Information Processing

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Stephen Hsu
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Physicist, Startup Founder, Blogger, Dad

Wednesday, May 14, 2014

What's New Since Montagu?

I wrote this to help a journalist who is trying to understand the current controversy over A Troubled Inheritance, the new book by NYTimes genetics correspondent Nicholas Wade. (Link above goes to earlier discussion on this blog, with additional useful links and figures.)

The anthropologist Ashley Montagu advanced the idea that race is a social construct rather than a biological reality. For Wade, Montagu is a foil against which to benchmark recent advances in human genomics.

> Wade: ... So I decided that I would write a book that explained what we know about race and what the consequences might be, and I think Montagu made a terrible mistake, though I share his motives.

Note the discussion below avoids using the term "race" and focuses instead on groups of humans that share ancestry. The degree of sharing can now be directly measured through genotypes.

> **What's New Since Montagu?**
>
> Two modern humans differ at about 1 in 1000 loci (out of ~ 3 billion in the human genome). There are a few million differences between any two individuals across their entire genome.
>
> A common argument is that 99.9 percent genetic similarity cannot leave room for "consequential" differences. But modern humans and Neanderthals are almost as similar (~ 99.8 percent; we have high accuracy sequences now for Neanderthals), and there are significant differences between us and them: both physical and cognitive. However, because humans and Neanderthals are known to have interbred, we are still part of the same species. (Would it be fair to refer to them as a separate "race"? Is the modern-Neanderthal difference merely a social construct?) Furthermore, this 0.1 percent genetic variation accounts for human diversity encompassing Confucious, Einstein, Shaq and Shakespeare.
>
> Genetic variation is patterned -- two individuals who trace their ancestry to the same geographical region (e.g., two Japanese) will have about 15 percent fewer total differences between them than if we were to compare individuals from widely separated ancestries (e.g., a Nigerian and a Japanese). This means hundreds of thousands of fewer differences between individuals from the same group than for two randomly selected people from different groups.
>
> Gene variants (alleles) which are common in one population (e.g., 90 percent of Japanese have version A) can be rare in another (e.g., only 20 percent of Nigerians have version A). Differences in allele frequencies are correlated across populations. From these correlations one can easily identify a genome (or even a small chunk of DNA as long as it includes many alleles) as belonging to a particular ancestral group. To oversimplify: just ask whether the DNA chunk in question has mostly the variants that are common in one group as opposed to another. Even if the differences in allele frequency are small -- e.g., allele X is 62 percent likely in Japanese, versus 57 percent likely in Nigerians -- once we consider thousands of such alleles the statistical signal becomes apparent. Each individual (or chunk of DNA) can be associated with a particular ancestral group.
>
> Is this genetic difference consequential? Does it make two Nigerians more similar, on average, to each other than to a random European? Obviously, on some superficial phenotypes such as skin color or nose shape, the answer is yes.
>
> But what about more complicated traits, such as height or cognitive ability or personality? All of these are known

to be significantly heritable, through twin and adoption studies, as well as more modern methods.

We can't answer the question without understanding the specific genetic architecture of the trait. For example, are alleles that slightly increase height more common in one group than another? We need to know exactly which alleles affect height... But this is challenging as the traits I listed are almost certainly controlled by hundreds or thousands of genes. Could population averages on these traits differ between groups, due to differences in allele frequencies? I know of no argument, taking into account the information above, showing that they could not.

In fact, in the case of height we are close to answering the question. We have identified hundreds of loci correlated to height. Detailed analysis suggests that the difference in average height between N and S Europeans (about one population SD, or a couple of inches) is partially genetic (N Europeans, on average, have a larger number of height increasing alleles than S Europeans), due to different selection pressures that the populations experienced in the recent past (i.e., past 10k years).

Many who argue on Montagu's side hold the prior belief that the ~ 50k years of isolation between continental populations is not enough time for differential selection to produce group differences, particularly in complex traits governed by many loci. This is of course a quantitative question depending on strength of selection in different environments. The new results on height should cause them to reconsider their priors.

It is fair to say that results on height, as well as on simpler traits such as lactose or altitude tolerance, are consistent with Wade's theme that evolution has been recent, copious, and regional.

Further extrapolation to behavioral and cognitive traits will require more data, but:

1) The question is scientific -- it can be answered with known methods. (I estimate of order millions of genotype-phenotype pairs will allow us to extract the genetic architecture of complex traits like cognitive ability -- perhaps sometime in the coming decade.)

2) There is no a priori argument, given what we currently know, that such differences cannot exist. (Cf. Neanderthals!) Note this is NOT an argument that differences exist -- merely that they might, and that we cannot exclude the possibility.

An honest Ashley Montagu would have to concede points 1 and 2 above.

The second part of A Troublesome Inheritance covers controversial topics such as genetic group differences in behavioral and cognitive predispositions, and their societal implications. Wade is mostly careful to present these as speculative hypotheses, but nevertheless his advocacy leaves him vulnerable to easy attack. What I have summarized above are the incontestable (albeit, in some circles, perhaps still controversial and poorly understood) new results that have accumulated through the last decade of genomic research.

See also Recent human evolution: European height and The Neanderthal Problem.

Note Added: Distinguished evolutionary biologist H. Allen Orr has written a review in The New York Review of Books which I find quite similar to mine.

There was some back and forth between Razib Khan, Orr and Jerry Coyne. I added the comment below.

My take on the book is similar to that of Orr/Coyne: does a decent job of explaining population structure; too much speculation in the second part.

However, I think Orr/Coyne/Wade all miss the most interesting piece of science regarding strength of recent selection: evidence that the N-S height gradient (about 1 SD of difference between the two regions) in Europeans is due to selection pressure. That would constitute an example of fairly strong (in the context of the debate over group differences in humans) selection pressure acting over relatively short periods of time (~ 10 kya or less). I would think this result, if it holds up, might require significant updating of priors for certain people. It also provides a good example of how science in this area should be done: observed phenotype group difference, large data sets (GIANT) teasing out the genetic architecture, tests for selection on associated genetic variants.

http://infoproc.blogspot.com/2014/05/whats-new-since-montagu.html
http://infoproc.blogspot.com/2012/08/recent-human-evolution-european-height.html

Another point, for the cognoscenti: Wade does a good job explaining the difference between soft and hard sweeps. Orr notes that small adjustments of allele frequencies is one of the primary mechanisms for evolutionary change (so nothing new in Wade's discussion; goes all the way back to Fisher), but many many readers, even biologists who aren't in population genetics, don't understand this point very well. So reading that section in the book would increase understanding for a large number of people.

35 Comments information processing Curt Doolittle

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Peter Connor • 5 years ago

Really Prof. Hsu, the "blank slate" hypothesis of Ashley Montagu (aka Israel Ehrenberg) and Marxist crooks like Stephen Jay Gould has absolutely zero scientific support at this point, as your work and BGI's is continuing to establish, along with rapidly developing genetic research on all fronts. For example, on the vital but academically toxic subject of intelligence, the very significant differences between various groups of people evolving in different environments, are highly correlated with statistics such as GDP/capita and scientific achievement. In the real world, it is game over for these politically motivated academics, but in academia we must assume that the witch hunts will continue for awhile.

8 ^ v • Reply • Share ›

Emil Kirkegaard • 5 years ago

There is already evidence of racial differences in g at the allele level. See:
http://openpsych.net/OBG/20...
http://openpsych.net/OBG/20...

and

Davide Piffer - Factor Analysis of Population Allele Frequencies as a Simple, Novel Method of Detecting Signals of Recent Polygenic Selection: The Example of Educational Attainment and IQ, Mankind Quarterly, Winter 2013.

6 ^ v • Reply • Share ›

Paul • 5 years ago

The way agenda-driven scientists mislead the public with the "99.9%" figure is absolutely shameful. Obviously in most everyday situations a difference of .1% would be trivial (e.g., most people wouldn't be too concerned about a .1% pay cut), and people like Gould et al. exploit that. But any honest person would of course mention (as you did) that that 0.1% of difference a) amounts to a large number of base pairs and thus b) *could* have significant implications given the function of the genetic code (even a single point mutation can be lethal etc.)

It seems as though Wade's book is being more or less ignored, much as Unz's article was a few months ago. This doesn't surprise me. In my experience, most people are highly averse to talking about (or even thinking about) these topics.

6 ^ v • Reply • Share ›

efalken • 5 years ago

you should read the review by Jerry Coyne, a guy who once wrote that as an evolutionary biologist he finds human evolution boring, which I really can't believe. He has this interesting ending:

"I am not absolutely opposed to all work on genetic differences in behavior between ethnic groups, populations, and sexes. That is a kind of scientific taboo which, as Steve Pinker has noted, has been enforced by social opprobrium based on the possibility of racism or sexism. I think the proper stand is that it's okay to study those questions that are interesting (but make sure you ask yourself why you find them interesting), and realize that a). we don't know the outcomes, and b). the fundamental equalities of all groups and all sexes don't depend on the results of such analyses."

So, it's OK to study as long as you first check whether it's politically correct, then admit you don't see anything and everyone's basically the same. Science!

http://whyevolutionistrue.w...

5 ^ | v • Reply • Share ›

steve hsu Mod ➚ efalken • 5 years ago

"... the fundamental equalities of all groups and all sexes don't depend on the results of such analyses"

I think he means that fundamental *rights* of individuals should not depend on the outcomes on group differences. I agree with this.

5 ^ | v • Reply • Share ›

efalken ➚ steve hsu • 5 years ago

I think he's being very disingenuous, because obviously your interpretation is completely reasonable, and I'm not aware of any serious researcher who would deny that (excepting maybe philosophers like Peter Singer who has stated babies should have less rights than some animals). So, interpreted that way it's indubitable.

If you've read enough of him, however, Coyne means all human classifications are the same on any trait that's important (eg, not skin color or epicanthic fold or genitalia). All human IQ researchers like Lynn, Wade, Murray, Rushton, and Jensen emphasize repeatedly that rights and human dignity are irrespective of IQ or any other trait, and they get labeled as crypto white supremacists all the time, so that statement as you interpret it is clearly not needed if that is its precise meaning.

4 ^ | v • Reply • Share ›

JayMan ➚ efalken • 5 years ago

I have a comment there that awaits approval. If it takes too long, I'll put it on my blog...

1 ^ | v • Reply • Share ›

Emil Kirkegaard ➚ efalken • 5 years ago

You are very wrong about Singer. He specifically wrote hard support for the above interpretation in his book Practical Ethics. It's in chapter 2.

^ | v • Reply • Share ›

efalken ➚ Emil Kirkegaard • 5 years ago

I thought he had an argument that debilitated humans, via injury or deformation, were less valid than some higher-functioning animals. It was meant to show there's nothing qualitatively different about humans. In his mind I think he meant to elevate animals, not bring down humans, but clearly you can see how this might not work as planned.

1 ^ | v • Reply • Share ›

Guest ➚ steve hsu • 5 years ago

That's how I read it, and that's what I would agree with as well.

^ | v • Reply • Share ›

Richard Seiter • 5 years ago

Readers of this blog interested in this topic and looking for background might find this course (underway now) of interest:
https://www.coursera.org/co...
The instructor is at U Minnesota (home of a notable twin study):
http://www.psych.umn.edu/pe...

Unit 2 is starting in on the MZ/DZ twin height and IQ scatter plots ;-)

This 2007 seminar syllabus is old but might also be of interest:
http://www.psych.umn.edu/as...
There is a version of this seminar running now, but I could not find the materials.

2 ^ | v • Reply • Share ›

BobSykes • 5 years ago

Cavali-Sforza et al's "The History and Geography of Human Genes" demonstrates (despite the Galilean disclaimer) that there are at least 30 distinct human races, and the difference between some of the race rises to the species level. Consider Pygmies and Eskimos. No honest taxonomist would group them into a single species, a genus yes.

The Dobzhansky-Mayr biological species definition applies at most only to animals, and even there most practicing taxonomists use other definitions. Hence we have dogs and wolves and coyotes, all of which interbreed in the wild.

2 ^ v • Reply • Share ›

Victor • 5 years ago

Geneticist Bryan Sykes, author of “The Seven Daughters of Eve,” used mtDNA to identify seven European-based haplogroups he referred to as “clans,” because each person whose DNA fell into one of these haplogroups shared a common female ancestor with everyone else in the same haplogroup. He describes this research in his later book, “Saxons, Vikings and Celts,” on pp. 102-107. The seven were labeled H, T, J, X, V, K and U. According to Sykes, “Over 95% of native Europeans are in one of the seven maternal clans.” The ages of these clans were estimated as ranging roughly between 45,000 ya to 10,000 ya, the estimated date of the period during which each clan “matriarch” was thought to have lived.

He then attempted to determine where each of these “matriarchs” had lived. Using a sampling of haplotypes from all regions of Europe, he was able to determine, for example, that haplogroup V (he named it Velda) “reaches its highest frequency in two places — northern Spain and among the Saami of northern Scandinavia.” Since V “has accumulated far more extra mutations in Spain than in Lapland,” he tentatively decided to place its point of origin in northern Spain, roughly 17,000 ya.

see more

1 ^ v • Reply • Share ›

Jason Ko • 5 years ago

There seems to be some excitement about the Klotho gene (specifically the VS allele) which has been found to have quite a large effect on cognitive traits in humans of all age groups (it was studied to see if it would protect against age-related cognitive decline as it had similar effects for cardiovascular health). Has the BGI cognitive genome project found any comparable results yet (or when do you think the scientific community will be able to see some of your results)?

The study on the aforementioned Klotho-VS allele:

http://www.cell.com/cell-re...

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efoss • 5 years ago

I haven't read the book, but I enjoyed this review by an evolutionary biologist whom I admire. A key quote:

"Knowing that natural selection has occurred, in some cases recently, but being unable to be more specific leaves a huge void – and it is into this void that Wade has inserted himself. He spends the first half of his book summarizing (albeit it inaccurately and incompletely) a decade of huge advances in human genomics, but then shifts abruptly from science to speculation.

In making the leap from the broad to the specific – from signature of natural selection in the human genome to explanations of the industrial revolution, Jewish Nobel Prizes and political turmoil in Africa and the Middle East – Wade tries to paint himself as a courageous scholar, going places with modern evolutionary biology that scientists WILL not go. But the truth is that scientists don’t go there, not because we are afraid to, but because we CAN’T. The data we have before us simply do not allow us to reconstruct human evolutionary history in this way."

Eric

-Eric

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steve hsu Mod ➚ efoss • 5 years ago

I agree with the part of Eisen's review that you quoted. I think he's a bit harsh on Wade in the remainder, but this is mainly a question of taste. How much speculation should someone be allowed, assuming they deliver explicit "THIS IS SPECULATION -- NO CONCLUSIVE EVIDENCE YET" warnings to the reader?

Reply • Share ›

Lemongrab • 5 years ago

Steve, when you say recent selection pressure how recent is recent ?
A number of non-professional commentators seem to be taking the general point you make above to suggest that meaningful changes to complex polygentic traits can happen very quickly, less than 1000 years, or even less than 500 years. As far as I understand, from reading Falconer's quantative genetics, this is really a maths question (to which some inputs are unknown) but changes on an approx 10,000 year scale seem much more likely than really rapid change (taking into account about population size and fitness). Do you have a prior on how fast this type of change can be in practice.

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steve hsu Mod ➚ Lemongrab • 5 years ago

http://infoproc.blogspot.co...

It all depends on selection pressure, assortative mating, etc. which no one can really calculate reliably in the deep past.

I would say ~1ky is very fast while ~10ky is easily plausible.

Poor Fisher, Kimura, Falconer, et al. So little of their theoretical work was testable. Only now is good data starting to become available -- we'll see big advances in our understanding of human evolution in the coming decades.

1 Reply • Share ›

Lemongrab ➚ steve hsu • 5 years ago

thanks

Reply • Share ›

Victor • 5 years ago

On the Eupedia website (http://www.eupedia.com/euro...,
we find a breakdown of European mtDNA haplogroups from a somewhat different perspective. (This one was last updated in 2013, so I'm assuming it's more up to date than Sykes' findings.) If you click on the link for haplogroups H&V, you'll find the following summary:

"H1, H3 and V are the most common subclades of HV in Western Europe. H1 peaks in Norway (30% of the population) and Iberia (18 to 25%), and is also high among the Sardinians, Finns and Estonians (16%), as well as Western and Central European in general (10 to 12%) and North-West Africans (10 to 20%). H3 is commonest in Portugal (12%), Sardinia (11%), Galicia (10%), the Basque country (10%), Ireland (6%), Norway (6%), Hungary (6%) and southwestern France (5%). Haplogroup V reaches its highest frequency in northern Scandinavia (40% of the Sami), northern Spain, the Netherlands (8%), Sardinia, the Croatian islands and the Maghreb. It is likely that H1, H3 and V, along with haplogroup U5, were the main haplogroups of Western European hunter-gatherers living in the Franco-Cantabrian refuge during the last Ice Age, and repopulated much

see more

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steve hsu Mod ➚ Victor • 5 years ago

Victor, you seem well-intentioned but confused about the sense in which individuals "cluster" into groups by genotype. These posts might help:

http://infoproc.blogspot.co...
http://infoproc.blogspot.co...

Old ideas about mtDNA, matrilineal lines, haplotypes, etc. don't capture the essence of the matter: there is a sense in which genome X is more similar to Y than to Z. Just count the number of places where the G,C,T,A base pairs differ. Visualize this geometrically by converting the number of differences into a Euclidean distance (in a very high dimensional space). Then you get clusters (see figures, etc.), and they correspond almost perfectly to self-identified race (Risch et al.)

Two individuals in the same cluster are *genotypically* more similar to each other than they are to individuals in other clusters. What this means in terms of *phenotype* is something we are still working out...

3 ^ v • Reply • Share ›

Victor ➚ steve hsu • 5 years ago

First of all, Steve, the analysis of mtDNA and Y based haplotypes and haplogroups is by no means "old" or outdated. It is in fact the only means we have of researching ancestry with any degree of accuracy. Most people, including Wade, associate "race" with ancestry, and the study of the haplotypes is still the best way to test the validity of that association. And as should be clear to you by now, it is in fact not valid. Human ancestry is far too complex to fit the racial stereotypes.

The clusters you've presented represent a very different, far more more general and hazy approach, which may well be valid in its own right, and does indeed strongly suggest geographical clustering, but calling it "racial" would be inaccurate, since, as we've seen, ancestry, as revealed by the haplogroups, is a far more complex and problematic matter than the simple clustering of "genes" by similarity.

According to the beautifully colored and fascinating pc graphs you display, the Hadza would represent a "racial" grouping fully comparable with all the others. Does that mean a new race has been discovered? Another problem is that Native Americans are represented in a different cluster than East Asians, which is NOT consistent with the traditional three-part grouping of the major races into Negroid, Caucasoid and

see more

1 ^ v • Reply • Share ›

steve hsu Mod ➚ Victor • 5 years ago

I'm really not interested in arguing about the meaning of a term like "race" -- it is used quite differently by cultural anthropologists, biologists, the man in the street, etc. Consequently it has become an impediment to understanding.

But we can still make well-defined statements such as "Allele frequencies tend to be more similar between two Nigerians than between a Nigerian and a Korean" or "The number of base pair differences between two Nigerians is less than between a Nigerian and a Korean". These are both now known to be true, but that was not the case 30 or 50 years ago. If you want to argue with me about what I mean by Korean or Nigerian then you are really just diverting the conversation, because those terms are about as well defined as "cat" or "car".

I don't want to make any strong claims about the *consequences* of these observations until the science is on firmer footing. It's an important first step to note that some claims about *genetic* level variation in humans (the Montagu/Lewontin-type claims still taught in university classes) turned out to be incorrect.

2 ^ v • Reply • Share ›

Victor ➚ steve hsu • 5 years ago

OK, good. If we're talking about allele frequencies and base pair differences then we are talking genetic science and that's fine. The problem is when people take for granted that these scientific terms can be applied to race, or that they somehow confirm that racial categories are scientifically meaningful. It's an easy trap to fall into and unfortunately it then confirms for a great many that their racial prejudices are justified. I tend to agree about Montagu and Lewontin, at least as far as their most publicized arguments are concerned. But not everything they wrote can so easily be dismissed.

2 · Reply · Share ›

Avatar This comment was deleted.

Victor ➚ Guest • 5 years ago

It's not the similarity that's the issue. It's associating such clusterings with race that's the issue. There are all sorts of morphological and genetic clusterings that can be produced from the data, and on many different levels. And an individual who appears in one cluster may appear in several others as well.

Too many people are too eager to associate such clusterings with races. But race is a far more rigid and circumscribed notion than genetic clustering, which is complex and multi-faceted.

It's certainly true that as far as "negroid", "mongoloid" and "caucasoid" are concerned, it does seem all too easy for the average man on the street to tell the difference. That's largely a reaction to morphological differences based to some extent on meaningful biological distinctions but also misleading stereotypes. If you could actually view a breakdown of some, let's say "mongoloid" individual's genome, you'd see how complex that person's ancestry is and how difficult it is to pigeonhole. Yes, he might cluster as East Asian in one study, but as Polynesian in another. Some of his ancestors might be Asian, but others might be Native American. He might look primarily E. Asian, but might well be primarily European.

And once we get away from the three most commonly cited "races," then things get really complicated. You might think you can spot a Mexican by the way he looks, but give him a different haircut, dress him in a banker's business suit and teach him the King's English, and he would probably look very European to you. And how many people of Native American descent can you spot I wonder? If you look at lots of photos of Native American faces made during the 19th century, when very few were of "mixed race," you'd see a wide variety of different types, many of which look Caucasian, at least to me.

2 · Reply · Share ›

Avatar This comment was deleted.

Victor ➚ Guest • 5 years ago

"I read a post by Steve Hsu in which he explained that there are 10^30,000 human genomes (under a set of assumptions). One can measure the distance between any two of these genomes by calculating the base pair difference at each gene, summing along the way, and the final sum is the genetic distance between the two genomes."

Well, first of all, that's only according to one research model. I can almost guarantee that another group analyzing the same data but using a different method would come up with different results. Secondly, in STRUCTURE you get a different clustering depending on the value of K. And sure you can look for a clustering that fits your hypothesis (confirmation bias), but there is no rule in STRUCTURE telling us which of these clusterings is the "correct" one. Thirdly, STRUCTURE uses nuclear DNA, which isn't capable of distinguishing male from female lineages and thus gives you only a vague result in which much information is lost. Phylogenetic trees based on haplotypes (mtDNA or Y chromosome) are

is lost. Phylogenetic trees based on haplotypes (mtDNA or Y chromosome) are much more accurate with respect to ancestry and in fact can identify the common female, or male (but not both) ancestor of any two people. According to Brian Sykes, there are 7 (or possibly 8) unique female ancestors of all Europeans. And

see more

1 · Reply · Share ›

botti ➚ Victor • 3 years ago

I think anthropologists like George Gill have written about this in terms of skeletal features in attributing race.

· Reply · Share ›

Oni ➚ Victor • 4 years ago

It's 9 months late that I'm reading this, but I thank you for your scientific insight on these matters. I feel it is the default predilection for humans to legitimize race and preserve traditional institutions that racism supports.

There are significant problems with separating Homo sapiens into various subspecies, and you have mentioned some. There's even more trouble grafting those subspecies onto traditional categorizations of "race". And even more trouble finding scientific value to some of these categorizations, as differences always occur statistically, not absolutely.

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Stevie Mac • 5 years ago

Questions:
1) you talk about allelles that occur in 20% of Nigerians and 90% of Japanese or 62 vs 57%. Are there allelles that occur close to 100% in one race an 0% in others or even 60% in one and 0% in others? How common are such allelles? I notice that pretty much all Black people have a certain kind of hair that all Europeans don't have.

2) Will the genetic architecture of cognitive ability be fully understood, including non-additive effects, such that it will be known with a high degree of certainty that one population is genetically advantaged and has a higher genotypic IQ than another? If only the linear effects are known, people may claim that one population- population y, although appearing to be less genetically endowed for IQ when only linear effects are taken into account, gets more of an IQ boost from non-additive effects than population X.

· Reply · Share ›

steve hsu Mod ➚ Stevie Mac • 5 years ago

1) Some alleles are (nearly) fixed differently (~ 100% frequency) in different populations. Wade gives some examples and discusses hair, skin color, etc. Buy the book! (Or use Google.)

2) Additive variance for cognitive ability is probably larger than non-additive. If I had to guess I'd say ~ 0.6 / 0.2 for additive and non-additive contributions to total h2 (error bars about 0.1 for each number). Given enough data we may be able to get the non-additive part as well (something I am working on ;-)

6 · Reply · Share ›

Stevie Mac ➚ steve hsu • 5 years ago

thanks. Without knowing the non-additive part, would it be likely that the non-additive effect (or additive:non-additive ratio if you like) would be the same size in all populations or is it a real possibility that the non-additive effect size could differ between populations? I'd intuitively think it would be the same...

1 · Reply · Share ›

steve hsu Mod ➚ Stevie Mac • 5 years ago

unknown territory ...

2 · Reply · Share ›

Stevie Mac ➚ steve hsu • 5 years ago

Here be dragons.

1 · Reply · Share ›

Peter Connor ➚ Stevie Mac · 5 years ago

The notorious MAO-A 2 copy "violence" gene is 5% in Africans, .1 % in Europeans….

1 · Reply · Share ›

Victor · 5 years ago

Ironically, the most controversial part of Wade's book, the notion of biological determinism with respect to values, intelligence and behavior, is the most scientific, because such hypotheses can indeed, at least in principle, be tested, as you say. Where he goes wrong is 1. in assuming that biological determinism is equivalent to racial determinism, a huge and unsupportable assumption; and 2. confusing correlation with causation, a fatal, though not uncommon error. There is no real scientific evidence for most if not all of the hypotheses he proposes, only confirmation bias by a closet racist.

The least controversial part of Wade's book, his attempt to demonstrate that race is indeed a meaningfully scientific principle and not a social construct, is, on the other hand, wrong in principle, and no amount of evidence can ever support it. I say that as a retiree with no fear of losing my position (currently I have none). I am also a card carrying member of the anti-political correctness league, and in fact a climate change skeptic (though not a denier, just a skeptic). Thus not your usual knee jerk liberal.

The reason so many professionals in the social sciences tend to be impressed by the evidence he's offered for the acceptance of "race" is that most of us have only the sketchiest notion of how the genetic research operates and what it means. I'll be presenting some examples in my next two posts that should clear that up. Even without such examples, however, the problem will be clear once you contemplate the difficulty of actually defining "race" in scientific terms. I know very well what a haplotype is. I know what an allele is. Etc. And yes, human populations can be grouped on the basis of genetic evidence. But that in itself tells us nothing about the validity of the term "race." Far too many simply associate one with the other, a huge mistake, as I will demonstrate.

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Stephen Hsu

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