

Lewontin's argument

Posted on [January 26, 2012](#) by [gcochran9](#)

Richard Lewontin argued that since most (> 85%) genetic variation in humans is within-group, rather than between groups, human populations can't be very different. Of course, if this argument is valid, it should apply to any genetically determined trait. Thus the variation in skin color within a population should be larger than the skin color differences between populations – except that it's not. The difference in skin color between Europeans and Pygmies is large, so large that there is no overlap at all. No European is as dark as the lightest Pygmy (discounting rare cases of albinism).

As it happens, we now know quite a lot about the genetic architecture of skin color. It is somewhat unusual, in that a handful of alleles shaped by recent selection account for light skin in Europeans and Asia (different alleles in Asia than in Europe). So, is skin color an exception? Maybe Lewontin's argument works on highly polygenic traits like height, that are influenced by many alleles of small effect. But no! Pygmies are notoriously short, while Bantus are about the same height as Europeans. We know that in a mixed population (part-Pygmy and part-Bantu) height goes up with the percentage of Bantu ancestry. So, there is a big, non-environmental difference in height (several standard deviations), even though height (itself highly heritable) is influenced by many genes of small effect.

So Lewontin's argument does not work. You can't predict group differences in trait values from the distribution of genetic variation – except in the limiting case where all of the variation is within-group, which means that the two populations are genetically identical. You know you can't apply it to other traits, whether they are influenced by a few genes or by many. It's not essential to know why it doesn't work – the mere fact that its predictions don't come true is reason enough to discard it.

We do know why, though. Selection generates correlated genetic differences. Selection for increased height causes changes in the frequency of many alleles, in principle at all loci that influence height, although that is still a small subset of the genome. What matter is the difference in that subset: the overall distribution of genetic variation tells you nothing. Moreover, imagine that in the ancestral population, there were two alleles for each of those loci – a short allele with a frequency of 0.7 and a tall allele with a frequency of 0.3. Suppose that after selection for height, the frequency of each short allele was 0.3 and the frequency of the tall allele was 0.7. This could significantly increase height. In that subset of the genome, about 85% of the variation between those two population is within-group while 15% is between-group.

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24 Responses to Lewontin's argument



Stephen Jay Phinker says:

January 26, 2012 at 4:23 am

“So Lewontin's argument does not work...”

Depends what you mean by “work”. It's not worked to advance science, but it's worked v. well to retard it.

[Reply](#)



Tschafer says:

January 26, 2012 at 11:18 am

And of course, retarding science was the whole purpose, so I would guess that it “worked” insofar as did what Lewontin wanted it to do. Ditto Stephen Jay Gould – I have no doubt that he thought that he was doing “good” science, because it advanced his political views, which were “good”. It's always important to remember, for leftists, politics and power trump everything...

[Reply](#)



Steve Sailer says:

January 26, 2012 at 6:04 am

Say there was a casino where 85% of the spins of the roulette wheel came up randomly, but 15% came up black if the croupier were black and red if the croupier were an American Indian. Would you like to know that?

[Reply](#)



TWS says:

January 26, 2012 at 8:28 am

Where is this casino? And more importantly, how do you play roulette? I've watched plenty of movies and tv and the only rule I can remember is the one Wesley Snipes gives in 'Passenger 57', “Always bet on black”.

[Reply](#)



Steve Sailer says:

January 27, 2012 at 3:51 am

It's right next door to Daniel Kahneman's casino:

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Gorbachev says:

January 26, 2012 at 6:40 am

The whole point is that people actually believe these things; the argument is not really over whether it's right or wrong. Most liberals are among the worst racists when you get them drunk.

The point is that we're not supposed to believe these things. Supposed to.

[Reply](#)



dave chamberlin says:

January 26, 2012 at 8:17 am

There is also a strange positive correlation between being liberal and living as far away from poor ethnic people as possible.

[Reply](#)



Jason Malloy says:

January 26, 2012 at 10:26 am

“So Lewontin’s argument does not work. You can’t predict group differences in trait values from the distribution of genetic variation”

Lewontin’s arguments were wrong on a number of different levels, but the distribution of genetic variation does predict group differences in trait values.

To take a [popular misconception](#), Africans are more genetically diverse, but that doesn’t necessarily imply greater diversity on any given phenotype because of natural selection (e.g. non-African populations are certainly more diverse in pigmentation). However the selectively neutral patterns in physical (and presumably psychological...) traits, such as [cranial](#) and [tooth](#) shape, map on to genetic diversity.

[Reply](#)



Jason Malloy says:

January 26, 2012 at 10:31 am

(WordPress thought I had too many links)

... [map on to genetic diversity](#):

“Multivariate analysis of craniometric variation shows results similar to those obtained from genetic markers and DNA polymorphisms: roughly 13% of the total diversity is among regions, 6% among local populations within regions, and 81% within local populations. This distribution is concordant with neutral genetic markers.”

[Reply](#)



jb says:

January 26, 2012 at 12:44 pm

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enormous amount of diversity in those genes, and we aren't interested in most of those genes, but it kind of obvious that

any number you might derive from a large set of genes wouldn't be particularly informative when you are interested in a trait controlled by a small subset of those genes? Even if the genes in the subset were completely disjoint, this would probably have little impact on any number you might generate for the entire set.

So yes, you're right. Richard Lewontin did not succeed in proving that Africans and Europeans are the same color, or that they are equal in any other trait that we care about.

[Reply](#)



Peter Frost says:

January 26, 2012 at 3:14 pm

Lewontin was comparing apples and oranges. Keep in mind that population boundaries are usually also boundaries between different environments, either physical environments or (as with humans) cultural environments. So a population boundary separates different selection pressures, with the result that genetic differences across the boundary tend to reflect differences in selection. In contrast, genetic differences within populations are less adaptively significant. They haven't been levelled out by similar selection pressures.

This isn't just theory. There are many sibling species that are anatomically and behaviorally distinct, yet they show the same pattern that Lewontin found between human races.

[Reply](#)



jb says:

January 26, 2012 at 3:55 pm

I'm sure there are such examples of sibling species, and it would be interesting to see a list, including the within/between group variations.

One reason I'm curious is that I've seen it stated that, like humans, different breeds of dogs also have more within-group variation than between-group. But the number I remember for dog breeds was something like 40% for between-group variation, as opposed to 15% for human races. This surprised me! Because dog breeds diverged so recently I would expect that the between-group variation would be even less than for humans. Am I missing something?

[Reply](#)



Peter Frost says:

January 27, 2012 at 11:00 am

Do you have the reference for that 40% figure? The only one I have on dog genetics is the following:

Coppinger, R., R. Schneider. (1995). Evolution of working dogs, in: J. Serpell (Ed.), *The Domestic Dog: Its Evolution, Behaviour and Interactions with People*, Cambridge University Press, Cambridge, pp. 21-47.

“[U]sing genetic and biochemical methods, researchers have shown domestic dogs to be virtually identical in many respects to other members of the genus. [...] Greater mtDNA differences appeared within the single breeds of Doberman pinscher or poodle than between dogs and wolves. Eighteen breeds, which included dachshunds, dingoes, and Great Danes, shared a common haplotype and were no closer to wolves than poodles and bulldogs. These data make wolves resemble another breed of dog. [...] there is less mtDNA difference between dogs, wolves and coyotes than there is between the various ethnic groups of human

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January 28, 2012 at 11:14 am

No reference; the figure was from memory, and it didn't come from a technical publication. One reason I posted was because I was hoping someone else would have a reference, and an explanation for why the figure was so large, or else would tell me I was wrong and give me a better number. I'd really like to know the authoritative figure for dogs corresponding to the 15% we are always hearing about for humans, because I think the example of dog breeds kills Lewontin's argument in a uniquely clear and transparent way. It's a counterargument that anyone can understand, even the most boneheaded cocktail party liberal, and that makes it worth getting the numbers right.

[Reply](#)



Bruce says:

January 27, 2012 at 9:57 am

So it sounds to me like Lewontin's logic was fallacious but also (as you imply, I think) that he was selective in what genes he chose to use as examples for his fallacy.

[Reply](#)



Nanonymous says:

January 27, 2012 at 10:13 pm

Just a historical note here: Edwards' 2003 article is widely cited as the one that pointed out the fallacy (first or, perhaps, most clearly). But essentially the same reasoning was presented by Jeffrey Mitton in 1977 (Genetic differentiation of races of man as judged by single-locus and multilocus analyses. The American Naturalist, 1977, 111(978):203-12). This was followed by three commentaries – from Lewontin himself, Ranajit Chakraborty, and Jeff Powell and Chuck Taylor (ibid., 112(988):1134-42). Mitton replied (ibid., 112(988):1142-4) with a PCA plot showing no overlap between racial groups using the same blood type markers that Lewontin used. And that was the end of it. Looking at this exchange today, I am amazed how many inks and smart words were expended on what is essentially a semantic argument. What's even more amazing is that the confusion persisted for over 25 years (does it continue to persist?).

[Reply](#)



harpend says:

January 28, 2012 at 6:53 am

“does it continue to persist?”

Is that a trick question? It has the status of Holy Writ in every anthropology textbook you can find.

[Reply](#)



Kiwiguy says:

February 2, 2012 at 7:05 pm

does it continue to persist?

PBS website – “Race the Power of an Illusion” – quick fact number 8.

“of the small amount of total human genetic variation, 85% exists within any local population, be they Italians, Kurds,

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Note, that 10 years ago Risch et al pointed out this wasn't the case:

“Genetic data ... show that any two individuals within a particular population are as different genetically as any two people selected from any two populations in the world.” [18]. This assertion is both counter-intuitive and factually incorrect [12,13]. If it were true, it would be impossible to create discrete clusters of humans (that end up corresponding to the major races), for example as was done by Wilson et al. [2], with even as few as 20 randomly chosen genetic markers. Two Caucasians are more similar to each other genetically than a Caucasian and an Asian.”

<http://genomebiology.com/2002/3/7/comment/2007>

[Reply](#).



gcochran says:

February 2, 2012 at 7:48 pm

Right. It is never the case that a Korean will be genetically closer to an Italian than to another Korean.

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