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A New Perspective on the Race Debate

Robin O. Andreasen

ABSTRACT

In the ongoing debate concerning the nature of human racial categories, there is a trend to reject the biological reality of race in favour of the view that races are social constructs. At work here is the assumption that biological reality and social constructivism are incompatible. I oppose the trend and the assumption by arguing that cladism, in conjunction with current work in human evolution, provides a new way to define race biologically. Defining race in this way makes sense when compared to the developments in other areas of systematic biology, where shared history has largely replaced morphological similarity as the foundation of a natural biological classification. Surprisingly, it turns out that cladistic races and social constructivism are compatible. I discuss a number of lessons about the way human biological races have been conceptualized.

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I was born in a century when the walls of race were clear and straight; when the world consisted of mutually exclusive races; and even though the edges might be blurred, there was no question of [the] exact definition and understanding of the meaning of the word . . . [Of late], the concept of race has . . . changed and presented so much . . . contradiction that as I face Africa I ask myself what it is between us that constitutes a tie which I can feel better than I can explain?

(W. E. B. Du Bois [1940], p. 116)

1 Introduction

Ashley Montagu led a lifelong campaign to rid science of the term ‘race’. In 1964, he made the prediction ‘Race is the phlogiston of our time’ (Montagu [1964] p. xii). Phlogiston, a substance believed to be given off during combustion, was once thought to be real. However, when Lavoisier determined the true nature of combustion, phlogiston turned out to be a mere chimera. Montagu believed that the concept of race should suffer a similar fate.

Most race theorists would say that Montagu’s prediction has come true.¹ Although the person on the street may still believe that races are biologically real, science has proven otherwise. Biological races are supposed to be ‘subspecies’—formal subdivisions of a species—yet according to most systematic biologists, the subspecies category is arbitrary and theoretically uninteresting. In addition, detailed work in human genetics purportedly reveals that, regardless of whether there are *non-human* subspecies, there are no *human* subspecies. A random sample of genes taken from different human populations classified by location reveals that these populations are too genetically similar to each other to justify dividing humans into races.

Although most race theorists think that races are biologically unreal, I disagree. Systematists and taxonomists have used two main approaches—typological and geographical—in their attempts to define subspecies. Neither of *these* work to define race. However, there is a third possibility that has largely been overlooked in the race literature—namely, the cladistic approach to subspecies. I will defend this account, arguing that races are ancestor–descendant sequences of breeding populations, or groups of such sequences, that share a common origin. Moreover, I will show that current work in human evolution supports this account and offers a new way of thinking about the biological reality of race. Races once existed, but they are on their way out. With the advent of the modern world came the intermixing of previously isolated populations and the gradual dissolution of racial distinctness. It isn’t that science must recognize that race, like phlogiston, never existed; rather, human activity is causing race to lose its biological reality.

Once I have defended this new approach, I will describe three lessons that the cladistic concept provides about the current state of the race debate. Most race theorists treat biological races as static categories. From the non-existence of current races, they argue that biological races are, and always have been, illusions that we have projected on the world. The account that I offer, however, shows that biological races are dynamic categories. Second, because biological concepts of race are used repeatedly to justify belief in racial superiority, many have come to associate the biological reality of race with racism. Although this reaction is perfectly understandable, I will argue that

¹ I am using the term ‘race theorist’ to mean someone who makes theoretical claims about race.

these concepts need not go hand in hand, and that the cladistic concept, specifically, lends no support to claims about racial superiority. Third, those who reject the biological concept of race often think that race is a *social construct*—it is a product of our social practices. Although there are many ways of being a constructivist about race, most constructivists assume that their view is incompatible with the idea that races are biologically real. I will argue, however, that these conceptions can be complementary; they should not always be viewed as competitors.

2 Two arguments against the biological concept of race

Today's race theorists cite two, purely biological, arguments to support their claim that race is not a biologically meaningful (or objective) category. In the first argument, they appeal to the practice of systematists. Most systematic biologists refuse to divide non-human species into subspecies on the grounds that the subspecies concept is theoretically meaningless. They add that if there is no justification for naming subspecies in biology, then there is no justification for dividing humans into biological races. The second argument allows that the subspecies concept might be useful in some contexts; here, theorists argue that there is a special reason why it should not be applied to humans.

Versions of both of these arguments have been presented before (Montagu [1941, 1959]; Barnicot [1964]; Ehrlich and Holm [1964]; Hiernaux [1964]; Livingstone [1964]), but for a long time they did not command general assent because the biological reality of race was thought to be 'self-evident'. However, the tide has turned; today, the dominant view in biology is that there are no biological races. As a result, the following arguments are now part of the mainstream in race theory.

2.1 The 'no subspecies' argument

Race, as a biological concept, is synonymous with subspecies. Human races are subspecies of *Homo sapiens* and, like the term 'race', 'subspecies' has had a tumultuous history. Two systematic definitions have been offered—one typological, the other geographical—but neither is acceptable. Additionally, many biologists feel that there is little reason to search for a better definition. Race theorists conclude that we should learn a lesson from systematic biology. If biologists rarely use the subspecies concept to describe variation in non-human contexts, we should not use it in the case of humans.

2.1a Problems with the typological subspecies concept

In the spirit of Aristotle, subspecies were first defined as *types*—as natural

kinds defined in terms of an *essential property* possessed by all and only the members of the same subspecies.² An attribute is 'essential' to an object if it is a *necessary, intrinsic, and explanatory* property that an object must have in order to be the kind of thing it is.³ For instance, it is a necessary truth that all samples of water have H₂O as their molecular structure.⁴ This property is 'intrinsic' because it depends for its instantiation only on the entity in which it is instantiated. It is also 'non-accidental': nothing can be water and lack this structure and anything possessing this structure must be water. Finally, this property is 'explanatory'. It allows one to make inferences about other properties that things of this type possess. Being made of H₂O explains many phenomenal properties of water such as its being clear and tasteless.⁵ Thus, the typological subspecies concept is the idea that subspecies ought to be objectively classified on the basis of a uniform association of characteristics, transmitted together due to the existence of an essential property.

Since there is extensive variability in nature, one rarely finds a single property possessed by all and only members of the same subspecies. Additionally, even if such a trait were to be found, it would probably not satisfy the modal and explanatory requirements demanded of an essential property. One might think that this is the straightforward reason why the typological subspecies concept is inadequate, but the essentialist has a way out. An Aristotelian essentialist can develop a 'natural state model' in order to explain, actually explain away, nature's variability (Sober [1980]). According to Aristotle, every object has a 'natural state' and a number of 'unnatural states'. An unnatural state is a deviation from the natural state, which occurs when an object is subject to an interfering force. By appeal to this distinction, then, typologists can view variability as a deviation from certain natural tendencies. More specifically, defenders of the typological subspecies concept can recognize unlimited variety within, and continuity between, subspecies—so long as one can expect to find discrete natural tendencies underlying this variation. In their search for natural tendencies, typologists gather numerical data on the phenotypic characteristics of organisms within a population. They then compute the mean and the standard deviation in order to construct a bell curve. The peak of the curve (the average) might be taken to represent the ideal type, and the variance around that mean might represent deviation from type due to interfering forces.

The problem with the typological subspecies concept, and with typological thinking in biology, is that evolutionary theory no longer uses a natural-state

² See Mayr [1963] for a brief discussion of the history of the subspecies concept in biology.

³ This is David Hull's [1978] version of Aristotelian essentialism.

⁴ Zemach ([1976], p. 120), who is sceptical about the existence of essential properties, challenges this example by arguing that 'there is no chemical constitution common to all bodies of water.' I will not address this criticism since my aim here is merely to provide an intuitive example.

⁵ Although this characterization of essentialism is fairly vague—for example, the concept of explanation needs more development—it should be good enough for my purposes.

model to understand biological diversity (Sober [1980]). When Darwin introduced his theory of evolution by natural selection, he introduced a new way of thinking, which Mayr [1959] calls 'population thinking'. Populationists define taxonomic categories in terms of the phenotypic differences existing between *populations as a whole*. In contrast, typological thinking involves defining taxonomic categories in terms of the properties possessed by *individual organisms*.

Population thinking eliminates the demand for natural tendencies by providing a new way to account for variability in nature. In Sober's words ([1980], p. 176, emphasis in the original):

Both typologists and populationists seek to transcend the blooming buzzing confusion of individual variation. Like all scientists, they do this by trying to identify properties of systems which remain constant in spite of the system's changes. For the typologist, the search for invariances takes the form of a search for natural tendencies. The typologist formulates a causal hypothesis about the forces at work on each individual within a population. The invariance underlying this diversity is the possession of a particular natural tendency *by each individual organism*. The populationist, on the other hand, tries to identify invariances by ascending to a different level of organization. For [the populationist], the invariant property across generations within a lineage is the amount of variability, and this is a property of populations.

Unlike typologists, populationists do not try to explain away nature's variability. Instead they treat it as real and work to explain the variation in one generation by appeal to variation in a previous generation and to the laws of heredity. This allows us to see why the typological subspecies concept won't work. Ever since Darwin, population models have played a central role in evolutionary theorizing; the ideas of type and of deviation from type at the species level, and at other taxonomic levels as well, do not feature in evolutionary laws and theories. The typological subspecies concept has no place in contemporary evolutionary biology.

2.1b Problems with the geographical subspecies concept

As one might expect, the typological subspecies concept was replaced with a population concept, which I will call the *geographical subspecies concept*. 'Geographical subspecies' are morphologically distinct geographic representatives of a species. More formally, a geographical subspecies is an aggregate of phenotypically and genetically similar intraspecific populations, inhabiting a geographic subdivision of the range of that species, and differing significantly from other conspecific populations (Mayr and Ashlock [1991], p. 43). According to this definition, it is not necessary for different subspecies to differ absolutely; it suffices that there be statistically significant differences in the mean values of the characters used to define subspecies membership. Furthermore, membership

must be defined with reference to many characteristics—enough to ensure that the addition of new characteristics will not alter subspecies groupings. If these conditions are not met, subspecies classifications will be arbitrary and theoretically uninteresting.

In contrast with those who support the typological subspecies concept, friends of the geographical concept deny that subspecies are natural kinds; instead they adopt a conventionalist stance. Subspecies are taken to be *conventional categories* that get individuated according to practical human interests. This does not mean, however, that geographical subspecies are arbitrary. On the contrary, for this concept to be biologically useful, some designations will have to be better than others. The meaningful designations will be the ones that allow biologically interesting generalizations to be formulated.

Over the years, there have been a number of criticisms of the geographical concept (Wilson and Brown [1953]; Gillham [1956]; Hagmeier [1958]; Mayr [1963, 1982]; Johnston and Selander [1964, 1966]; Storer [1982]; Zusi [1982]); most of them point to the fact that intraspecific variation is often not discrete. It is generally gradual across geographic regions (clinal) and it often ranges in many different directions (discordant). For example, a bird species might gradually increase in size from the southern to the northern regions of its habitat. At the same time, a different pattern of variation, say from light to dark, might range across the east–west regions of the habitat. When intraspecific variation displays such a pattern, there is no principled way to designate geographical subspecies. Designations would be mere subjective partitions of continuous variability. They would be neither stable nor repeatable, nor theoretically interesting.

Although I think that biologists have come to the right conclusion—namely, that geographical subspecies are arbitrary and unreal—they have come to this conclusion for the wrong reason. The above argument demands that there be a precise boundary between different subspecies, but this is unreasonable. It is like demanding that there be a precise line of demarcation between baldness and having a full head of hair, or between being rich and being poor. Just because there are line-drawing problems in these cases does not mean that these properties (wealth and baldness) should be rejected as arbitrary. Similarly, geographical subspecies might be real, even if the boundaries between them are vague.

The real problem with the geographical concept is that it is a *phenetic* concept. Pheneticists define taxonomic groupings based upon overall similarity. For example, a phenetic subspecies is a set of phenotypically and genetically similar conspecific organisms that are distinct from other such sets. Perhaps the worst problem with pheneticism is that there is no reason to believe that the resultant taxa reflect any important biological phenomena. Pheneticism defines

taxa using similarity *alone*, but there is no reason to believe that overall similarity represents an objective (or theoretically interesting) feature of reality. A second problem with this concept is that there is rarely a unique way to describe the similarities and differences between pairs of taxa. For example, a pheneticist might attempt to classify a set of organisms into subspecies by pointing to a number of characteristics possessed by one group, but not by the others. However, for each of these characteristics, it is possible to describe others that entail quite different similarity groupings. Finally, the concept of similarity itself can be spelled out in different ways, which further augments pheneticism's embarrassment of riches (Ridley [1986]).

Systematists once thought it possible to provide a biologically meaningful definition of 'subspecies'. Today however, many biologists question this assumption (Wilson and Brown [1953]; Mayr [1963, 1982]; Johnston and Selander [1964, 1966]; Storer [1982]; Zusi [1982]). Some argue that, due to the dynamic nature of intraspecific variation, it will be difficult to come up with a biologically meaningful subspecies concept. Designating subspecies entails identifying *distinct units* and giving them formal names. Yet the boundaries between 'subspecies' are rarely fixed or definite. Others argue that the subspecies concept is superfluous; biologists can use multivariate analysis to study the clinal and discordant variation within a single species. As a result, it is generally accepted that the subspecies category is (at best) a unit of taxonomic convenience. Race theorists conclude that the implications for human race ought to be obvious. If the subspecies concept is inadequate for defining non-human subspecies, we should not use it to divide humans into biological races.

2.2 The 'no human subspecies' argument

The second argument against the biological concept of race is a special case of the first. Race theorists who present this argument are agnostic about the overall value of the subspecies category, allowing that it might result in biologically meaningful designations in some non-human contexts. What they argue is that when the geographical concept gets applied to humans, the result is a number of biologically insignificant 'racial' groupings. Thus, even if there are non-human subspecies, there are no *human* subspecies.

Over the past fifty years, geneticists have been gathering copious data on the genetics of contemporary human populations in order to measure the genetic differences among individuals, populations, and 'races'.⁶ Studies indicate that the variation within major 'races' is slightly greater than the variation

⁶ For the purposes of these studies, 'racial' categories were assumed to correspond with major skin-colour groupings.

between local populations. Moreover, the variation between individuals within a population is substantially greater than the variation between populations or 'races'. Approximately 85% of human genetic variation is between individuals within the same local populations. About 8% is between the local populations found within major 'racial' groups, and the remaining 7% is between 'races' (Lewontin [1972]; Nei and Roychoudhury [1972; 1974]; Cavalli-Sforza [1974]; Lewontin, Rose, and Kamin [1984]; Cavalli-Sforza, Menozzi, and Piazza [1994]). Using these statistics, race theorists argue that there can be no justification for recognizing human geographical races. Populations are clustered so closely together that any partitioning into races would be merely subjective.

Like the general argument against the biological reality of subspecies, this argument does not deny the existence of human variation. It merely claims that racial classification is not the best way to understand such variation. At first sight, this argument provides a strong reason to reject the biological concept of race—especially when it is coupled with the previous argument. Nevertheless, I will show that appearances are deceiving; these arguments are inconclusive.

3 Why not cladism?

Biologists have often been too quick to infer the general failure of the subspecies concept, and most race theorists have been too quick to reject the biological reality of human race. In this section, I will argue that there is a third option for defining subspecies that has been largely overlooked in the race literature. Using the principles of cladistic classification, we can think of subspecies as (groups of) ancestor-descendant sequences of breeding populations that share a common origin. I will call this the *cladistic approach* to subspecies. Additionally, by appeal to current work in human evolution, I will show that this account can be applied successfully to humans. This will provide a new way to define race that is untouched by the above arguments.

The philosophical debate concerning the status of scientific categories provides a background for my argument. Given the human propensity to divide the world into different sorts of things—gold, humans, bachelors—it is natural to ask which of these categories are artificial kinds, invented by us, and which are natural kinds, corresponding to real divisions in nature. Two answers to this question have been prominent in contemporary philosophy. Essentialists claim that natural kinds are defined in terms of essential properties possessed by all and only members of a kind (Kripke [1972]; Putnam [1975]). Conventionalists, on the other hand, argue that all categories are individuated according to practical human interests (Dewey [1938]; Lewis [1946]; De Sousa [1984]; Sidelle [1989]). Some categories may be more interesting

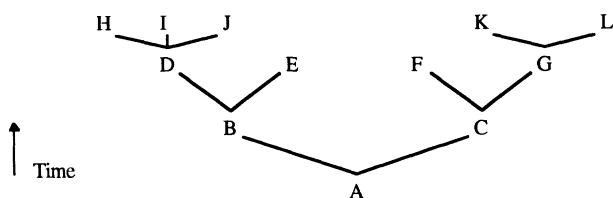


Fig 1.

than others, but all categories have the same metaphysical status. However, when it comes to certain categories—namely, evolutionary ones—the possibility arises that neither position is adequate. Both of the above philosophies of classification hold that classifications must be based on the idea of similarity; typological classification requires a shared essential property and the geographical concept requires overall similarity. There is a third possibility, however, that is present in the biological literature—namely, that a natural classification is one that reflects the genealogical relationships among organisms (Darwin [1859]; Hennig [1966]; Ghiselin [1974]; Hull [1978]; Sober [1988]). Darwin was among the first to make this suggestion, but Hennig is the one who gave it rigour.⁷

Hennig is the founder of the systematic school called *cladism* which individuates taxa in terms of common ancestry. By organizing sets of well-defined species into a branching structure, a *phylogenetic tree*, one can depict the relationships between ancestors and their descendants and classify organisms into higher taxa (anything above the species level).⁸ (Later I will discuss how this taxonomic philosophy can be extended to lower taxonomic categories such as subspecies.) For example, Figure 1 represents an ancestral species, A, giving rise to two daughter species, B and C, which then eventually give rise to the terminal taxa H-L as depicted.

In this diagram, the nodes represent the species whose evolutionary relationships are depicted and the branches represent speciation events. Provided that each object in the tree has a unique immediate ancestor—that is, provided that there is branching without reticulation—we can define a taxonomic unit as a *monophyletic unit*, a group composed of an ancestor and

⁷ In addition to essentialism, pheneticism, and cladism, there is a fourth school of classification—*evolutionary taxonomy*—which uses both genealogy and adaptive similarity for individuating taxa. I mention this school only to set it aside; it fails to offer a nonarbitrary criterion for when adaptive similarity matters more than propinquity of descent, and vice versa (Sober [1993]).

⁸ It is important to recognize the difference between a phylogenetic tree and a cladogram. Cladograms represent only one feature of phylogenetic development, namely, branching sequence. Phylogenetic trees, on the other hand, represent a number of features such as branching sequence and the relation between ancestors and descendants.

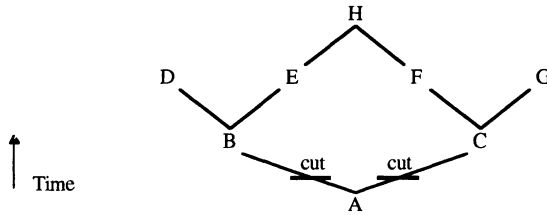


Fig 2.

all of its descendants. Sober [1993] applies what he calls ‘the cut method’ to explain the concept of monophyly. If you draw a cut across any branch, the nodes immediately above that cut comprise a monophyletic group. For example, in Figure 1, E is a monophyletic group, so is DHIJ, and so are many other groupings.

Two facts about monophyly are worth noting. The first is that the complement of a monophyletic group is not itself a monophyletic group. By applying the cut method to Figure 1, it is possible to see that DHIJ is monophyletic, but that the rest of the tree (ABCEFGKL) is not. Furthermore, monophyly is a property of a *bifurcating tree* (a point that will have considerable importance later on). Although the concept of monophyly *can* be applied to a reticulate structure, such as the one depicted in Figure 2, it results in a partial overlap between monophyletic groups. Again the cut method is useful for seeing why this is so.

Applying the cut method to this reticulate structure produces two groups (BDEH and CFGH), both of which contain species H. Most systematists choose not to develop classifications in such cases. The reason is that when reticulation is extensive, partial overlap will also be extensive, resulting in a nonhierarchical classification scheme.

Cladistic classifications have both a conventional and an objective aspect. The way that monophyletic groups get assigned to a taxonomic level is conventional. According to Hennig the smallest terminal taxa—for example, H, I, J, E, F, K, and L in Figure 1—represent current species; the next largest monophyletic units—DHIJ and GKL—represent genera, and so on up the taxonomic hierarchy.⁹ Yet there is nothing to keep us from arranging things differently. For example, one might decide that DHIJ and GKL comprise genera, or that they make up families. There is no fact of the matter at issue here. This conventional aspect, however, should not obscure the fact that the

⁹ It has been argued that species cannot be required to be monophyletic. If species are monophyletic, then ancestral species cannot exist. On this view, an ancestral species *belongs* to monophyletic groups, but they cannot *be* monophyletic groups. Thus, although the monophyly criterion is useful for classifying superspecific taxa (and, as I will argue, subspecific taxa), it is not an appropriate criterion for designating species (Sober [1993]).

branching structure and the nested hierarchy of monophyletic groups exist objectively. They exist objectively because they reflect the patterns and processes of evolution, which are themselves objective. It is this that makes cladistic classifications objective. We may not always know when we have the right phylogeny, but when we do, the resulting classification will reflect something that exists independently of our classifying activities.

We are now in a position to see why we ought to consider a cladistic view of subspecies. Defenders of the typological approach embrace essentialism and defenders of the geographical approach adopt a conventionalist stance, yet discussions about the biological reality of subspecies have taken place without seriously considering the cladistic approach. Since this third possibility has been immensely important when it comes to defining other categories in the taxonomic hierarchy and, as I am about to demonstrate, it can be adapted for defining subspecies, it is premature to conclude that subspecies are biologically meaningless.

3.1 Cladistic subspecies

A cladistic view of subspecies would require constructing a phylogenetic tree out of the *breeding populations* in a single species. A 'breeding population' is a set of local populations linked to one another by reproductive ties that are, for the most part, reproductively isolated from other such populations. For example, a gaggle of geese living in Vilas Park constitutes a local population. When there is interbreeding between this population and other local populations due to migration, these local populations constitute a breeding population. In our tree, then, the nodes would represent breeding populations and the branches would represent the birth of new breeding populations. A breeding population is born when a local subpopulation becomes separated from its parent population and is, for the most part, reproductively isolated from the parent population. Suppose that a few rabbits get separated from the breeding population to which they belong due to a river's changing course. On the assumption that the rabbits cannot cross the river, this constitutes the birth of a new breeding population. Referring again to Figure 1, we can define subspecies in the following manner. The terminal taxa (H, I, J, E, F, K, and L) represent current breeding populations, the more inclusive monophyletic units (DHJ, GKL, BEDHIJ, and CFGKL) represent a nested hierarchy of subspecies, and the whole tree represents the species.

There are two reasons why biologists have, by and large, ignored the possibility of defining subspecies cladistically. The first is mere force of habit—cladistic classification is traditionally used for defining membership of higher taxa; to apply it to subspecies would deviate from Hennig's original intention. Second, many authors think that tree reconstruction is too difficult

for lower taxonomic levels (Bremer and Wanntorp [1979a, b]; Arnold [1981]). They argue that cladism is appropriately applied whenever groups are diverging. Two groups are likely to diverge when, over long periods of time, there is limited gene flow between them. But in the case of subspecies, divergence rarely occurs because there is often considerable interbreeding between local populations. I think that this point is overstated. Many commonly recognized sexual species have subpopulations between which there is little or no genetic exchange (Ehrlich and Raven [1969]). Furthermore, low levels of interbreeding can be allowed; interbreeding is only a problem when it is extensive enough to cause reticulation. Third, systematists and human evolutionists have come up with methods for estimating degrees of interbreeding, and hence can work around some of the problems that it poses (Nei and Roychoudhury [1993]; Templeton [1993]; Cavalli-Sforza, Menozzi, and Piazza [1994]). Finally, current work in human evolution illustrates that it is possible to reconstruct a phylogenetic tree of human breeding populations—and this means that it is possible to apply cladistic classification below the species level. It is to this possibility that I now turn.

4 Races as clades

Reconstructing a human phylogenetic tree has been a goal of human evolutionists for some time, but until recently this was only a remote possibility. Early attempts at tree reconstruction were, for the most part, unsuccessful because they were based solely on palaeontological and archaeological data (mainly fossilized bones and artefacts). Due to the incompleteness of the fossil record and the limitations of early dating techniques, these data were met with scepticism. Today, however, the prospects of reconstructing a human phylogeny are quite promising. Not only have dating techniques improved, but new fossil evidence is being discovered quite rapidly. More importantly, however, recent developments in human genetics provide a new and independent source of data. This new source, in conjunction with improved palaeontological and archaeological data, is allowing human evolutionists to approach their goal.

A chief tool for reconstructing human phylogenies is a quantitative measure called *genetic distance*. This is a measure of the difference in gene frequencies between two breeding populations. In this context, it is used for estimating degrees of relatedness between human populations. Roughly, the smaller the genetic distance between two populations, the closer their ancestral relation. The reasoning here is that all humans share a common origin; we all evolved from a single ancestral population at some point in our distant past. Thus as local subpopulations migrated out of their original location and formed new

breeding populations, mutations occurred and differences accumulated. Genetic distance, therefore, serves as a means by which to calibrate human evolutionary history.

We should be aware, however, that the assumed correlation between time and genetic distance is only rough; a number of factors can disturb it, resulting in an imperfectly reconstructed tree. When two previously distinct populations live in similar environments, natural selection may cause them to converge (i.e. to develop similarities). The effect of convergence on tree reconstruction is an over-estimation of their degree of relatedness. Secondly, rapid genetic drift in small populations will cause them to evolve more rapidly than larger populations. In such cases, smaller populations appear to be older (more divergent) than they in fact are. Finally, interbreeding between two previously isolated populations can occur, resulting in an overestimation of their degree of relatedness.

These difficulties, however, are not insurmountable. Geneticists can minimize potential biases in a number of ways. They address the problem of convergence by using selectively neutral DNA segments, such as 'junk DNA' (DNA that serves no apparent function) or mitochondrial DNA. Secondly, rates of evolution are likely to be uniform when drift is a major cause of change and when populations are roughly the same size on average. Independent evidence confirms the former assumption and careful selection of populations makes the latter probable (Cavalli-Sforza [1991], p. 105). Furthermore, geneticists can greatly reduce the problems posed by hybridization by studying *aboriginal populations*—breeding populations that occupied their present location before the great migratory waves that began with the voyages of discovery in the mid-to late fifteenth century. A fourth source of confirmation comes from agreement with historical, archaeological, and palaeontological data. Finally, and perhaps most importantly, biases can be 'washed out' by averaging over many genes in calculating genetic distance. The greater the number of measured differences, the more confidence one can have that a tree is unbiased. Fortunately, thousands of genes are known.

For the past fifty years, geneticists have been gathering extensive data on the genetics of living populations (Nei and Roychoudhury [1982]; Cavalli-Sforza *et al.* [1988]; Cavalli-Sforza [1991]; Vigilant *et al.* [1991]; Wilson and Cann [1992]; Cavalli-Sforza, Menozzi, and Piazza [1994]). Their purpose is to infer major patterns of human evolution. For example, Cavalli-Sforza and colleagues calculated the genetic distances between 120 different gene states for forty-two aboriginal populations. Using these data, they inferred the phylogenetic tree depicted in Figure 3.

Cavalli-Sforza and colleagues tested the accuracy of their phylogeny by comparing measured genetic distances with a number of widely accepted dates suggested by the geological record. The genetic distances between Africans

and non-Africans exceeded all other measures. Moreover, this distance was approximately twice that between Australians and South East Asians, and the latter was more than twice that between Europeans and North East Asians (Cavalli-Sforza [1991], p. 106). The corresponding times of separation suggested by paleoanthropology are in similar ratios. Archaeological and palaeontological data indicate that anatomically modern humans evolved in Africa ~200,000 years ago. Thus, the first major split—which separates Africans from all other groups—represents a racially undifferentiated stock of *Homo sapiens* migrating out of Africa ~100,000 years ago. The second split separates Pacific and South East Asians from all other non-Africans. The breeding populations of native Australia and Papua New Guinea reached their location ~50,000 years ago. Within this supercluster, there was a later separation between the Pacific Islanders and the South East Asians. The breeding populations of native Australia and Papua New Guinea reached their location ~50,000 years ago. Within this supercluster, there was a later separation between the Pacific Islanders and the South East Asians. Prior to this split, however, there was a division in the third major branch; the North Eurasians separated from the Caucasians. An approximate date for this event is 40,000 years ago. Finally, a series of divisions occurred in the North Eurasian supercluster.

An interesting result comes from applying cladistic classification to Cavalli-Sforza's tree. People standardly divide humans into three (or more) major races—Africans, Caucasians, Asians. The cladistic concept of race, however, results in racial categories that cross-classify these standard groupings. More specifically, the folk category 'Asian' is not a cladistic race. We can see why by looking at the nested hierarchy of monophyletic groups in Figure 3. Caucasian and African are monophyletic groups, but Asian is not. South East and North East Asians are in two distinct major branches. North East Asians are more closely related to Amerindians and to Caucasians than they are to South East Asians. Similarly, South East Asians are more closely related to Australians than to North East Asians. This conclusion is interesting because it illustrates

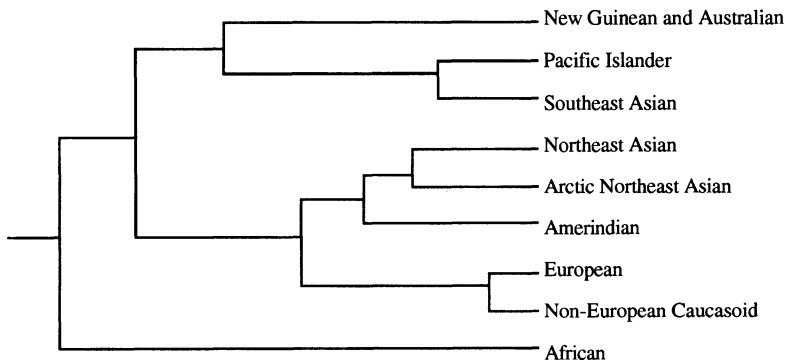


Fig 3.

that the existence of biological races does not depend upon our folk taxonomy being right.

The above results, although fascinating, are somewhat controversial. For example, Cavalli-Sforza (Cavalli-Sforza, Menozzi, and Piazza [1994]) denies that his phylogeny can be used to define race. He relies on the conventional aspect of cladistic classification to support his claim: human phylogenies provide a nested hierarchy of monophyletic groups, and there is no biological reason to apply the term 'race' at one level rather than others. However, there is no need to choose a unique level of monophyly that defines racial categories—we can simply define 'race' as a nested hierarchy of monophyletic groups. In addition, Cavalli-Sforza's point applies to races no more than it applies to other monophyletic groups in a cladistic hierarchy. For these reasons, we should not accept this argument against the biological reality of races.

Secondly, a number of theorists have criticized Cavalli-Sforza for using phenetic methods—specifically, Nei's genetic distance—to make phylogenetic inferences (O'Grady *et al.* [1989]; Bateman *et al.* [1990a, b]; Bayard [1990]); they argue that cladistic methods provide a better way to measure propinquity of descent. I will address this issue, as well as a number of others, at the end of this section. At present, however, my concern is to address a different matter. This criticism appears to contradict my proposal that we use *cladistic* classification to define race, since it asserts that Cavalli-Sforza uses phenetic rather than cladistic methods of phylogenetic inference. To understand why this contradiction is only apparent, it is important not to confuse the problem of *phylogenetic inference* (which concerns how one is to infer what the phylogenetic tree is for a given set of taxa) with the problem of *classification* (which concerns how one is to organize sets of organisms into taxa (Felsenstein [1984])).¹⁰ There is no contradiction between using phenetic methods for reconstructing trees and using cladistic methods for constructing a classification scheme (Sober [1993]).

Finally, in addition to the controversy surrounding Cavalli-Sforza's methods of phylogenetic inference, there is some controversy over the specifics of his tree. For example, although Cavalli-Sforza's results agree with one line of fossil evidence, there is some disagreement with other palaeoanthropological data (Stringer [1990]). Additionally, other research groups have inferred phylogenies that show a somewhat different pattern of migration and subsequent divergence

¹⁰ I have already discussed the distinction between cladistic and phenetic methods of classification—pheneticism uses overall similarity to define its taxa and cladism uses monophyly. Here is the difference between pheneticism and cladism when it comes to phylogenetic inference. *Pheneticists* use overall similarity to measure degrees of relatedness. When two breeding populations are found to be more similar to each other than either is to the third, a pheneticist would conclude that the first two are more closely related to each other than either is to a third. *Cladists*, on the other hand, distinguish between two types of similarity—those that are derived through descent from a common ancestor (synapomorphies), and those representing retained ancestral characters (symplesiomorphies)—and argue that only the former count as evidence when assessing degrees of relatedness.

(Nei and Roychoudhury [1982, 1993]; Vigilant *et al.* [1991]; Wilson and Cann [1992]). For example, Wilson's group obtained a phylogeny in which Asian is monophyletic, but African is not. Nei and his colleagues, on the other hand, found that all three major races are monophyletic. Finally, Cavalli-Sforza's tree supports a hypothesis (the 'out-of-Africa' hypothesis) that sees racially undifferentiated modern humans as evolving in Africa about 200,000 years ago and subsequently spreading around the world. Under this hypothesis, racial differentiation occurs after the initial migration out of Africa as a result of incomplete but effective reproductive isolation among groups. Some human evolutionists, however, reject this hypothesis (Wolpoff, Wu, and Thorne [1984]; Wolpoff *et al.* [1988]; Wolpoff [1989a, b]; Thorne and Wolpoff [1992]). Instead, they defend what is called the 'multiregional evolution' hypothesis. This theory holds that, as a result of genetic continuity over time and gene flow among contemporaneous populations, modern humans evolved not only in Africa but also in Europe and Asia from their already racially differentiated *Homo erectus* forebears.

In spite of the issues that remain to be resolved, we should not lose sight of the great importance of this research. Cavalli-Sforza's work illustrates that human evolutionists are approaching their goal; they are on their way towards reconstructing a human family tree that accurately reflects the patterns and processes of human evolution. This carries with it important implications for the race debate. It means that it is possible to give a biologically objective definition of race. Races are monophyletic groups; they are ancestor-descendant sequences of breeding populations, or groups of such sequences, that share a common origin. Even if the empirical details change, this conceptual point—as well as others that I am about to make—will remain in place.

5 Lessons

I have just argued that cladistic classification, in conjunction with current work in human evolution, vindicates the biological reality of race. My aim in this section is to discuss the impact that this has on the current state of the race debate. Specifically, I will discuss three lessons that the cladistic view provides about the way race theorists have traditionally understood the biological concept of race.

5.1 Biological races are dynamic

Current race theorists tend to think of biological races as static categories. The presupposition is that biological races have either always existed or they have never existed. Although this type of thinking is rampant in the race literature, it

is best illustrated by Montagu's prediction. Montagu thought that biological races don't exist and that they never have. Racial categories are merely convenient fictions invented by humans in order to render intelligible their observations of human differences.

The cladistic concept of race, however, shows that biological races are dynamic categories; races once existed, but due to recent historical events, they are on their way out. As noted in Section 3, cladistic classification requires that evolution take the form of a branching process. Subspecific evolution takes this form when a species splits into several breeding populations that experience different evolutionary forces under a significant degree of reproductive isolation. Current work in human evolution illustrates that this condition was met in the past. Specifically, the genetic data used to reconstruct phylogenetic trees indicates that Old World human populations had low levels of genetic contact for a substantial portion of time (Nei and Roychoudhury [1993]; Templeton [1993]; Cavalli-Sforza, Menozzi, and Piazza [1994]). Further support comes from the fossil record. Had there been substantial interbreeding among ancestral populations, the fossil remains of our ancestors would show significantly more continuity than they in fact show (Stringer and Andrews [1988]; Stringer [1990]; Aiello [1993]; Shreeve [1995]). From this evidence, and from Cavalli-Sforza's tree, we can conclude that races once existed.

Yet these newly reconstructed phylogenetic trees do not indicate the existence of current races. They describe racial ancestry—this is why human evolutionists focus on aboriginal populations (such as the Australian aborigines who, even today, remain reproductively isolated to a very high degree) and attempt to control for any outbreeding that has occurred in more modern times. The importance of this point can be seen by returning to the 'no human subspecies' argument. Unlike the data used to reconstruct phylogenetic trees, the data used in this argument come from modern (i.e. non-aboriginal) populations. For example, when measuring the frequencies of various gene states, Lewontin used black and white Londoners and Nei and Roychoudhury used African and Caucasian Americans as representatives of the African and Caucasian 'races' (Nei and Roychoudhury [1972]; Lewontin, Rose, and Kamin [1984]). Additionally, there were no attempts to control for outbreeding when these studies were done. These data, in conjunction with the fact that there has been reduced reproductive isolation in modern times, indicate that races are fading out of existence. Ever since the voyages of discovery, colonization and immigration have been blurring racial distinctness.

Thus, if we focus on the synchronic question—is there any justification for dividing current populations into races—the answer may very well be 'no'. The boundaries between races are becoming blurry due to a lack of reproductive isolation. This is, or at least should be, the upshot of the 'no human

subspecies' argument. But we should not conclude from this, as Lewontin and others have done, that race is merely an illusion that we have projected on the world. The cladistic concept focuses on a diachronic question about the biological reality of race; it seeks to define race via evolutionary history. If we focus on this type of question, a better conclusion to draw is that *ancestral races* existed, but biological races are anastomosing.

5.2 The relation between biological races and racism

Anyone who attempts to argue that races are biologically objective should do so with great trepidation. Appeals to the biological reality of race have been used repeatedly to justify the belief that some races are biologically superior to others; this, in turn, gets used to justify oppressive social practices. As a result, people have come to associate any talk of the biological objectivity of race with racism. One particular concern is that some might think that Cavalli-Sforza's diagram—with Africans splitting off first and Caucasians last—is itself racist. Does the diagram entail that Africans are the most 'primitive' of races and that Caucasians are the most 'advanced'? The answer is 'no'. Cavalli-Sforza's tree tells us nothing about the relative 'values' of different races; this is so for two reasons.

Claims about biological objectivity entail claims about biological difference, but they do not justify conclusions about racial superiority. As Hume taught us, one cannot infer normative conclusions from purely descriptive premises. It follows that inferences from biological difference to biological superiority are fallacious. Statements about biological differences are descriptive; they are statements of empirical fact. Assertions of racial superiority are normative claims that are born out of social and political motives. They are a result of imposing a value system upon the fact of biological variation, and this value system has no intrinsic relationship to biological diversity itself. In Cavalli-Sforza's words, '[p]olitical convenience, and a variety of motives totally unconnected with science are the basis of racism' (Cavalli-Sforza, Menozzi, and Piazza [1994], p. 19).

In addition, even if one could sometimes draw conclusions about the relative values of different races from facts about biological differences, Cavalli-Sforza's tree does not support such an inference. As I argued above, this tree represents facts about racial ancestry. Specifically, it illustrates that in our distant past, there was little genetic contact between human breeding populations. As a result, we can conclude that ancestral races existed. However, as I also argued above, the current situation is much less clear cut. With the advent of the modern world came an explosion of migration resulting in a great increase of interbreeding among previously isolated populations. Consequently, the boundaries between current human populations are becoming increasingly

fuzzy. Given this, it makes no sense to use this concept to argue for biological superiority. If it is unclear that races exist today or in our recent past, and I have argued that it is, surely this fact provides no basis for drawing racist conclusions.

5.3 The relation between the cladistic account and constructivist accounts

Those who reject the biological reality of race often think that race is a *social construct*—it is a product of our social practices. Although it is often assumed that ‘social constructivism’ has a single well-understood meaning, this is not the case. Constructivists often use the metaphor in a variety of ways, and rarely distinguish between its many uses. For example, although most forms of constructivism oppose realism about natural kinds, this opposition can be either *local* or *global*.¹¹ ‘Local constructivists’ accept that some kinds might be natural; they merely deny that the category in question is a natural kind. ‘Global constructivists’, however, deny that any kind is natural. At this point, one can draw a distinction between *causal* and *conceptual* forms of constructivism. ‘Conceptual constructivism’ is the idea that some (or all) categories conceptually depend for their existence and features on the way that human inquirers think about things. This thesis is most often formulated as a global thesis that is intended to apply to *all* categories (see, for example, Goodman [1978]; Latour and Woolgar [1979]; and Woolgar [1988]), yet it also can be stated as a local thesis about some limited set of categories (see, for example, Appiah [1986, 1992, 1996] and Goldberg [1993]).¹² In contrast with conceptual constructivism, ‘causal constructivism’ is usually formulated as a local realist thesis; it holds that humans can create socially real kinds as a result of their causal interactions with the world. For example, some constructivists argue that the act of classifying people can cause these classifications to become real and causally meaningful (McIntosh [1968]; Foucault [1978]; Hacking [1986, 1988, 1991, 1992]). Human kinds become real when the act of classifying people influences their self-understandings and behaviours, causing them to act in conformity with a label. To see the difference between these two constructivisms, consider the following example. A conceptual constructivist might hold that the existence of individual dinosaurs, or of dinosaur taxa, depends on how we think about the world; the meaning of the term ‘dinosaur’ inevitably involves considerations that have to do with human capacities. In contrast, a causal

¹¹ Constructivism, in addition to being a thesis about kinds, can be a thesis about objects, properties, or reality. I am focusing on the social construction of kinds because of my interest in race as a social construct.

¹² See Scheffler [1980], Wolterstorff [1987], Giere [1988], Stove [1991], and Devitt [1991] for persuasive criticisms of global conceptual constructivism.

constructivist would never say that dinosaurs depend for their existence and features on us—at least not if dinosaurs existed before human beings started to interact with the world.

Using this brief taxonomy of constructivisms, we can better understand what it means to say that race is a social construct. Race constructivism is most often (and most sensibly) formulated as a *local* thesis; race constructivists deny that race is a biologically real category, while allowing the biological reality of other categories (such as species). Moreover, although most race theorists agree that races are not biologically real, they disagree over the metaphysical implications of this. Appiah [1986, 1992, 1996] and Goldberg [1993], for example, argue that races are neither biologically real nor socially real. For them, races are *conceptual constructs*—they are merely a product of the way that we think about human differences. Many race theorists, however, find this view implausible. They argue that race is a central element in many people's identities; it also plays a prominent role in how people identify and treat others. For these theorists races are *causal constructs*; as a result of the way that people treat others in the name of race, races have become socially real categories (on a par with categories such as marital status, class, and religion). Defenders of this view hold that race ought to be defined in terms of socially normed biological and cultural factors (Du Bois [1940]; Omi and Winant [1994]; Outlaw [1995]).

The third lesson that I want to draw from the cladistic concept of human race is that it poses no threat to the constructivist project; in fact, there is a sense in which the two conceptions are complementary. The reader is probably wondering how this could be: if the cladistic approach provides a biologically objective definition of race and constructivists deny the biological reality of race, how can the two coexist? The answer is that the cladistic account falls outside the constructivist's domain of enquiry. Questions about biological classification can be about ordinary language classifications, or they can be about scientific classifications. For example, the question 'is there a biologically objective way to define race' could be asking whether biology vindicates our common-sense notions of race. Alternatively, it could be asking whether there are *any* biologically objective ways to divide humans into races. The second question is more general than the first; it accepts the possibility that our conventional racial categories may be unjustified while allowing that biological races might still exist. As it turns out, constructivists are interested in the first question only. I, however, am using the cladistic account to address the second question. Moreover, since the cladistic account supports the biological reality of human race without vindicating popular conceptions, it is not in competition with constructivist accounts.

Evidence that constructivists are interested in the first question and not the second comes from two sources. First, there is the practice of constructivists; as

a matter of fact constructivists have focused their studies on popular racial categories. Second, there is the constructivist project. Constructivists are concerned with the sociology of race and race relations. In order to make sense of the problems of interracial conflict, they seek to understand the role that the race concept has played in modern Western thought and experience, and this understanding is gained by critically examining popular conceptions of race. Specifically, constructivists are interested in the commonly held belief that there are at least three biological races (Caucasians, Africans, and Asians) that differ significantly in their morphological, behavioural, and intellectual characteristics. Their concern with this conception stems from their belief that it forms the core of many common-sense notions about race. For example, it is (unfortunately) often only a short step from beliefs about morphological, behavioural, and intellectual traits to beliefs about biologically based racial superiority.

When constructivists deny the biological reality of race, they are denying that biology vindicates our common sense notions; they are not disagreeing with the conclusions generated from the cladistic account. We learn two main lessons from applying cladistic classification to Cavalli-Sforza's human family tree: firstly, biological races once existed, and the conditions necessary for maintaining racial distinctness no longer exist; and secondly, what subdivisions there are in the human species are being rapidly diminished by extensive outbreeding. Neither of these lessons helps constructivists achieve their goals. Constructivists are interested in the impact of popular biological conceptions on human behaviour. Yet scientists did not seek scientific backing for popular conceptions of race until around the seventeenth century (Banton and Harwood [1975]). By this time, biological races were already on the road to obsolescence. Moreover, it is likely that if current races *do* exist, they cross-classify folk racial categories. For example, most people believe that African-Americans are more closely related to the Bushmen than they are to Caucasian-Americans. The cladistic account, however, would lead to the opposite conclusion. The reason is that the Bushmen are aboriginal populations that have remained largely reproductively isolated (even in more modern times). African-Americans and Caucasian-Americans, on the other hand, have not been reproductively isolated. Hence, the latter two groups would probably be in the *reticulated* part of the tree, while the Bushmen might get their own distinct branch. This constitutes further evidence that popular notions of race are indeed social constructions without any basis in biological fact.

By clarifying the ambiguity in questions about the existence of biological races, it is possible to appreciate the importance of both conceptions of race. The cladistic conception helps systematists understand the patterns and processes of human evolution. Constructivist conceptions,

on the other hand, aid our understanding of social and political implications of current uses of the term. Both perspectives should be recognized as legitimate.

6 Conclusion

I have argued that race theorists have been too quick to reject the biological reality of race. Cladistic classification, in conjunction with current work in human evolution, shows that biological races once existed, but they may no longer exist. It is possible to accept a biological account of race without accepting odious claims about genetically based racial superiority. Furthermore, the historical character of the cladistic concept means that it is not in conflict with most constructivist views.

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