

Are human races cladistic subspecies?

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In the article titled 'A New Perspective on the Race Debate', Robin O. Andreasen argues that contrary to popular scientific belief, human races are biologically real — it is just that we are wrong about them. Andreasen calls her contemporary biological concept of race 'the cladistic race concept' (or CRC). Her theory uses theory from cladistics — a systematic school founded by entomologist Willi Hennig in 1950 — to define human races genealogically as cladistic subspecies. In this paper I will argue that despite its promise as a biological definition of human races, Andreasen's CRC is unconvincing. In particular, I will show that the central problem of the CRC is its attempt to apply cladistics below the species level. In other words, there is good reason not to think that cladistic subspecies are not real, and therefore, they cannot be the target of a realist concept of race.

Introduction

Much of the consensus that race is biologically unreal follows Richard Lewontin's (1972) oft-cited claim that racial classification in humans is biologically meaningless because there is more genetic variation within so-called 'races' than between so-called 'races'. Since significant genetic difference between races is often part of the biological concept of race, Lewontin argues that the actual genetic homogeneity across races means that the human species is too genetically similar to be divided into discrete gene pools that might qualify as 'races'.

Andreasen (1998, 2000, 2004, 2005, 2007) proposes that contrary to popular scientific belief, races are biologically real — it is just that we are wrong about them. She argues that where theorists like Lewontin are incorrect in their analysis of human race is by assuming that *similarity* should be the basis of 'an objective classification scheme in systematic biology' (Andreasen 2000: p. S657). These theorists have not considered a *genealogical* definition of human races as

cladistic subspecies (p. S657). Andreasen contends that human races, as cladistic subspecies, are biologically real and that cladistic subspecies suitable as candidates of human race.

In this paper I argue that Andreasen's defence of human races as cladistic subspecies is unconvincing. In particular, I will show that the main problem with Andreasen's Cladistic Race Concept (CRC) and the cause of its failure as a biological definition of race is its attempt to define race by applying cladistics *below the species level*. In other words, there is good reason to think that cladistic subspecies are not real, and therefore, they cannot be the target of a biological conception of race.

In the next section, I begin by describing Andreasen's CRC and I explain how the CRC posits human races as cladistic subspecies. In the subsequent section, I argue that human races cannot be defined cladistically because of the problems encountered with applying cladistics below the species level. I show that Andreasen fails to provide sufficient evidence that human races are indeed cladistic subspecies. Moreover, that cladistic subspecies are theoretically useful is doubtful.

Cladistic Races?

Problems of classification

After systematists rejected biological essentialism because it conflicted with evolutionary theory, biologists began to consider two different schools of classification (Andreasen 2000: p. S656). The first is pheneticism and it classifies taxa according to *overall similarity* (p. S655). Groups of organisms are classified as species using the criterion of resemblance, and the same process is used for higher taxa and subspecies as well. The second school of classification is phylogenetic classification and it defines taxa (particularly, higher taxa — anything above the species level) solely on the basis of *common ancestry*. That is, 'species that share a recent common ancestor belong to the same genus; species that share a more distant common ancestor belong to the same family, etc' (p. S655).

Andreasen argues that while both schools of classification are thought to be objective, only phylogenetic classification is in fact objective. Specifically, the goal of phylogenetic classification is to illustrate the branching process of

evolution — phylogeny tells us the criterion according to which organisms should be grouped (Sterelny and Griffiths 1999: p. 186). Andreasen claims that since this evolutionary process does not depend on any human classification system, phylogenetic classifications are themselves also objective.

The problem with phenetic classifications, in contrast, is that determining the overall similarity between any two things seems to be a largely arbitrary matter because there are so many different measures of similarity.

Firstly, because individual organisms possess countless traits, it is difficult to decide which of these traits counts as a character. A character is an attribute that all members of a specific taxon have either in its original state or in a transformed state. In contrast, a trait is an attribute that occurs in only some but not all members of a taxon (Davis and Nixon 1992: p. 421). But the problem is that there are different types of traits — for example, there can be a genotypic trait, or there can be a phenotypic trait. Additionally, even within these different types of traits, there are numerous other traits.

Secondly, pheneticism encounters the ‘problem of weighting’ — this is problem of assessing which trait is important and which is not (Andreasen 2000: p. S656). For example, Biologist A could argue that wing pattern is a good weighting method of butterfly similarity. Biologist B, on the other hand, could argue that it is wing shape that is a better measure of butterfly similarity since the wing pattern varies with seasons. Although pheneticists argue for various weighting of traits, there is no clear-cut way to settle the kind of debate Biologist A and B might have.

Finally, there are also a variety of ways in which to spell out similarity. This adds to the pheneticism’s mounting problems. The point here is that if these species of butterflies are similar organisms that could be classified according to a number of different measures of similarity, then phenetic classifications are in fact very subjective (Sterelny and Griffiths 1999: p. 184).

We can now understand why Andreasen suggests that theorists, including Lewontin, have been mistaken in their ideas about race. These theorists assume that racial classifications ought to be based on similarity, without considering genealogy as the basis of an objective classification scheme. For example, according to the typological species concept, organisms must share a common

essence in order to be considered members of a specific species. On the other hand, the geographical concept classifies taxa according to overall similarity. Both these concepts are based on phenetic methods whose objectivity we have just called into question. Andreasen argues that since it is now genealogy, and not similarity, that is considered a basis for an *objective* classification scheme in most areas of systematic biology, races should also be defined genealogically, much like taxa are defined in cladistics (Andreasen, 2000: p. S655). But what exactly is cladistics and why does Andreasen maintain that it can be successfully adapted to defining human races?

In 1950, East German entomologist, Willi Hennig founded cladism, which defines higher taxa according to common ancestry. Usually, the evolutionary process takes the form of a branching pattern. If species with a unique, immediate ancestor are organised into a phylogenetic tree (a tree representing descent), higher taxa can be classified as monophyletic groups — that is, as Andreasen has defined them, ‘groups composed of an ancestor and all of its descendants’ (p. S657).

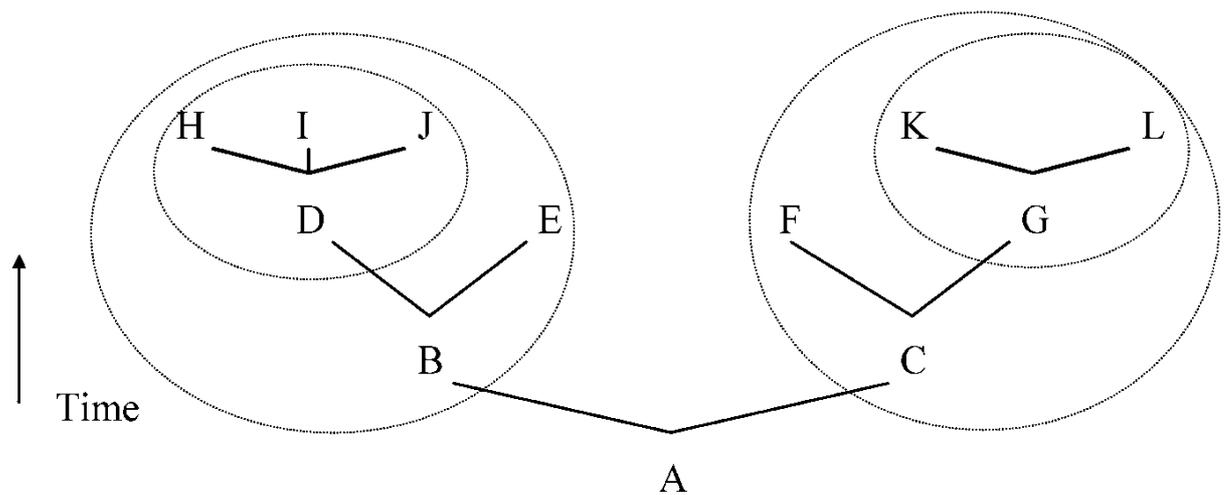


Figure 1. (Andreasen 2004: p. 426)

Figure 1 is a phylogenetic tree in which the terminal nodes or relations (A, B, C etc.) designate well-defined species. Each of the branches represents cases in which a daughter species (for example, ‘E’) has split from the lineage of a parent species (e.g. ‘B’) as a result of reproductive isolation. The circles in the tree (e.g. GKL or DHIJ) each represent a ‘nested hierarchy of monophyletic groups’ (Andreasen 1998: p. 209) — if you consider this phylogeny in relation to Linnaeus’

taxonomy, the smallest monophyletic group identifies genera, the largest group after that identifies a family etc. (p. 208). Andreasen also states that an important feature of cladistic classifications is that they are objective because they are based on common ancestry (p. 200).

How is common ancestry itself objective? Andreasen provides the same argument for the objectivity of cladistic classifications as the one used to express the objectivity of phylogenetic classifications. Recall that she states that the processes of evolution are objective. The goal of phylogenetic classifications is to represent these processes of evolution therefore Andreasen maintains that these phylogenetic classifications must themselves also be objective. Cladistic classifications, Andreasen explains, are objective in a similar way to phylogenetic classifications because cladistic classifications represent the branching process of evolution and monophyletic groups 'which exist independently of human classifying activities' (p. 200).

The Cladistic Race Concept (CRC)

Although cladistic classification was, as mentioned above, developed to define higher taxa, Andreasen (2000: p. S655) contends that it can be used to define subspecies, and therefore human race. Instead of creating a phylogenetic tree from species, as is customary in cladistics, a cladistic definition of human races (as subspecies) would create such a classification from human breeding populations. These populations are 'set[s] of local populations that exchange genetic material through reproduction and are reasonably reproductively isolated from each other' (Andreasen 2000: p. S657).

Roughly, let us take a breeding population of Africans 200 000 years ago as the parent population. We could say that a European breeding population was 'born' or split from this African one as a result of geographic barriers (like the rivers and oceans between Europe and Africa) or certain socio-cultural factors (Kitcher 1999). The European population would then represent a new branch on the human phylogenetic tree because there is limited gene flow between the two populations. If we were to input this scenario into Figure 1, terminal node A would identify the African breeding population, B or C would identify birth of the new

European breeding population, and the whole phylogenetic tree would represent the human species.

If we now go back to our discussion of race, the CRC posits races as *cladistic subspecies*. According to the CRC, cladistic subspecies or races should be defined as 'a nested hierarchy of monophyletic groups' within the human species (Andreasen 1998: p. 209). Turning again to Figure 1, the monophyletic groups GKL, DHIJ, BEDHI etc. represent all and only the descendants of the human species and therefore constitute a nested hierarchy of human races. Formally, according to the CRC, human 'races are ancestor-dependant sequences of breeding populations that share a common origin' (p. 200).

Andreasen states that support for extending cladistic classification to defining human races as cladistic subspecies can be found in recent work by human evolutionists. For over fifty years now, by gathering extensive genetic data of living populations, a number of human evolutionists (e.g. Cavalli-Sforza et al. 1994) have tried to reconstruct a phylogenetic tree that denotes the evolutionary relations of reproductively isolated human breeding populations. Using genetic distance, which measures the frequency in genes between different populations, these evolutionists attempt to estimate the degree of relatedness between human populations. They reason that human beings share a common origin. As human populations migrated out of Africa, mutations occurred and differences between populations accumulated. If two populations have a close genetic distance, it is hypothesised that they are also closely related ancestrally.

At this point, it is important that I address a worry that may arise in the reader's mind. It may seem that these evolutionists' attempts to construct phylogenetic trees are based on the same (phenetic) assumption that Lewontin (1972) makes, namely, that in order to define human races there must be genetic homogeneity within races. In what Andreasen (2007: p. 463) calls 'Lewontin's genetic argument', Lewontin argues that the fact that there is more genetic distance *within* common sense human races (like the African race) than between human races (like the African and the Caucasian race) precludes a meaningful biological definition of race.

But note that Lewontin insists that genetic distance between human races is a *necessary condition* of a *definition* of race. For him without significant genetic

distance between human populations, there can be no races. These evolutionists, however, use genetic distance between populations as *evidence* of the different lines of evolutionary descent between human populations (that is, as evidence that populations have been reproductively isolated). As such, their classification does not make genetic distance a necessary condition for defining human races. For this reason, Lewontin's argument affects neither the attempt to create a human phylogenetic tree nor the cladistic definition of races Andreasen proposes.

Consider Figure 2, which Andreasen (1998: p. 212; 2000: p. S660) references as an example of such a branching diagram.

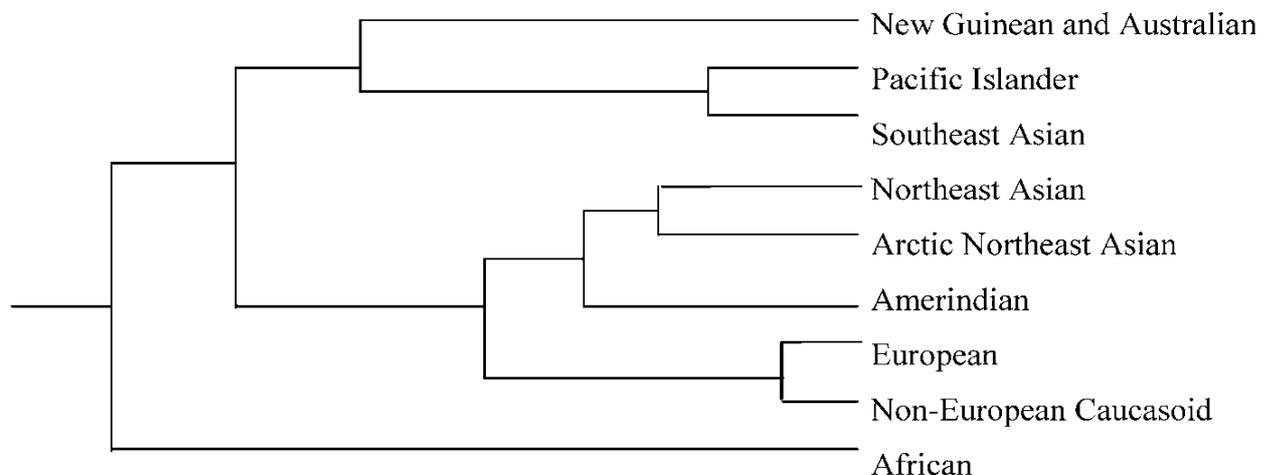


Figure 2. (Andreasen 1998: p. 212; 2000: p. S660)

Cavalli-Sforza et al. (1994) inferred this phylogenetic tree by calculating 'the genetic distances between 120 different gene states for forty-two aboriginal populations' (Andreasen 1998: p. 211). The trunk of this phylogenetic tree represents a population of racially undifferentiated human Africans. The first split from this trunk identifies a local subpopulation of these Africans who became reproductively isolated from their 'parent' population by migrating out of Africa. Therefore, Africans and non-Africans have the greatest genetic distance. Each subsequent split, or branching point, represents further migration and reproductive isolation of breeding populations. In this hierarchy of monophyletic groups, Caucasoid, Amerindian and African, for example, are monophyletic groups, and therefore cladistic races.

Importantly, Andreasen maintains that this phylogenetic tree shows that ancestral cladistic human races *once existed* — that is, there once was evolutionary

branching in the human species. But since that initial branching, there has been a large amount of interbreeding between different human breeding populations. As such, according to Andreasen, today ‘races [...] are on their way out’ due to the relative lack of reproductive isolation required to demarcate cladistic races (p. 215).

Problems with the CRC

To be sure, for Andreasen, so long as 1) human evolutionists are able to reconstruct a human evolutionary tree that represents evolution; and 2) this tree represents a branching pattern, it remains the case that races can be defined cladistically.

In what follows, I argue that Andreasen’s defence of cladistic subspecies as human races is unconvincing. In particular, I will show that the main problem with the CRC, and the cause of its failure as a biological definition of race, is its attempt to define race by applying cladistics *below the species level*. In other words, there is good reason to think that cladistic subspecies are not real, and therefore, they cannot be the target of a biological conception of race.

I wish to explain why races cannot be defined cladistically through the following four-step dialectic:

- (i) **The objectivity objection (OO):** Andreasen has failed to establish the objectivity of cladistic subspecies.
- (ii) **The epistemic usefulness reply (EUR):** Andreasen might retort by claiming the usefulness of cladistic subspecies.
- (iii) **The arbitrariness objection (AO):** There are, however, reasons to think that treating human breeding populations as cladistic subspecies is *not* epistemically useful.
- (iv) As such, cladistic races are neither objective nor epistemically useful. Cladistic subspecies are not real and cannot be part of a biological conception of race.

In what follows I elaborate on each of these points.

The objectivity objection (OO): Andreasen has failed to establish the objectivity of cladistic subspecies

Assumptions

Before I begin with my argument, notice the assumptions Andreasen makes in her definition of race. Firstly, although she states that biologists use the term 'race' and 'subspecies' interchangeably, Andreasen assumes that a definition of the one ('subspecies') suffices for the other ('race'). Pigliucci and Kaplan (2003) have defined biologically meaningful human races as ecotypes and what they do in their definition is look to the ways in which 'race' is used in nonhuman biology. What they find is that in some contexts, 'race' is explicitly connected with and defined as 'subspecies' — even Darwin, for example, defined race as subspecies (*ibid.*). But what these authors stress is that in the current biological literature, the connection between race and subspecies is much more ambiguous. Templeton (1999: p. 632) also highlights that it is unclear just what the precise definition of 'subspecies' is. What I am getting at here is that the match between arguing for race versus arguing for subspecies is not as matter-of-factly clear-cut as Andreasen assumes. There are many ways to define race. Indeed, Pigliucci and Kaplan, who are unconvinced by Andreasen's CRC, maintain that arguments against the biological races are strongest against definitions of human race as incipient species.

Secondly, Andreasen assumes a realist account of natural kinds. Phillip Kitcher, who has independently argued for a definition of race similar to the CRC, describes this realist account as the view that the task of the sciences is to trace the 'objective fault-lines' on which nature runs (Kitcher 2007: p. 299). The idea is that nature exists and is divided independently of our human classifying activities. A division of species, for example, by 'interruption of free reproduction' is seen as an objective boundary upon which to demarcate natural kinds (*ibid.*). To see how Andreasen adopts this realist account of natural kinds in her definition of race, consider how she describes systematists' interest in defining race.

Andreasen argues that when systematists search for a biologically objective definition of race, their goal 'is to determine whether race represents an *objective* feature of reality' (Andreasen 2000: p. S661; *emphasis added*). That is, systematists are interested in whether races 'exist objectively' or if races 'exist independently of human classifying activities'. Indeed, she calls her CRC a 'biologically objective definition of race' (pp. S656–S657). The task Andreasen

creates for herself then is to establish the objectivity of cladistic subspecies as races. This is the point on which the objectivity objection turns — does Andreasen actually establish the objectivity of cladistic subspecies?

Objectivity?

I have two things to say about this. The first is that ‘objectivity’ is a high bar for a theory of race and it assumes a certain transparency of nature to us. Interestingly, in his 2007 paper entitled ‘Does Race Have A Future?’ Kitcher argues that the realist account of race he took in his early definition of race is no longer persuasive for several reasons. He notes that nature does not just come ‘nicely organised with fence-posts’ — the divisions we see in nature very much depend on the particular enquiries we undertake (Kitcher 2007: p. 299). He adds that this is not to say, and I agree with him here, that there is no world independent of us. He adopts a pragmatist account of natural kinds and insists that there are many ways to demarcate objects in the world. There are, for example, many species concepts. But even within one species concept like the Biological Species Concept, there will be many different ways in which to go depending on how one conceives of what, for instance, a population is.

What many philosophers have done in theorising about race is get into metaphysical debates about natural kinds, and this, I think, takes away from more fruitful and specific questions we can ask about race. I think that we should separate the general question of realism about natural and especially biological kinds, from the question of whether it is possible to pull out an interesting concept of race and do something with it. I also do not mean to imply that pragmatism is or should be rampant in biology. My point here is that it is not that nature simply ‘exist[s] independently of human classifying activities’ (Andreasen 2000: p. S657) — nature is shaped by the particular enquiries we undertake.

Andreasen assumes that human phylogenetic trees are objective and she downplays the historically and socially contingent aspect of human phylogenies. As Gannett (2004: p. 332), who criticises Andreasen’s CRC, points out, populations are the base units of the human phylogenies Andreasen talks about. What this reflects is our *particular* interest in *populations* when it comes to human evolutionary history — for these phylogenies could just as well be constructed

with chromosomes as base units, for example. This might very well lead to a human phylogenetic tree that looks different from the Cavalli-Sforza tree Andreasen uses. Much like the Biological Species Concept example, even if we agree to take populations as the basic units for human phylogeny, how we demarcate the boundaries between populations will depend on the definition of a population we hold. Andreasen's CRC does not capture this conventional aspect of classification.

My second point about objectivity is that if the CRC is the 'biologically objective definition of race' Andreasen argues it is, then surely she should provide some more empirical evidence that cladistic subspecies are indeed races.

To see why this is the case, consider the kind of support Andreasen cites for the CRC. Andreasen thinks that we are able to define races cladistically — that is, apply cladistics below the species level — because human evolutionists, like Cavalli-Sforza et al. (1994) and several other research groups, are able to reconstruct a human phylogenetic tree (recall Figure 2) (Andreasen, 2007: p. 472). The aim of phylogenetic analysis is the discovery of descent relations among species, and the goal of cladistics is to reconstruct descent relations among biological taxa in a purely genealogical way. Therefore Andreasen argues that cladistic races are objective because they aim to reflect the hierarchy of a branching human phylogenetic tree, which is itself objective. Andreasen maintains that as long as human evolutionists can create accurate human phylogenetic trees, we can infer the existence of cladistic races from these trees.

Now there are a number of controversies surrounding Cavalli-Sforza's tree — these include the method of tree construction and the fact that Cavalli-Sforza argues that this phylogenetic tree should not be used to ground theories of race. Andreasen acknowledges these controversies but she insists that 'these difficulties need not concern us here' (Andreasen, 1998: p. S661). For her, the empirical details of Cavalli-Sforza's tree do not matter. As long as such trees can be created, the conceptual point remains that races can be defined cladistically. We need more than this conceptual point to mark cladistic subspecies off as human races.

There are two models of human evolutionary history — the candelabra and the trellis model (Templeton, 1998: p. 636). The candelabra model, on which

Cavalli-Sforza's tree is based, fits well with Andreasen's definition of cladistic races as inbred lineages within the human species. It posits the out-of-Africa thesis in which different geographical groups (like the Europeans and the Asians) split off from the parent African population. These geographical groups can therefore be portrayed as independent branches on the evolutionary tree.

But Templeton favours the other model of human evolutionary history. In the trellis model, human evolution does not have a branching structure. The trellis model posits extensive gene flow throughout human history. According to this model, there can be no separation of the human species into distinct evolutionary lineages. As such, 'human races are not valid subspecies' (p. 636). The difficulty for Andreasen is that, as Gannett (2004: p. 330) highlights, her defence of the CRC is premature without definitive evidence in the way of the validity of the candelabra model of human evolution. Until a definitive branching structure for human evolution has been established, the CRC is underdetermined by available evidence.

Andreasen (2007) address this and other criticisms. She argues that Templeton's criticism is of limited scope because there are other ways in which to generate a phylogenetic tree, other than using genetic distance as the candelabra or trellis model would do. I agree that does limit Templeton and Gannett's criticism but there is no definitive evidence for the kind of separation into lineages that Andreasen's CRC requires. In fact Andreasen herself acknowledges that if the trellis model were the right one, whether or not there are other ways to generate a human phylogenetic tree, there could not have ever been any cladistic subspecies. All that Andreasen establishes is that one is allowed to consider the possibility that races can be defined cladistically. To reiterate the objectivity objection, Andreasen has not given definitive evidence that cladistic subspecies in humans 'exist objectively' and exist 'independently of our classifying activities' (Andreasen 1998:209). As I will explain in the arbitrariness objection (AO), what we need is empirical evidence from Andreasen of the kind that humans races do represent separate cladistic subspecies because at some time humans did not interbreed.

The epistemic usefulness reply (EUR): Andreasen might retort by claiming the epistemic usefulness of cladistic subspecies

One way in which Andreasen might respond to the OO is to claim that cladistic subspecies as human races play some sort of useful role in biology. In the OO, I mentioned that objectivity is a high bar for a theory of race. Questions of objectivity often lead to murky scientific realism issues. Even if there are objectively real natural kinds, we cannot assume that all or most of them lie within our epistemic scope (Spencer 2011: p. 189). If one holds objectivity as the bar for one's theory, some kind of empirical evidence is needed to support one's theory, but even still, exactly how much evidence is needed to mark a kind off as objective is questionable.

Andreasen's CRC is liable to the OO because of her contentious metaphysical stance that race must be a natural kind, i.e. objective to be biologically real (Andreasen 2000: p. S655). I agree with Kitcher (2007: p. 298) and Spencer (2011: p. 196) that this contentious metaphysical assumption is unnecessary in the race debate. Much less controversially, and much more practically, Andreasen could seek to determine if cladistic subspecies are useful in biology, or if they play some sort of epistemically useful role in cladistics. Let me explain what I mean by epistemically useful role and the EUR. For this I will borrow some terminology from Spencer's (2011) account of genuine kinds.

Spencer looks at cases of good classification in science, and asks why kinds like electron or gene are important in science. He argues that these kinds are important because they allow biologists to answer questions in biology in a theoretically interesting way (p. 199). Spencer defines genuine kinds as valid kinds in scientific research programmes (or SRPs) (p. 186). These kinds are valid because they play an epistemic role of scientific kinds in SRPs. The reason why scientists posit these kinds in the first place is because of this epistemic usefulness role.

The epistemic role of valid kinds in science is threefold. First, a valid kind in an SRP plays the role of 'observational usefulness' — it underwrites observational generalisations that are important in a certain epistemic context (p. 187). Second, a kind can be valid if it plays the role of 'theoretical usefulness' in an SRP — that is if it underwrites theories in the SRP. Third, a valid kind plays the

epistemic role of ‘presuppositional usefulness’ — it underwrites ‘presuppositions of experience, such as fundamental laws and definitions’ (p. 187).

Spencer explains that for a kind to be valid in an SRP it must be epistemically useful in one or more of the ways described above. Moreover, that kind must be *epistemically justified* in an SRP. There are two ways to justify valid kinds and these correspond with the epistemic usefulness a kind has. A kind whose usefulness comes from it underwriting presuppositions is called a ‘relativised a priori kind’ (p. 190). This kind is epistemically justified in an SRP so long as it is ‘well-motivated according to the aims and epistemic values of that SRP’ — if a kind promotes empirical adequacy in an SRP, for example, then it is well motivated (p. 190). A kind whose usefulness comes from it underwriting theories is called a properly empirical kind. If this kind explains observational laws in an SRP, then it is epistemically justified in an SRP.

Spencer provides several good examples of valid kinds, one of which is a monophyletic group as an example of a relativised a priori kind. Since I have already explained cladistics, and I need to explain the match between Spencer’s account of genuine kinds back to the CRC and the EUR it will be useful to explain in some detail why a monophyletic group is considered a genuine kind in cladistics. What Spencer shows with this example is that a monophyletic group is epistemically useful in cladistics. Also, although alternative kinds could have been used to define taxa in cladistics, only a monophyletic group is well motivated, or epistemically justified, according to the aims of cladistics.

If William and Harry are all of Prince Charles of Wales’ children for example, the group Prince Charles, William and Harry is a monophyletic group (adapted from Spencer 2011: p. 190). Recall that in cladistics, higher taxa are defined as monophyletic groups of species. To be sure, cladists could have defined higher taxa as paraphyletic groups or polyphyletic groups. A paraphyletic group consists of an ancestor and only some of the descendants of the ancestral species (Grant 2003: p. 1264). Prince Charles and Prince William are an example of a paraphyletic group. A polyphyletic group, on the other hand, includes an ancestor and some descendants in such a way that one or more of the descendants in the group do not descend from ancestor. For example, Prince Charles, Prince Harry and myself form a paraphyletic group because I am not a descendent of Prince

Charles (Spencer 2011: p. 190). However, monophyletic groups are uniquely useful in cladistics because only they promote cladistics' aims and epistemic values.

One essential aim of cladistics is to classify taxa in a purely genealogical and hierarchical way. A hierarchical classification of taxa means that a current taxon must be generated by either a subdivision or a replication 'of previously existing ancestors' (David and Nixon 1992: p. 435). There are two major reasons why monophyletic groups are uniquely useful in cladistics. The first is that paraphyletic and polyphyletic groups guarantee a hierarchical classification of taxa, but neither guarantees a *purely* genealogical classification (Spencer 2011: p. 190). Presumably, empirical adequacy is an empirical value of cladistics, as such monophyletic groups are epistemically justified because they promote empirical adequacy in cladistic classification (p. 190).

Moreover, Grant (2003: p. 1264) explains that paraphyletic groups are often rearranged into monophyletic groups to create an accurate cladistic classification. What this underwrites is that monophyletic groups have *good reason* to feature in cladistics. Monophyletic groups support various generalisations and facilitate the aims of cladistics in a way in which paraphyletic and polyphyletic groups cannot. To use Spencer's terminology, monophyletic groups are both epistemically useful and justified in cladistics.

If I bring this discussion back to defining race and the CRC, despite the flaws in his arguments, Lewontin (1972) (and indeed most race theorists) is clearly brought to the discussion of race by the presumption that in order for race to make its way biologically, it has to *do* something. There must be good reason for race to feature in biology. Race should facilitate biology or make useful predictions in biology.

I want to apply Spencer's notion of why kinds are posited in science to the CRC. By usefulness, henceforth, I mean a positive answer to this question: Are cladistic subspecies epistemically useful in any of the three ways spelt out by Spencer? Do cladistic subspecies have any observational, theoretical or presuppositional usefulness in cladistics? My hope is that this will suggest an answer to this underlying question: Are races-as-subspecies epistemically

justified in cladistics, that is, justified as an epistemic tool for investigating and theorising about the world?

One way in which Andreasen could respond to my objectivity objection is to relinquish objectivity as a standard for her theory, and instead argue that cladistic subspecies are like other useful kinds in biology, such as gene or population. This is the epistemic usefulness reply or EUR. In keeping with what is actually happening in biology — that is, in keeping with how kinds are posited by biologists in the first place because of how these kinds are epistemically useful — Andreasen could instead ask if cladistic subspecies play either one of the epistemically useful roles I mentioned in explanation of Spencer's notion of genuine kinds.

The epistemic usefulness of a race concept in cladistics would avoid potentially problematic commitment to realism about kinds. In this regard, it would perhaps be in keeping with the epistemic attitude of biology as a science. Arguably, biology is fairly pragmatic, where issues of kind-hood are concerned. There are a number of cases in biology where the epistemic usefulness of a kind matters more than the question of whether that kind is objectively real: the concept of organism and the concept of species, for example. On the epistemic usefulness reply, the concept of race might be added to this list of ontologically uncertain but epistemically useful concepts.

Consider again the case of species in biology. There may not be objectively real species like ecological species or molecular species. In fact, intellectual battles continue about the existence of species and their status as objectively real natural kinds. Yet biologists continue to use different species concepts for different kinds of generalisations in biology. In what follows, I argue that Andreasen's CRC would still fail even if she took this epistemic usefulness line of defence for her CRC — there are many reasons to think that cladistic subspecies in humans are not epistemically useful.

The arbitrariness objection (AO): Moreover, there are reasons to think that treating human breeding populations as cladistic subspecies is not epistemically useful

The arbitrariness of classification

Firstly, using cladistics, Andreasen defines races as monophyletic groups. However the a priori objection to taxonomic 'lumping' of humans into large groups is its arbitrariness. An uncertainty arises about where to label the boundaries between taxa. If you consider that every lineage in a phylogenetic tree includes sub-trees, then the level at which you label this or that sub-tree as a hierarchy of monophyletic groups becomes arbitrary. It seems that no classification of races in this way is more correct than any other (Levin 2002: p. 30). The arbitrariness of classification is a conceptual problem for Andreasen's CRC because it introduces a conventional aspect in not just her classification but also in the phylogenetic classifications on which she supports the objectivity of her tree.

Andreasen's (1998: p. 213) first reply to the arbitrariness of classification is that it applies to any and all narrower or wider classifications — it is true but trivial that all classifications could be arbitrary in this way. But if arbitrariness is a problem for every classification, then this gives us no reason to adopt Andreasen's specific classification over any other in defining race. Again, Andreasen will have to argue why her classification is more useful than other classifications.

Andreasen's second reply to this objection is that 'we can simply define "race" as a nested hierarchy of monophyletic groups' (p. 213). What this means is that cladistic subspecies or human races represent an *entire* nested hierarchy of monophyletic groups. In this way the arbitrariness of classification is circumvented because there is no need to label a specific sub-tree as a monophyletic group. Instead, the whole nested hierarchy of human monophyletic groups represents races.

But if human races are an *entire* nested hierarchy of monophyletic groups, then there are also nested hierarchies at every level of the human phylogenetic tree. So there will be a lot of races. Indeed we will have races (nested hierarchies of monophyletic groups) *within* races (nested hierarchies of monophyletic groups). This could go on all the way down to the family level. This should definitely strike us as a strange definition of race because we do not think of human races as races within races. We cannot even call these nested hierarchies within nested hierarchies sub-races because according to Andreasen's definition,

they *are* races, or cladistic subspecies. Not only is this an odd definition but it not particularly useful either. It is unclear in which kind of context such a definition of race could be useful.

Are cladistic subspecies justified?

I have just argued that cladistic subspecies are not epistemically useful in the way scientific kinds should be, but are they somehow epistemically justified in cladistics?

There exists the problem that cladistics was specifically designed to define higher taxa, not any taxa below the species. The question is: if human races as subspecies can be defined cladistically, then why have biologists been reluctant to apply cladistics to lower taxonomic levels? Is it just because of 'mere force of habit' on the part of biologists as Andreasen (1998: p. 209) argues or is there more to it? In what follows I argue that it is not justified or well motivated according to aims in cladistics to apply cladistics to subspecies. If we start with reasonably recognisable species in cladistics, we can infer higher taxa. However, if we start with human breeding populations — if we attempt to infer taxa below the species level — we cannot infer cladistic subspecies.

It will be useful here to explain the aims of cladistics. Hennig 'initially described phylogenetic analysis as a means of reconstructing hierarchic descent relationships among species' and this is why he meant for cladistic classification to be applied to higher taxa (David & Nixon, 1992: p. 422). Cladistics uses species (as terminals) to infer relations of higher taxa because species are already hierarchically related to each other — a branching structure is clear in the relation of species. Moreover, because a cladistic classification does not necessarily demonstrate the hierarchic descent relationship that underlies the patterns it reflects, it must be determined that the phylogenetic analysis satisfies what I will call the 'hierarchic descent condition'.

Therefore according to cladistics, if Andreasen seeks to represent the phylogenetic relation of human populations in a cladistic classification of races, she must either prove that the terminal relations (the relations between breeding populations) are hierarchic, or she must somehow show that their hierarchic nature is not important for her classification.

So why does Andreasen use breeding populations as the terminal nodes of her cladistic classification of human phylogeny? For Andreasen's definition to hold, and for her to justify using human breeding populations as nodes, she must show that human populations are or once were hierarchically organised — that is, that breeding populations were once sufficiently reproductively isolated to form incipient species and therefore arose from the subdivision of ancestral populations into two or more descendant populations.

Recall my discussion of the two models of human evolution — the trellis and the candelabra model. In order for a species to diverge, gene flow must be limited for long amounts of time. Gene flow is the transfer of alleles from one group to another. It is gene flow that is the main evolutionary force shaping human genome diversity (Marks 2010: p. 268). To define races as clades is to assume that there once was sufficient limited gene flow between human populations so that distinct evolutionary lineages (subspecies or monophyletic groups) within the human species were formed and which we can call races. The CRC requires that that these lineages were indeed formed. These lineages mean that evolution does indeed take a branching structure and that human populations were once hierarchically organised.

However, there seems to be more support for the trellis model — that is for the idea that human populations never did form inbred lineages. Pigliucci and Kaplan argue that gene flow has been rampant in human populations for tens of thousands of years:

There are no extant populations of our species that are plausible candidates for being incipient species. Further, the current distribution of genetic variation within *H. sapiens* implies that at no time in the past were any of the (currently extant portions of the) population evolving independently (2003: p. 1164)

The CRC requires that human subspecies were once a) genetic differentiated, b) over long periods of time historical continuity — yet support for this is not forthcoming (Templeton 1999). To be sure, I am not making the same mistake as Lewontin to assume that the current low genetic distance between

racism precludes a partitioning of the human species into distance lineages (i.e. races). I agree with Andreasen that Lewontin's results actually agree with the CRC, since the CRC maintains that races are dying out. As such, little genetic variation between races is expected. Rather, in the same way that Andreasen uses phylogenetic trees to go back in time and define race there, I am examining whether there ever was the limited gene flow and reproductive isolation (the 'hierarchical descent condition' of breeding populations) needed to produce different human evolutionary lineages (i.e. races) at that time before colonisation. Since there is little support for phylogenetically distinct human populations, cladistic subspecies are not justified in cladistics. Andreasen has not shown that cladistic subspecies are real, and because there is in fact great reason to think they are not real, cladistic subspecies cannot be candidates for a realist concept of human race.

Conclusion

I have presented Andreasen's CRC as a contemporary way to define human races biologically. I have argued that Andreasen does not establish the objectivity of cladistic subspecies as she aims to do. Moreover, I have argued that cladistic subspecies are not epistemically useful or justified in cladistics as a scientific kind should be. Andreasen's CRC ultimately fails by trying to define race by applying cladistics below species level. From this paper, I hope that more discussions can be had about the biological basis of race and about contemporary approaches to defining race biologically.

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