Race Differences: A Very Brief Review

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Race Differences: A Very Brief Review

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The nature of race differences, and even the mere "existence" of human races, continues to be a major source of controversy and confusion. This brief review summarizes the empirical evidence about race differences and the conceptual issues related to taxonomy, as well as practical implications for medicine and the social sciences. The review shows that human races are distinctive phenotypically and genotypically, the latter with regard to the frequencies of a very large number (millions) of alleles. Distributions of these traits are clinal rather than discrete, and human races are subject to continuous change across evolutionary time.
Key Words: Human races, Skin color, Allele frequencies, Genome-wide association studies, Admixture, Evolution

Differences between human racial groups are perhaps the most controversial topic in all of the social sciences, with almost every conceivable fact being contested by two or more opposing factions. The matter is also scientifically challenging because a comprehensive account of such differences and their origins involves findings from a large number of scientific (sub)fields including evolutionary psychology, differential psychology, psychometrics, sociology, anthropology, population genetics, genomics, behavioral genetics, history, archaeology, and almost every interdisciplinary field between these. On top of this comes the fact that the topic became heavily politicized in Western countries after World War II. The following account attempts a cautious summary of the current thrusts of the research, which will unavoidably be seen as unsatisfactory by some.

Semantic, ontological and historical status

To begin with, both the current and historical meaning of the word *race* is disputed. The most popular view in the West currently among social scientists is

that *race* denotes a concept of discrete/typological populations in an ancient Greek sense (Platonic/essentialist), and that genomic data shows that such discrete populations do not exist. Hence human races do not exist in any biological sense, but only as (at least somewhat) arbitrary social categories (e.g. James, 2017; Kitcher, 2007; Ousley, Jantz & Freid, 2009; Pigliucci & Kaplan, 2002; Smedley & Smedley, 2005; Sussman, 2014). The contrary minority view is that *race* denotes a subspecies, breeding population, genetic cluster, extended family (or some other biologically-based idea along those lines), and that genomic data shows that these exist, and have or might have important relationships to socially valued phenotypic traits among humans (e.g. Andreasen, 2000; Barnes, 2018; Fuerst, 2015; Levin, 1997; Lynn, 2015; Relethford, 2009; Rushton, 2000; Sarich & Miele, 2004; Sesardic, 2010; Spencer, 2015). In line with standard terminology in philosophy (Miller, 2016), the first view will be denoted the social constructivist view (or sometimes, anti-realist), and the second the realist view ("race realism"). This is not meant to be an endorsement of the realist view as being more realistic in the everyday sense of the word, but only as a descriptive term meaning the reality of something is asserted. Therefore, the difference is essentially semantic rather than substantive.

Fuerst (2015) reviewed 12 surveys of anthropologists, anatomists and biologists, which asked about agreement with statements such as "There are biological races in the species *Homo sapiens*" (see also Lieberman et al., 2004). Agreement with race realism is lower among researchers in the USA and higher in East Europe and East Asia, however, there are substantial numbers of experts with both views in every survey. Furthermore, agreement is higher among physical as opposed to cultural anthropologists, lower in recent years in the US/West[1], and higher among biologists and anatomists than anthropologists. Agreement ranged from 14% to 75% depending on the survey year, exact question, country, and type of researcher. Partly in response to the above compilation, another large US survey was carried out which polled about 1900 anthropologists and included many variant question formulations (Wagner et al., 2017). The patterns of that study replicate those above in that contemporary US anthropologists mostly are to be found in the anti-realist or social constructivist

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1 Working population geneticists in the West have generally avoided the term *race* since it fell out of political favor, opting instead for synonyms or closely related terms such as *genetic cluster, population, genetic ancestry* and so on (Frost, 2014). In medical genetics, the currently preferred term is the somewhat unwieldy *biogeographical ancestry* (Mersha & Abebe, 2015; Shriver & Kittles, 2004; Tishkoff & Kidd, 2004), though this is not to say that this term does not also have its detractors (Gannett, 2014).

camp, but it depends on the specific framing of the question. Similarly, Horowitz et al. (2019) surveyed 301 US anthropologists about various topics. One question included was "The social construct of 'race' has no corresponding biological reality", with which 76% of their sample agreed, and 15% disagreed (9% don't know/other). All in all, we can say that opinion seems to be moving against the realist view, but that there is not yet a consensus level of agreement, even among anthropologists.

There is no non-question-begging way to even write about race differences since using *race* as normally done would implicitly appear to assume a realist position of some sort, while adding scare quotes ('race') would indicate the opposite. This entry does not take a position on the question but uses the normal writing style for ease of reading. For the matters at stake, the ultimate fate of the word *race* is immaterial because the ancestry associations will be there no matter what we call them, and no matter how well typical racial classification schemes are congruent with ancestry variation.

Overview of human populations

There is consensus in the field that when human genomic data is analyzed with methods such as principal components analysis or cluster analysis, certain non-arbitrary patterns can be seen in the data (J. L. Baker, Rotimi & Shriner, 2017; Cavalli-Sforza, Menozzi & Piazza, 1994; Reich, 2018a). Specifically, for persons who don't belong to 'recent migrant' populations, those who are geographically close tend to go together or cluster (in some sense) in the results. Recent migration usually refers to peoples that have moved since 1492, in the post-Columbus period. This date is a somewhat arbitrary but convenient choice since mass migration to the Americas started at that time. There is a large number of mathematical approaches to doing such clustering with no agreement on a single best method (Padhukasahasram, 2014; Yuan et al., 2017). Because of this, results from multiple methods will be summarized. Figure 1 shows the results of a principal components analysis on a large genomic dataset from populations across the world. It is evident there is some patterning in the data related to geographic location.

Principal components analysis works by constructing a new dimension (variable) based on the data such that it 'best explains' the existing data in the sense of having the highest possible variance in common with the input variables (here, variation in genetic loci). This process is usually repeated multiple times, giving a set of principal components. Hence, the first principal component (PC1) summarizes the largest possible amount of the data in a single dimension. Of the remaining variation, PC2 best summarizes that, and so on. In the figure, the two

first dimensions are shown and the subjects are colored by their geographical origin (or origin of their remote ancestors). It is evident that similarly colored persons are usually close to each other. There are some exceptions, however. Mexicans (MEX) are not well separated from Indians (GIH). They are however far apart in genetic space if one considers more than the first two dimensions, but this is difficult to convey in a two-dimensional image.
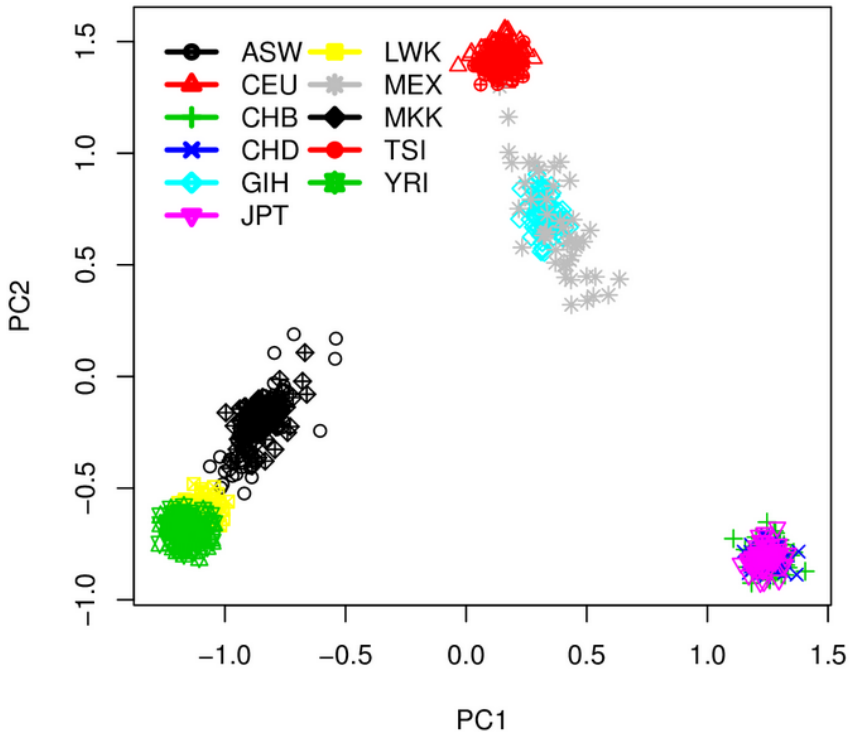

Figure 1. *Principal components analysis of HapMap3 data. Each dot is a person. Axes are the first two principal components of the SNP (single nucleotide polymorphism) data. Populations: ASW = African American in USA; CEU = Central European from Utah, USA; CHB = Chinese from Beijing; CHD = Chinese from Denver, USA; GIH = Gujarati Indians in Houston, USA; JPT = Japanese from Tokyo, Japan; LWK = Luhya Africans from Kenya; MEX = Mexicans from Los Angeles, USA; MKK = Maasai Africans from Kenya; TSI = Italians from central Italy (Toscani); YRI = Yuruba Africans from Nigeria. Figure reproduced from Abraham and Inouye (2014).*

An alternative approach is to construct a phylogenetic tree (dendrogram, tree plot) based on the most likely estimated relationships between the groups in terms of evolutionary divergence. An example is shown in Figure 2.
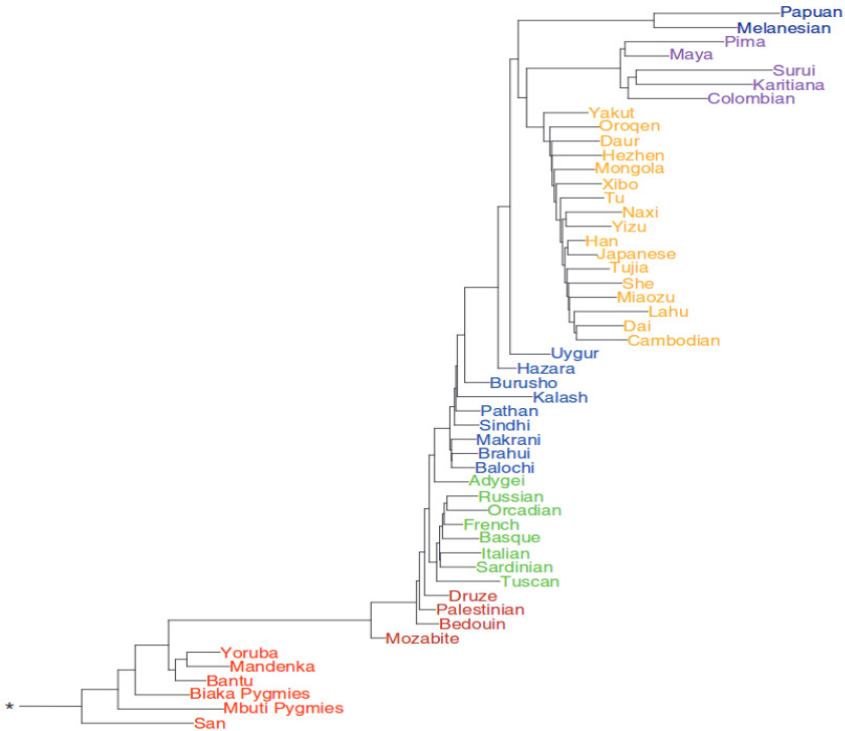

Figure 2. *Dendrogram based on data from 51 populations in the Human Genome Diversity Panel. Colors represent the 7 continental clusters. Reproduced from Jun et al. (2017).*

As before, one can clearly see that geographically close populations tend to 'join up'. Some other relations are more surprising and reflect older migrations that are now mostly forgotten. For instance, northern Indians are related to Europeans, and indeed speak related languages from the Indo-European family (Reich et al., 2009). In general, language relatedness reflects earlier migrations and thus genetic relatedness as well (J. L. Baker et al., 2017). There are various exceptions to this general pattern, such as the Hungarians (a central European population). Their language is related to those of Finns and Estonians (northeast

European populations), who live about 1,500 kilometers (900 miles) away across several national borders and bear little genetic resemblance to Hungarians. Various language isolate populations speak languages (apparently) unrelated to their neighbors, with the most well-known being Basque (located in north of Spain).

The degree to which genetic relatedness mirrors geographical distance can be impressive. Figure 3 shows a scatterplot of the first two principal components with a map of Europe shown on top.
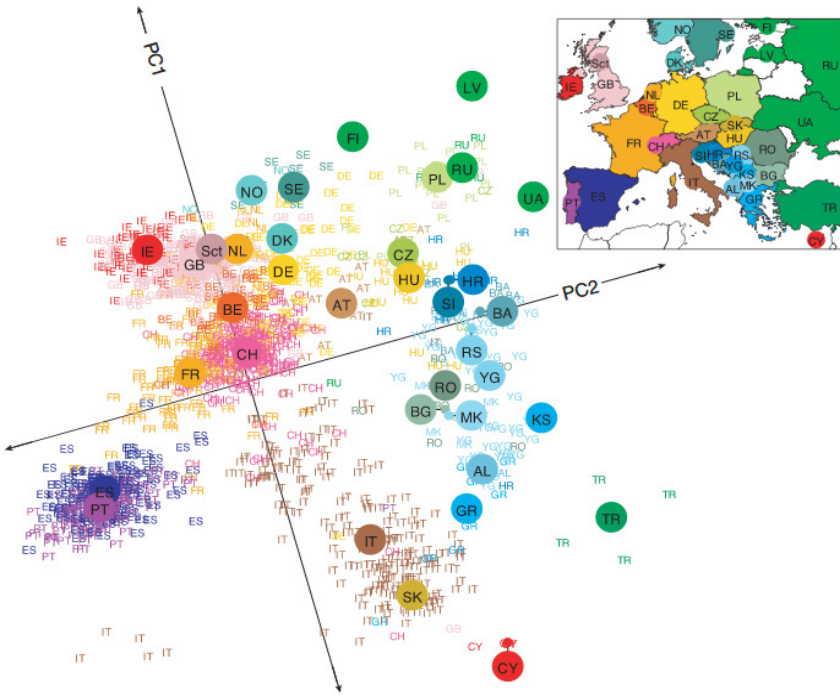

Figure 3. *Map of European populations' genetic distance with a map of Europe. From Novembre et al. (2008).*

The relationship between genetic distance and geographic distance is good but not perfect, thus indicating some recent population movements or inaccuracies in the data. More fine-grained differences can also be detected, including ones inside a single country of relatively homogeneous people. Recent studies have looked at the relationships between geographic location and genetic distances in the British Isles (Abdellaoui et al., 2018; Byrne et al., 2018; Kandt, Cheshire & Longley, 2016; Leslie et al., 2015), Belgium (Van den Eynden et al.,

2018), France (Karakachoff et al., 2015), and the Nordic countries (Athanasiadis et al., 2016; Kerminen et al., 2017).

The two approaches to analyze the data used above hail from two different ways of looking at the genetic data. In the first approach, one is concerned with continuous distances between persons and groups, and there are no rigid boundaries. In the other approach, one thinks of the populations more as discrete units which can be descended from one another. Reality is somewhere in between these two extremes, which is called the clinal vs. cluster debate of human genetic variation (Rosenberg et al., 2005). Both sides recognize the fact that genetic distance between populations correlates strongly with geographic distance (again, for populations that haven't migrated 'recently'). Depending on theoretical assumptions and definitions, finding certain low (high) levels of clinality might indicate the absence (reality) of human races. Figure 4 shows a world map overlaid with relative rates of migration.
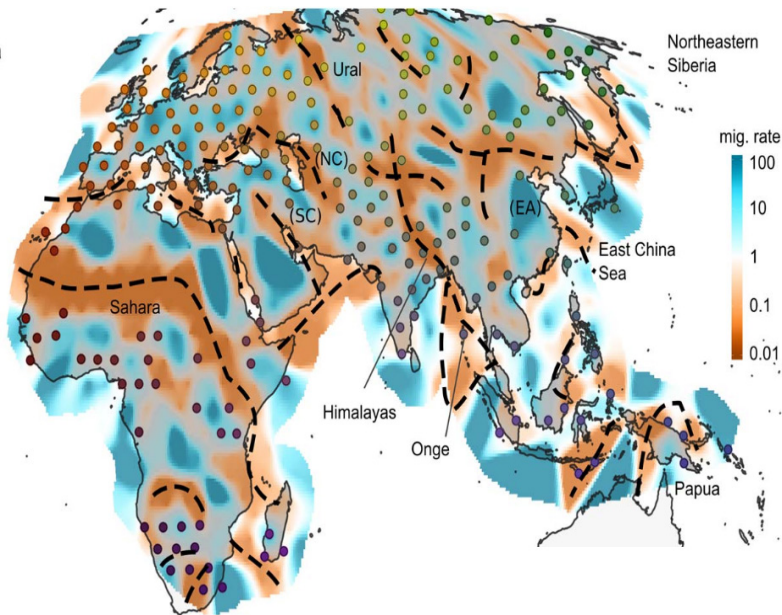

Figure 4. *Large-scale patterns of population structure in the Old World. Color coding shows estimated rate of migration with brown indicating 'troughs', i.e. areas across which there was little human intermixing. Reproduced from Peter et al. (2018).*

While all human variation is clinal to some degree, some areas have more migration (and thus gene flow) than others. The areas with particularly low migration usually correspond to geographical barriers: oceans, mountains and deserts. With regards to the clines vs. clusters debate, the authors of the study that produced the above map concluded:

> Our rugged migration landscapes suggest a synthesis of the clusters versus clines paradigms for human structure: By revealing both sharp and diffuse features that structure human genetic diversity, our results suggest that more continuous definitions of ancestry in human population genetics should complement models of discrete populations with admixture.

This might be taken as a reasonable middle position on the clines vs. clusters debate.

Ancestry estimates and social race

When clustering methods are used to analyze genetic data, the results allow one to score a given individual on their proportion of genetic ancestry — or *biogeographic ancestry* as it is often called in medical genetics (Shriver et al., 2003) — from each cluster identified in the analysis. Such ancestry (or admixture) analysis has since become big business (dubbed consumer genomics or recreational genomics) with multiple competing companies offering ancestry estimation services based on microarray data obtained from customers (Khan & Mittelman, 2018). At the beginning of 2018, about 10 million people had been genotyped this way. Essentially, the customer purchases a small kit (a tube with liquid), deposits spit into it, mails it to the laboratory for analysis, and then 2-3 weeks later receives a report on a website. Ancestry analysis and presentation is somewhat of an art, not exact science (Khan, 2017a,b), but provides valuable information to many people who are curious about their origins. The services can also identify distant or lost family members (most commonly siblings adopted away, or unknown half-siblings). The ability to do this has also led to the arrest of multiple people suspected of serious crimes based on DNA evidence left at the crime scene that for decades could not be matched to a person but which could be found by matching to distant relatives (Regalado, 2018; Wilson, 2018).
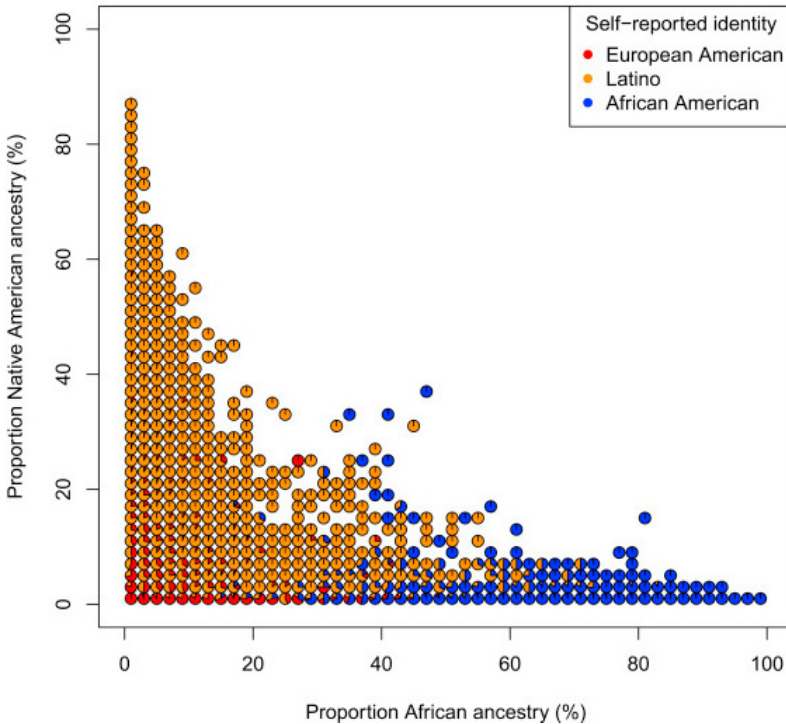
Figure 5. *Individual ancestry estimates for three US race groups with European, Amerindian and African ancestry. Reproduced from Bryc et al. (2015) based on 23andme customer data.*

Figure 5 shows an example of an ancestry distribution for the United States from the consumer genomics company 23andme. Each mini-pie chart represents the distribution of self-reported race/ethnicity for a given combination of genetically measured ancestry. European (White) Americans are almost entirely European on average (about 99%) but Latinos and African Americans show considerable variation, almost every person having some degree of admixture compared to reference populations (Africans in Africa and Amerindian populations without interbreeding since the European conquest). The mixed nature of many human groups, especially in Latin America, and somewhat imperceptible nature of precise genetic ancestry means that typical social labels such as White, Black/African American, Mestizo do not map up exactly with genetic ancestry, and in some cases, not well at all (Ruiz-Linares et al., 2014). Still, the terms are widely used as rough proxies for genetic ancestry, which can

be valuable in situations where genetic data is missing, both in medicine (Bonham, Sellers & Woolford, 2014; Rosenberg et al., 2002) and in other research (Fulford, Petkov & Schiantarelli, 2016; Putterman & Weil, 2010).
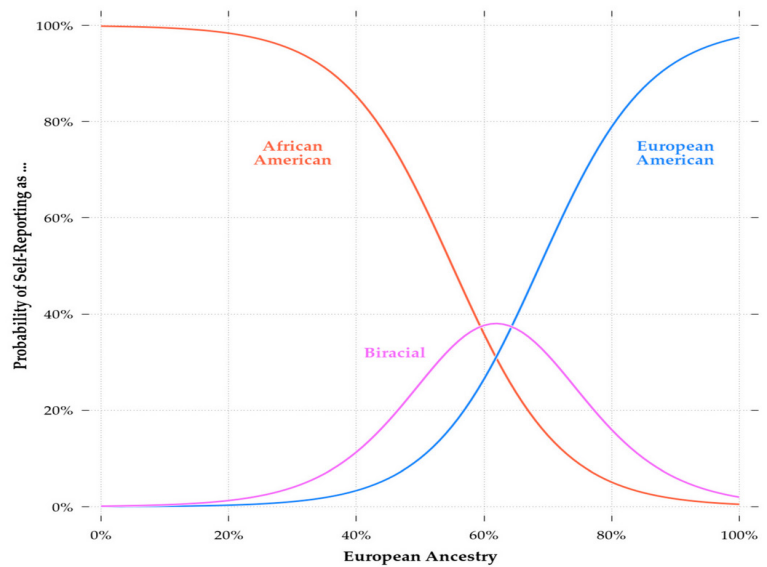

Figure 6. *Self-identified race among a sample of American blacks and whites from Philadelphia. Biracial are those that identified as both black and white. Figure from Lasker et al. (2019)*

Figure 6 shows a sample of Americans and their self-identification as a function of their genetic ancestry. In this dataset, only persons who self-identified as White, Black or both were included. One can see that individuals with nearly 100% ancestry from either group have a nearly (but not entirely) 100% chance of identifying as White or Black. However, for persons of mixed ancestry, the probabilities were intermediate almost but not entirely in line with their ancestry. It would make more sense to have the doubly identifying group exactly in the middle, but instead we see that such persons are somewhat more European genetically than would be expected with a maximum probability around 60%. This seems to be a remnant of the so-called one drop rule (or law) that was present in the USA in past times (Guo et al., 2014); or it simply means that in the US, most individuals identifying as biracial have a white parent who is nearly 100% European and a "black" parent with substantial European admixture. Other

research has shown that a person's visual characteristics (skin color, nose shape etc.) and social status also affect how they self-identify above and beyond their actual genetic ancestry (Ruiz-Linares et al., 2014; Telles & Paschel, 2014).

Physical differences

Physical differences between races are much less controversial than mental ones, at least, insofar as they relate to traits unrelated to social status or other valued traits. The most obvious physical trait related to race is skin color. Figure 7 shows a world map of estimated skin color.
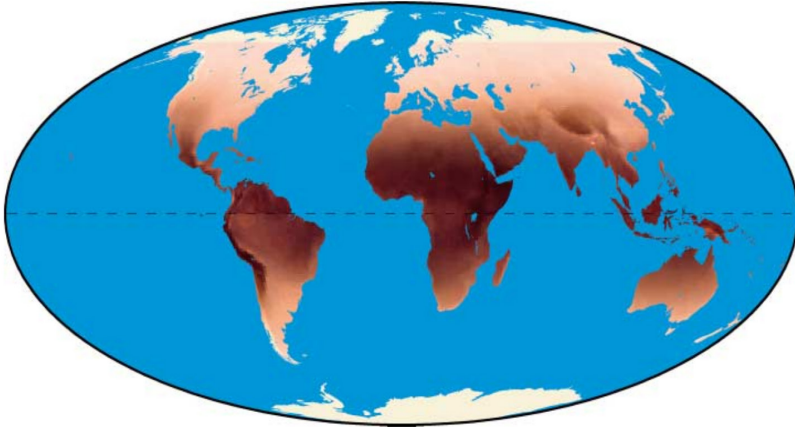

Figure 7. *Worldwide distribution of human skin color, as estimated by Jablonski (2004).*

There is geographical clustering which is related to the amount of UV radiation that people in different parts of the world are exposed to. Other visible traits that strongly covary with skin color and geographic location include tannability, freckles, hair color, hair texture (straight, curly etc.), eye color, lip and nose thickness (J. R. Baker, 1974). A variety of less visible physical differences also exist, and can in many cases be identified from skeletal remains to infer the likely ancestry/race of the decedent (Albanese & Saunders, 2006; Kennedy, 1995). Detailed cranium measures can also be analyzed with the same methods used for large genetic datasets and tend to give similar results (Reyes-Centeno, Ghirotto & Harvati, 2017). Another human trait that shows large race differences is height (NCD Risk Factor Collaboration, 2016). Human height has increased considerably during the last 100 years in almost every country while the between country differences have generally remained large ("A rising tide lifts all boats, but tall sails remain high"). The tallest people in the world 100 years ago (e.g. Dutch

and Scandinavians) are also among the tallest people now, but gained about 10 cm. Meanwhile some populations increased in the relative ranking, such as post-war Japan and South Korea coinciding with rapid economic growth (North Koreans stayed short, however). This temporal relationship between development and height has led economic historians to create large databases of historical data for human height for use in research as a proxy for development, or measure of health of a population (Baten, 2000, see https://clio-infra.eu/Indicators/Height.html).

What is common for the traits discussed above is that few researchers dispute that differences between race groups are the result of genetic differences (though the secular trend in height is attributed to environmental improvements). However, for more socially valuable traits, the relative contributions of genetics, environment and their potential interactions are heavily debated. Since large health datasets began to be collected, medical researchers have noted that race groups differ in various disease rates. Many of the rare diseases have relatively simple genetic causes (single-gene/monogenic/Mendelian disorders), with one or only a few genes involved (Tibayrenc, 2017). The genetic etiology of race differences is not disputed for these, probably because most of them are quite rare (though not sickle cell disease) and the molecular causes are often known to some degree. Populations that have had recent migration-related bottlenecks usually have their own collection of special disorders they acquired from the genetic drift induced by the bottleneck. Ashkenazi Jews, for instance, suffer from higher than average European rates of Tay-Sachs disease, Gaucher's disease, and BRCA-related breast cancer among others (Slatkin, 2004). Other populations with well-known elevated rates for rare single-gene disorders include French speaking Canadians (Scriver, 2001), Finns (Martin et al., 2018), and Amish (Mitchell et al., 2015).

Since the advent of large datasets with SNP (single nucleotide polymorphism, a location in the genome with a variable base) data, it has become possible to estimate the fractional admixture of people with mixed ancestry for large samples of people with known phenotypes. This information can then be related to having a given disease, or the value of some continuous trait (e.g. height, body mass index). Hundreds if not thousands of such studies now exist that find many relationships between genetically estimated ancestry and disease traits, which usually replicate those seen for the corresponding socially defined racial groups (e.g. African Americans, AA). Such associations are often interpreted causally, especially when the most plausible environmental causes were controlled in a regression. For instance:

The role of genetic predisposition in this disparity is supported by two admixture mapping studies of AAs which demonstrated that greater proportion of European ancestry was inversely associated with fibroids in AA women. (Giri et al., 2017; two other examples: Bidulescu et al., 2014; Meigs et al., 2014)

It should be mentioned that some researchers advise against such causal interpretations (Cooper, 2004), on account that the associations with ancestry might just reflect a relevant but omitted environmental variable. More advanced methods based on local ancestry analysis exist, but are not yet as widely used as global ancestry analysis (for a brief introduction, see Shriner, 2013). These methods have been used to examine both diseases (Tibayrenc, 2017) and physical traits that are thought to have evolved recently by natural selection (Chacón-Duque et al., 2018). For instance, Jeong et al. (2014) examined a population of mixed Tibetan and Han (Chinese) ancestry, and found that those with more Tibetan ancestry did better in higher altitudes. Furthermore, local ancestry analysis revealed particular blood-related genes which were much more distinctive than the rest of the genome in comparisons between Han and highland-adapted Tibetans, indicating a causal protective effect of these.

More controversial is the topic of race differences in sports (Dutton, 2015; Epstein, 2014). A commonly noted difference is that West Africans (the ancestors of most Africans in the New World) tend to do very well at short distances while East Africans tend to do well at long distance running. Currently, all top 25 records for the 100 meter dash are held by persons of West African descent (Wikipedia, 2019a), whether born in Africa or to ancestors who emigrated to somewhere. In contrast, the current top 25 male (and female) record holders for half marathons (21 km) all are of Kenyan or Ethiopian descent (Wikipedia, 2019b). It seems difficult to argue that other groups lack an interest in this sport considering the millions of people in Western countries who enjoy running, including competitively (Deaner, 2015). It is also hard to argue that these people don't have the necessary wealth to pursue training and the requisite nutrition. Yet they are being beaten consistently by persons who either hail from or grew up in very poor states, and which are geographically distant. Thus, to many researchers (Dutton, 2015; Entine, 2016; Epstein, 2014) it seems likely that genetics plays some role in these differences.

Psychological differences

Psychological differences between race groups are controversial, perhaps the most controversial topic in all of social science (Horowitz, Haynor & Kickham,

2018; Hunt & Carlson, 2007; Tabery, 2015; Yee et al., 1993). The literature on the topic is enormous and goes back to the 1860s with Victorian English polymath Francis Galton's pioneering work (Galton, 1869). Although there are many ways to categorize psychological traits, I will employ a binary division according to which psychological traits can be roughly divided into cognitive and noncognitive domains (e.g. as used in Kaestner & Callison, 2011). *Cognitive* refers to cognitive ability/intelligence related traits such as working memory, long term recall, 3d spatial ability, verbal fluency, general intelligence and many more (Carroll, 1993). *Noncognitive* refers to everything that isn't cognitive, which is a very heterogeneous remainder category that includes personality traits (both broad and narrow), interests, dispositions, beliefs, and psychiatric diseases. These various traits are of course often statistically related, including across the binary classification, and sometimes strongly enough that one might question their independence. In other cases, the traits themselves admit both cognitive, noncognitive and mixed conceptions, such as with emotional intelligence (O'Boyle et al., 2011). However, to attempt a summary, we must allow for some level of simplification.

Noncognitive differences
Personality

There is broad agreement that personality is multi-dimensional. Several approaches exist that attempt to distill personality variation to a few latent dimensions. The most popular of these is the Big Five/Five factor model/OCEAN approach, which summarizes personality as variation in Openness, Conscientiousness, Extraversion, Agreeableness, and Neuroticism/Emotional Stability (McCrae & Costa, 2006). Social group differences, including racial, in OCEAN traits are difficult to investigate due to implicit group comparisons in the scales, sometimes called the reference group effect (Heine et al., 2002). Most of the data about human personality comes from subjects rating themselves on adjectives or short phrases. These ratings are implicit comparisons to other people, but which other people exactly? When asked whether one often attends parties, the reference frame is some kind of typical party-going rate among other humans in comparison to which one might be above average or not. This problem becomes especially troublesome when one does personality comparisons across countries where most people have little or no experience with other groups (Kajonius & Mac Giolla, 2017; Meisenberg, 2015). Such country-level comparisons of OCEAN traits find sizable gaps, which depending on the demographics of the countries, may or may not reflect racial group differences. The psychometric quality of the measurements is unfortunately low and

confounded with other traits such as intelligence (Kajonius & Mac Giolla, 2017; Meisenberg, 2015; Meisenberg & Williams, 2008; Nye & Drasgow, 2011). Heine et al. (2008) compared national stereotypes (termed national character perceptions) to measures of conscientiousness from self- and other reported personality scales, as well as objective data based on e.g. precision of public clocks and speed of postal workers. They found that the typical personality measures had negative (self report, mean r's -.43 and -.19) and null associations (other report, $r = .06$) with national stereotypes, but that objective measures had sizable positive correlations with stereotypes ($r = .61$). Based on this, one might conclude that the stereotypes were accurate and the self-report personality data is problematic.

To reduce the reference group problem, we might instead consider racial group differences in OCEAN traits within a country. A very large (k = 567) meta-analysis by Tate and McDaniel (2008) found that gaps between African Americans and Whites in the United States were small or trivial in size: openness $d = 0.02$, conscientiousness $d = 0.02$, extraversion $d = 0.18$, agreeableness $d = 0.09$, and neuroticism $d = 0.06$ (where positive values mean whites are higher). Racial group personality differences on other personality inventories have rarely been reported in large samples or meta-analyses and are thus hard to describe. These results were replicated by Foldes et al. (2008) who included data from over 700 studies. While Tate and McDaniel (2008) only covered the black-white comparison, Foldes et al. (2008) covered data from Whites, Blacks, Hispanics, and Asians (heterogeneous as these groups are). Generally, their findings agree with the previous study in that they find overall small gaps. The gaps are not consistent in direction within each trait (e.g. conscientiousness), so that while whites seemed to be favored on one facet (e.g. dependability, $d = 0.05$) blacks where higher on others (e.g. cautiousness, $d = -0.16$). Results were similar for the other comparisons. Exceptions related mainly to small samples, as would be expected by sampling error alone (e.g., Asian-White gap was $d = 0.63$ for agreeableness, but the Asian sample for this was only n = 93).

In general, the findings should be viewed with suspicion in the light of existing stereotypes, which tend to be especially accurate for demographic groups (Jussim, 2018). The question then boils down to: are the stereotypes quite incorrect for personality traits, or are we not measuring personality correctly? The matter requires more research to clarify. It seems unlikely that the existing approach of collecting more self-report data can clarify matters, so it is recommended that researchers try other approaches as well as better statistical methods to clarify measurement invariance (Church et al., 2011; Mõttus, Allik & Realo, 2010; Schmitt, Golubovich & Leong, 2011).

Occupational interests

Occupational (job) interest scales such as the Holland Occupational Themes are used for guidance counseling. These tests attempt to summarize variation in occupational interests with a few dimensions. RIASEC is the acronym of a popular 6-factor model (Lubinski, 2000)—Realistic, Investigative, Artistic, Social, Enterprising, Conventional—though much recent research has used a simpler 2-dimensional model that distills variation down to a people-things dimension and a data-ideas dimension (Su, Rounds & Armstrong, 2009; Tay, Su & Rounds, 2011). Studies using occupational interest scales and racial group are rare, but Schmitt et al. (2011) reported gaps for the usual black and white comparison (in Cohen's d, positive values mean whites are higher): R = 0.31, I = 0.28, A = -0.42, S = -0.51, E = -0.45, C = -0.17. Their design was stronger than usual because they also used multi-group confirmatory factor analysis to guard against measurement bias. The same study, however, also examined OCEAN traits and found only minor differences, the same as in the meta-analysis discussed previously. These results are in need of replication to reach firm conclusions.

Psychiatric traits

Table 1. *Odds ratios of mental disorders by US racial groups, compared to the White prevalence scaled as 1.00. Table from Coleman et al. (2016), who calculated them based on large samples. * indicates the odds ratio was not statistically different (p>.05), all other values differed with p<.001.*

Disorder	Asian	Black	Hispanic	Mixed	Native Amer. & Alaska Native	Hawaiian/Pacific Islander
Anxiety disorder	0.43	0.65	0.83	0.68	1.09	0.47
Any psychiatric diagnosis	0.36	0.69	0.72	0.64	1.03	0.47
Bipolar disorder	0.24	0.65	0.44	0.65	1.34	0.33
Depressive disorder	0.32	0.68	0.70	0.66	0.99*	0.46
Schizophrenia spectrum disorder	0.77	1.98	0.72	0.88*	1.18*	0.67
Other psychosis	0.50	1.13	0.61	0.34	0.80	0.51

Racial differences in rates of psychiatric disorders have long been noted, though they are hard to estimate accurately. Table 1 shows odds ratios of mental disorders from major US racial groups. With the exception of Native Americans who have similar prevalence rates as whites, for most of the disorders in the table, whites have the highest rate (the odds ratios for others are below 1). This pattern may be caused by ascertainment bias with whites being more likely to admit

psychiatric problems, seek help, afford evaluation, or some combination of factors, or simply by them having the highest genetic liability. The main exception to this pattern is the higher rate of schizophrenia and other psychosis seen for blacks, which is a heated topic of debate in the literature (Curtis, 2018).

An increasingly popular view is that psychiatric disorders are mainly a continuation of normal personality variation. In a slogan, abnormal is normal (Plomin et al., 2016). Based on this, one might consider race differences in psychiatric disorders to be measures of race differences in normal personality variation, which could result from evolutionary trade-offs (Del Giudice, 2018; Sikela & Quick, 2018). In line with this approach, the MMPI (Minnesota Multiphasic Personality Inventory), spans both 'non-diseased' personality variation and psychopathology (Sellbom & Ben-Porath, 2005). Evidence going back to the 1970s indicates that blacks outscore whites on some of the scales of this battery (Castro et al., 2008). Unfortunately, the scales lack good descriptive names, so it is not easy to summarize the nature of these findings. The meta-analysis by Hall et al. (1999) indicates that these gaps are small in size, with Cohen d's around 0.20. More controversially, Lynn (2002) reviewed evidence from studies of psychopathy (broadly speaking) and found that East Asians have the lowest levels, Europeans intermediate and Africans the highest. His conclusions have however been contested by others (e.g. DeLisi, 2018). Generally speaking, aside from a few facts such as the higher rate of depression among whites compared to blacks and schizophrenia among blacks compared to whites, there is not much agreement in the field about the relationships between race and psychiatric disorders.

Cognitive differences

Soon after the start of the 1900s when the first modern cognitive tests were invented, a large research effort began with the purpose of documenting and understanding racial gaps in various tested abilities. This was by no means limited to the study of blacks (vs. whites) in USA, but also covered Aborigines in Australia, Maori in New Zealand, Indians in South Africa, and so on (Herrnstein & Murray, 1994; Lynn, 2015; Shuey, 1966). Most of the early studies were very simple since they were chiefly concerned with detecting whether racial cognitive gaps existed, and whether these were due to faulty tests or real differences. The question of measurement bias remains very much a central topic of active research, though the methods employed have markedly improved from the earliest studies. Much current research is interested in the question of national differences in cognitive ability (Jones, 2016; Lynn & Becker, 2019; Rindermann, 2018), which is of course strongly related to the deeper question of racial gaps

due to the varying demographics of countries. Lynn (2015) provides a review of typical IQ scores for each of 12 major racial groups, shown in Table 2.

Table 2. *Mean IQ scores by racial group. All groups measured in their native habitat (e.g. Africans measured in Africa, not in Western countries). IQ normed to UK British norms (white British = 100/15). Based on Lynn (2015).*

Racial group	Brain size (cm^3)	Mean IQ	Number of studies
Arctic Peoples	1443	91	18
Northeast Asians	1416	105	75
Europeans	1369	100	162
Native Americans	1366	86	31
South Asians	1293	84	77
North Africans	1293	83	26
Bushmen	1270	55	5
Sub-Saharan Africans	1280	71	143
Australians	1225	62	17
Southeast Asians	1332	87	51

The values given by Lynn cannot be taken as final estimates because many are based on small, old samples and with unclear levels of test bias. For instance, it is difficult to accept that the true level of intelligence among Australian Aborigines is about 60 without strong evidence of measurement invariance. As far as the author knows, there are no recent, large, advanced measurement studies for this population, and studies from the early 20th century can hardly be considered informative about present-day intelligence levels. A particularly contentious topic is the best estimate of African intelligence, with other researchers estimating either about 80 or about 75 (Rindermann, 2013; Wicherts, Dolan & van der Maas, 2010). Still, however, the numbers are reasonably consistent and quite stable across time and place.

Neither can the values be taken at face value to indicate what one might call genetic level of intelligence. Both sides in the debate recognize the importance of environmental variation, especially for the lower scoring groups. Unfortunately, it is difficult to estimate the relative importance of genetic and environmental factors since these are usually correlated in practice—countries with good nutrition also have high intelligence levels, but which causes what? A few modern genetic

studies have been done on psychological traits and are worth summarizing. Piffer (2019) found that when looking at 26 quasi-national populations, their mean polygenic score for educational attainment/intelligence was correlated .80 to .90 with estimates of intelligence. However, it is well known that simple comparisons of polygenic scores across groups are hard to interpret due to biases in their construction which is mainly based on genotyping of European-origin individuals (Berg et al., 2018; Curtis, 2018; Duncan et al., 2018; Kerminen et al., 2018; Sohail et al., 2019). One can avoid this problem by using ancestry analysis instead, and there are two such published studies. Kirkegaard et al. (2019) studied ~1400 US children and youth and found that genetic ancestry predicted IQ scores even controlling for parental education. Lasker et al. (2019) analyzed data from ~7200 US children and youth, and found that genetic ancestry predicted IQ scores even when including a genetic score for skin color in the regression. So far, however, no study using the stronger design of local admixture analysis has been published, and the aforementioned studies all have limitations that make a substantial role of genetics plausible but not conclusive. They do, however, conform to predictions made by hereditarian researchers back in the 1960s (e.g., Jensen, 1969).

Finally, it is worth noting that experts have not yet reached any consensus on this topic with regards to causation. There exist at least four surveys of experts which asked about causes of racial or national gaps (Friedrichs, 1973; Rindermann, Becker & Coyle, 2016; Sherwood & Nataupsky, 1968; Snyderman & Rothman, 1988). All of these found that a sizable minority believes the gaps to result purely from environmental causes. The average opinion, however, seems to be that there is some unclear mix of genetics and environmental causes. For instance, the most recent survey by Rindermann et al. (Becker, 2018; Rindermann et al., 2016; Rindermann, Becker & Coyle, 2020) was conducted 2013 to 2014 by surveying authors who had published in the journal *Intelligence*, the highest impact factor journal in the field. 86 experts answered a question about the causes of the US black-white intelligence gap. They estimated a genetic contribution of on average 49% (SD = 31%), with 16% believing environmental factors to be the sole cause, and 6% believing genetics to be the sole cause. The large standard deviation of the mean estimate indicates that experts strongly disagree with one another, and the question remains a topic of ongoing scholarly debate.

Conclusion

The present review is necessarily quite limited in scope. However, it is hoped that it has provided a useful summary of the main findings of the many scientific

fields that contribute towards the study of race. Regarding the causes of the many racial group differences noted above, the present author expects that advances in genomics will relatively soon (less than 10 years from now, probably sooner) provide crucial evidence on the relative role of genetics in causing or not causing such gaps. David Reich, a population geneticist with impeccable credentials, explained what we might expect in a recent *New York Times* article (Reich, 2018b):

> Recent genetic studies have demonstrated differences across populations not just in the genetic determinants of simple traits such as skin color, but also in more complex traits like bodily dimensions and susceptibility to diseases. For example, we now know that genetic factors help explain why northern Europeans are taller on average than southern Europeans, why multiple sclerosis is more common in European-Americans than in African-Americans, and why the reverse is true for end-stage kidney disease.
>
> I am worried that well-meaning people who deny the possibility of substantial biological differences among human populations are digging themselves into an indefensible position, one that will not survive the onslaught of science. I am also worried that whatever discoveries are made — and we truly have no idea yet what they will be — will be cited as "scientific proof" that racist prejudices and agendas have been correct all along, and that those well-meaning people will not understand the science well enough to push back against these claims.
>
> This is why it is important, even urgent, that we develop a candid and scientifically up-to-date way of discussing any such differences, instead of sticking our heads in the sand and being caught unprepared when they are found.

For readers interested in more in-depth reviews about race differences, see (more realist view: J. R. Baker, 1974; Fuerst, 2015; Jensen, 1998; Lynn, 2015; Rushton, 2000; Rushton & Jensen, 2005; Sarich & Miele, 2004; Wade, 2014; Winegard, Winegard & Boutwell, 2017; less realist view: Conley & Fletcher, 2017; Evans, 2019; Nisbett, 2009; Nisbett et al., 2012; Sussman, 2014).

Background

   This review was originally written with intent to send to the *Encyclopedia of Evolutionary Psychological Science*, as I was invited to submit an entry for their encyclopedia. However, upon completion, the editor, Todd Shackelford, sent me

an email letting me know that "After further discussion, we have decided to eliminate this entry. You are now free to send to a different publication." This series of events should probably be interpreted in the light of a recent shaming of Shackelford by a journalist, which happened in between the invitation and the submission of the entry, which has made him more wary of taking on "controversial" material (Schulson, 2018; for context, see Carl & Woodley of Menie, 2019 and Woodley of Menie et al., 2018).

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