.75	75.939	0.717
SUR	Suriname	Sovereign	0.40	0.60	0.00	74.141	0.698
SXM	Sint Maarten (Dutch)	ONS					
TCA	Turks & Caicos	ONS	0.09	0.91	0.00	79.26	0.746
TTO	Trinidad & T.	Sovereign	0.24	0.63	0.13	87.065	0.8
URY	Uruguay	Sovereign	0.83	0.09	0.08	88.488	0.837
USA	United States	Sovereign	0.79	0.14	0.07	97.401	0.934
VCT	St. Vincent & Gr.	Sovereign	0.13	0.81	0.07	70.443	0.717
VEN	Venezuela RB	Sovereign	0.56	0.19	0.25	86.394	0.712
VGB	British Virgin Islands	ONS	0.07	0.82	0.11	76.14	0.839
VIR	Virgin Islands (US)	ONS	0.31	0.64	0.04	72.32	0.781
CAN	Canada	Sovereign	0.90	0.06	0.04	100.669	0.935
MEX_AGU	Aguascalientes	Mexico state	0.433	0.060	0.507	92.12	0.784
MEX_BCN	Baja California	Mexico state	0.540	0.063	0.397	87.47	0.765

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
MEX_BCS	Baja California Sur	Mexico state	0.578	0.045	0.377	86.87	0.79
MEX_CAM	Campeche	Mexico state	0.131	0.090	0.779	85.22	0.75
MEX_CHP	Chiapas	Mexico state	0.287	0.027	0.686	80.27	0.655
MEX_CHH	Chihuahua	Mexico state	0.578	0.080	0.342	90.47	0.757
MEX_COA	Coahuila	Mexico state	0.518	0.055	0.428	88.52	0.781
MEX_COL	Colima	Mexico state	0.417	0.081	0.502	91.37	0.785
MEX_DIF	Distrito Federal (Mx)	Mexico state	0.346	0.040	0.608	93.32	0.859
MEX_DUR	Durango	Mexico state	0.505	0.054	0.441	87.32	0.755
MEX_GUA	Guanajuato	Mexico state	0.410	0.027	0.563	87.17	0.736
MEX_GRO	Guerrero	Mexico state	0.206	0.047	0.744	80.57	0.684
MEX_HID	Hidalgo	Mexico state	0.250	0.110	0.640	87.17	0.724
MEX_JAL	Jalisco	Mexico state	0.417	0.081	0.502	90.62	0.764
MEX_MEX	Mexico, the state	Mexico state	0.228	0.078	0.692	88.37	0.739
MEX_MIC	Michoacán	Mexico state	0.344	0.052	0.603	85.07	0.721
MEX_MOR	Morelos	Mexico state	0.265	0.051	0.681	87.62	0.746
MEX_NAY	Nayarit	Mexico state	0.567	0.053	0.380	86.72	0.752
MEX_NLE	Nuevo León	Mexico state	0.540	0.047	0.418	91.52	0.78
MEX_OAX	Oaxaca	Mexico state	0.134	0.020	0.846	80.87	0.682
MEX_PUE	Puebla	Mexico state	0.242	0.066	0.692	86.87	0.713
MEX_QUE	Querétaro	Mexico state	0.330	0.068	0.602	90.47	0.753
MEX_ROO	Quintana Roo	Mexico state	0.224	0.065	0.711	87.77	0.746
MEX_SLP	San Luis Potosí	Mexico state	0.423	0.043	0.535	86.12	0.728
MEX_SIN	Sinaloa	Mexico state	0.567	0.054	0.380	87.02	0.76
MEX_SON	Sonora	Mexico state	0.616	0.028	0.356	87.17	0.778

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
MEX_TAB	Tabasco	Mexico state	0.235	0.058	0.707	81.02	0.746
MEX_TAM	Tamaulipas	Mexico state	0.428	0.047	0.525	88.07	0.769
MEX_TLA	Tlaxcala	Mexico state	0.246	0.088	0.666	85.07	0.738
MEX_VER	Veracruz	Mexico state	0.280	0.068	0.652	85.22	0.711
MEX_YUC	Yucatán	Mexico state	0.316	0.041	0.643	86.87	0.746
MEX_ZAC	Zacatecas	Mexico state	0.449	0.040	0.511	86.87	0.74
USA_AL	Alabama	US state	0.733	0.244	0.022	93.35	0.88
USA_AK	Alaska	US state	0.790	0.063	0.147	96.35	0.903
USA_AZ	Arizona	US state	0.788	0.073	0.139	95	0.898
USA_AR	Arkansas	US state	0.809	0.158	0.033	95	0.875
USA_CA	California	US state	0.743	0.100	0.157	93.2	0.913
USA_CO	Colorado	US state	0.846	0.070	0.084	98.45	0.923
USA_CT	Connecticut	US state	0.827	0.119	0.054	99.95	0.939
USA_DE	Delaware	US state	0.752	0.211	0.037	97.85	0.916
USA_DC	District of Columbia	US state					
USA_FL	Florida	US state	0.749	0.168	0.083	96.2	0.9
USA_GA	Georgia	US state	0.678	0.286	0.036	95.45	0.89
USA_HI	Hawaii	US state				93.8	0.922
USA_ID	Idaho	US state	0.906	0.040	0.054	98.15	0.903
USA_IL	Illinois	US state	0.781	0.157	0.062	97.25	0.917
USA_IN	Indiana	US state	0.864	0.108	0.028	98.6	0.9
USA_IA	Iowa	US state	0.917	0.057	0.026	99.05	0.919
USA_KS	Kansas	US state	0.868	0.083	0.049	99.2	0.911
USA_KY	Kentucky	US state	0.886	0.096	0.018	96.95	0.885
USA_LA	Louisiana	US state	0.684	0.292	0.024	93.5	0.873
USA_ME	Maine	US state	0.942	0.042	0.016	99.5	0.918
USA_MD	Maryland	US state	0.680	0.284	0.036	97.85	0.93
USA_MA	Massachusetts	US state	0.867	0.091	0.042	101.45	0.949
USA_MI	Michigan	US state	0.825	0.150	0.025	96.95	0.906
USA_MN	Minnesota	US state	0.892	0.077	0.031	100.4	0.937
USA_MS	Mississippi	US state	0.654	0.330	0.017	92	0.863
USA_MO	Missouri	US state	0.851	0.128	0.021	98.3	0.897
USA_MT	Montana	US state	0.902	0.036	0.062	99.95	0.906
USA_NE	Nebraska	US state	0.885	0.071	0.044	98.75	0.918

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
USA_NV	Nevada	US state	0.780	0.110	0.110	93.95	0.895
USA_NH	New Hampshire	US state	0.941	0.042	0.018	100.55	0.942
USA_NJ	New Jersey	US state	0.774	0.155	0.070	100.1	0.94
USA_NM	New Mexico	US state	0.714	0.060	0.226	93.35	0.881
USA_NY	New York	US state	0.756	0.172	0.071	97.7	0.927
USA_NC	North Carolina	US state	0.747	0.210	0.043	97.1	0.897
USA_ND	North Dakota	US state	0.905	0.042	0.053	100.25	0.917
USA_OH	Ohio	US state	0.850	0.132	0.018	98.75	0.907
USA_OK	Oklahoma	US state	0.801	0.096	0.102	95.9	0.881
USA_OR	Oregon	US state	0.892	0.050	0.058	98	0.913
USA_PA	Pennsylvania	US state	0.851	0.122	0.027	99.05	0.918
USA_RI	Rhode Island	US state	0.865	0.082	0.053	96.5	0.927
USA_SC	South Carolina	US state	0.717	0.259	0.025	95.75	0.885
USA_SD	South Dakota	US state	0.877	0.043	0.080	99.65	0.91
USA_TN	Tennessee	US state	0.808	0.168	0.023	95.3	0.884
USA_TX	Texas	US state	0.723	0.139	0.138	97.1	0.889
USA_UT	Utah	US state	0.896	0.044	0.059	97.85	0.917
USA_VT	Vermont	US state	0.945	0.040	0.015	100.55	0.934
USA_VA	Virginia	US state	0.765	0.199	0.036	98.6	0.919
USA_WA	Washington	US state	0.874	0.067	0.059	98.75	0.921
USA_WV	West Virginia	US state	0.928	0.060	0.012	94.85	0.88
USA_WI	Wisconsin	US state	0.882	0.085	0.034	99.35	0.922
USA_WY	Wyoming	US state	0.906	0.040	0.053	98.9	0.903
BRA_AC	Acre	Brazil state	0.510	0.160	0.320	79.5	0.679
BRA_AL	Alagoas	Brazil state	0.547	0.266	0.187	77.1	0.681
BRA_AP	Amapá	Brazil state	0.480	0.240	0.280	80.7	0.726
BRA_AM	Amazonas (Br)	Brazil state	0.465	0.138	0.397	79.2	0.685
BRA_BA	Bahia	Brazil state	0.554	0.367	0.079	81.15	0.706
BRA_CE	Ceará	Brazil state	0.758	0.133	0.109	82.2	0.713
BRA_DF	Distrito Federal (Br)	Brazil state					0.819
BRA_ES	Espírito Santo	Brazil state	0.741	0.134	0.125	87.6	0.783

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
BRA_GO	Goiás	Brazil state	0.640	0.240	0.120	81.9	0.786
BRA_MA	Maranhão	Brazil state	0.420	0.190	0.390	77.1	0.654
BRA_MT	Mato Grosso	Brazil state	0.640	0.240	0.120	80.4	0.767
BRA_MS	Mato Grosso do Sul	Brazil state	0.588	0.259	0.153	87.15	0.772
BRA_MG	Minas Gerais	Brazil state	0.601	0.304	0.095	86.7	0.781
BRA_PA	Pará	Brazil state	0.550	0.157	0.292	79.95	0.679
BRA_PB	Paraíba	Brazil state	0.580	0.270	0.150	84.75	0.71
BRA_PR	Paraná	Brazil state	0.710	0.175	0.115	86.25	0.794
BRA_PE	Pernambuco	Brazil state	0.568	0.279	0.153	79.35	0.714
BRA_PI	Piauí	Brazil state	0.580	0.270	0.150	83.25	0.689
BRA_RJ	Rio de Janeiro	Brazil state	0.706	0.192	0.101	84	0.796
BRA_RN	Rio Grande do Norte	Brazil state	0.580	0.270	0.150	82.05	0.723
BRA_RS	Rio Grande do Sul	Brazil state	0.794	0.095	0.110	87.45	0.798
BRA_RO	Rondônia	Brazil state	0.510	0.160	0.320	82.8	0.742
BRA_RR	Roraima	Brazil state	0.510	0.160	0.320	79.35	0.703
BRA_SC	Santa Catarina	Brazil state	0.797	0.114	0.089	87.3	0.815
BRA_SP	São Paulo	Brazil state	0.673	0.220	0.108	86.25	0.805
BRA_SE	Sergipe	Brazil state	0.580	0.270	0.150	82.65	0.713
BRA_TO	Tocantins	Brazil state	0.510	0.160	0.320	79.95	0.721
COL_AMA	Amazonas (Co)	Colombia state	0.31	0.11	0.59	72.97	0.686
COL_ANT	Antioquia	Colombia state	0.45	0.12	0.44	82.87	0.746
COL_ARA	Arauca	Colombia state	0.46	0.08	0.47	82.27	0.72
COL_ATL	Atlántico	Colombia state	0.33	0.26	0.41	79.87	0.743
COL_DC	Bogata (capital)	Colombia state	0.47	0.06	0.47	90.22	0.781

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
COL_BOL	Bolívar	Colombia state	0.30	0.34	0.36	74.92	0.713
COL_BOY	Boyacá	Colombia state	0.47	0.06	0.47	88.12	0.695
COL_CAL	Caldas	Colombia state	0.46	0.07	0.47	84.37	0.754
COL_CAQ	Caquetá	Colombia state	0.46	0.08	0.46	79.57	0.642
COL_CAS	Casanare	Colombia state	0.47	0.06	0.47	84.37	0.759
COL_CAU	Cauca	Colombia state	0.26	0.30	0.44	78.97	0.641
COL_CES	Cesar	Colombia state	0.43	0.13	0.45	78.07	0.679
COL_CHO	Chocó	Colombia state	0.17	0.59	0.24	70.12	0.614
COL_COR	Córdoba	Colombia state	0.30	0.27	0.43	74.92	0.679
COL_CUN	Cundinamarca	Colombia state	0.47	0.07	0.46	87.67	0.733
COL_GUA	Guainía	Colombia state	0.23	0.12	0.65	76.27	0.66
COL_GUV	Guaviare	Colombia state	0.45	0.09	0.47	78.07	0.691
COL_HUI	Huila	Colombia state	0.47	0.06	0.47	83.92	0.708
COL_LAG	La Guajira	Colombia state	0.26	0.19	0.55	74.02	0.636
COL_MAG	Magdalena	Colombia state	0.33	0.26	0.41	73.87	0.672
COL_MET	Meta	Colombia state	0.47	0.07	0.47	84.37	0.732
COL_NAR	Nariño	Colombia state	0.38	0.18	0.44	83.47	0.689
COL_NSA	Norte de Santander	Colombia state	0.48	0.06	0.47	84.67	0.717
COL_PUT	Putumayo	Colombia state	0.38	0.11	0.51	81.52	0.709
COL_QUI	Quindío	Colombia state	0.47	0.07	0.46	83.32	0.784
COL_RIS	Risaralda	Colombia state	0.46	0.09	0.47	85.87	0.771
COL_SAP	San Andrés y Prov.	Colombia state	0.25	0.48	0.27	76.12	0.713
COL_SAN	Santander	Colombia state	0.47	0.07	0.46	88.57	0.749
COL_SUC	Sucre	Colombia state	0.30	0.28	0.42	75.82	0.697

Abbrev.	Full name	Group	Euro %	African %	Amerind. %	Ability	S
COL_TOL	Tolima	Colombia state	0.46	0.06	0.48	82.42	0.715
COL_VAC	Valle del Cauca	Colombia state	0.30	0.34	0.36	82.42	0.759
COL_VAU	Vaupés	Colombia state	0.22	0.13	0.65	74.92	0.655
COL_VID	Vichada	Colombia state	0.30	0.11	0.59	75.37	0.657

22. Appendix B – Path model results

The complete path model terms, from Section 10, are shown below. The output is from the *lavaan* package for R.

Variable	Relation	Variable	Stand. β
Euro	-->	ACH	0.549
Euro	-->	S-factor	0.218
Euro	<-->	Euro	1.000
ParaNH	-->	ACH	-0.283
ParaNH	-->	S-factor	-0.146
ParaNH	<-->	Euro	-0.119
ParaNH	<-->	ParaNH	1.000
Cold	-->	ACH	0.342
Cold	-->	S-factor	0.138
Cold	<-->	Euro	0.568
Cold	<-->	ParaNH	-0.440
Cold	<-->	Cold	1.000
Anglo	-->	ACH	-0.021
Anglo	-->	S-factor	0.307
Anglo	<-->	Euro	0.330
Anglo	<-->	ParaNH	-0.716
Anglo	<-->	Cold	0.556
Anglo	<-->	Anglo	1.000
Tourist Exp.	-->	S-factor	0.051
Tourist Exp.	<-->	Euro	-0.064
Tourist Exp.	<-->	ParaNH	-0.472
Tourist Exp.	<-->	Cold	0.050
Tourist Exp.	<-->	Anglo	0.484
Tourist Exp.	<-->	Tourist Exp.	1.000
ACH	-->	HIV	-0.662
ACH	-->	S-factor	0.327
ACH	<-->	ACH	0.189
HIV	<-->	S-factor	-0.431

Variable	Relation	Variable	Stand. β
HIV	<-->	HIV	0.561
1	-->	ACH	0.177
1	-->	S-factor	0.066
1	-->	HIV	-0.008
1	-->	Euro	0.654
1	-->	ParaNH	0.327
1	-->	Cold	0.558
1	-->	Anglo	-0.337
1	-->	Tourist Exp.	-0.852