

Troubles for Cluster Conception of Species

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Abstract:

In the face of the difficulties that plague the hypothesis that there exist intrinsic properties both necessary and sufficient for membership in any given biological kind, some philosophers (e.g., Dupré 1981, 1993) have come to argue that the properties that characterize biological species at least tend to “cluster,” and that membership in biological species accordingly depends on the possession of *enough* of the characteristic properties of the kind, rather than of *all* the typical properties of the kind. The cluster theory may in fact be characterized as an attempt to salvage essentialism about natural kinds by loosening up the definition of an essence. Cluster theories come in various forms. The similarity approach to species requires that members of a species be more similar to one another than to any non-member, and comes in two varieties, depending on whether its proponents postulate that *all* similarities or only genetic similarities must be taken into account in grouping individuals into species as well as into higher order taxa. In this paper, I critically evaluate the two most prominent versions of the cluster thesis as it applies to biological species—namely the “overall” similarity approach (better known as the phenetic approach) and the genetic similarity approach—in order to determine whether some attenuated form of intrinsic essentialism about species can be salvaged.

1. Introduction

In the face of the difficulties that plague the hypothesis that there exist intrinsic properties both necessary and sufficient for membership in any given biological kind, some philosophers (e.g., Dupré 1981, 1993) have come to argue that the properties that characterize biological species at least tend to “cluster,” and that membership in biological species accordingly depends on the possession of *enough* of the characteristics properties of the kind, rather than of *all* the typical properties of the kind. To put the point differently, although species cannot, according to cluster theorists, be defined in terms of single characters or in terms of several *universally* co-varying characters, they may nonetheless be defined *polythetically*, that is, in terms of *statistically* co-varying properties (Hull 1984). Dupré’s conception of species provides a good example of this view:

The existence of species, I suggest, may be seen as consisting in the following fact. If it were possible to map individual organisms on a multidimensional quality space, we would find numerous clusters or bumps. In some parts of biology these clusters will be almost entirely discrete. In other areas there will be a continuum of individuals between the peaks. It can be seen as the business of taxonomy to identify these peaks (Dupré 1981, 82).¹

Since the cluster theory does not require that any property occur in all and only the members of a given species, it is not, strictly speaking, an essentialist doctrine. It nonetheless closely resembles essentialism in characterizing species in terms of similarities in the intrinsic properties of their members. The cluster theory may in fact be characterized as an attempt to salvage essentialism about natural kinds by loosening up the definition of an essence. Cluster theories come in various forms.

¹ As will be discussed below, Dupré’s approach to taxonomy is in fact pluralistic (or rather *was* pluralistic, since he has recently shifted towards what he calls a “feeble monism” (1999, 18)). Following the passage quoted above Dupré goes on to say that “this picture also makes clear why the deliverances of taxonomy need not provide the distinctions that are relevant for more specialized interests When the classificatory problem is approached from a more restricted point of view, that is, with an interest only in a certain range of properties, many peaks will disappear, while others may be emphasized” (Dupré 1981, 82).

The similarity approach to species requires that members of a species be more similar to one another than to any non-member, and comes in two varieties, depending on whether its proponents postulate that *all* similarities or only genetic similarities must be taken into account in grouping individuals into species as well as into higher order taxa. In this section I critically evaluate the two most prominent versions of the cluster thesis as it applies to biological species—namely the “overall” similarity approach (better known as the phenetic approach) and the genetic similarity approach—in order to determine whether some attenuated form of intrinsic essentialism about species can be salvaged.

2. The Phenetic Approach

The overall similarity approach to biological kinds is endorsed by the phenetic school of taxonomy of Sneath, Sokal and Crovello, which had its hay-day in the sixties and seventies (Sneath and Sokal 1963; Sokal and Crovello 1970). By contrast to the vast majority of taxonomists who argue that the division of organisms into biological taxa should be based on known genealogical relations, pheneticists claim that biological classifications should be as theory-neutral as possible. Pheneticism in fact emerged in reaction to the genealogical approach to biological taxonomy discussed above, and, as we will see, many of the arguments that have typically been presented in its favor are in effect arguments against the alternative, phylogenetic or genealogical, approach to biological classification.

The nature of the dispute between advocates of the genealogical and pheneticist approaches to species and other taxa can be expressed in terms of the distinction between monophyletic and paraphyletic taxa on the one hand, and polyphyletic taxa on the other. What genealogical taxonomists claim and pheneticists deny is that only homologies should be used in constructing classifications so as to ensure that

polyphyletic taxa are excluded. As I noted before, genealogical taxonomists want to exclude polyphyletic taxa from biological classifications on the grounds that the homeoplastic similarities on the basis of which organisms are grouped into polyphyletic taxa do not result from a single evolutionary event, but rather from disparate evolutionary events. Homologous similarities, by contrast, ensue from a common evolutionary event, since homologous characters are (by definition) passed down to various organisms from their common ancestor. The members of taxa constructed on the basis of homologies alone (rather than on the basis of both homologies and homoplasies) are thus linked by genealogical relations, as desire the proponents of the view that taxonomy should reflect evolutionary processes.

Pheneticists, by contrast, argue that the homology/homoplasy distinction should be abandoned because it has too little, if any, operational value. To know whether a trait is a homology rather than a homoplasy, phylogenies must be known. But pheneticists argue that the methods by which phylogenetic relations are determined are too uncertain for practical use, and that classifications of organisms according to their phylogenetic relations thus inevitably end up being subjective, depending on the personal preferences and whims of the classifier (Sneath and Sokal 1963). More generally, pheneticists point out that the greatest source of error in early biological classifications was taxonomists' reliance on scientific theories that were later discovered to be false. If a biological classification system was instead erected independently of any theoretical considerations, it could remain unchanged regardless of changes in our allegiances to particular scientific theories. According to pheneticists, such a theory-neutral classification system would also have the advantage of serving as an "all-purpose" classification system that would be useful

not only to evolutionary biologists but also to scientists interested in all other aspects of biology.²

Pheneticists maintain that, for all these reasons, biological classification should not be driven by any theoretical considerations, but should reflect degrees of *overall* similarity between the organisms classified. According to pheneticists, taxonomists should proceed by first observing organisms and recording all their characters. Statistical techniques should then be used to form clusters by aggregating the organisms that are “nearest” to each other with respect to the traits recorded. On this view, species in particular correspond to those groups of organisms that have *the most* overall similarity, where overall similarity is understood as similarity with respect to *all* characters, without any prior weighting of the various respects of similarity considered.³

Several objections have been raised against the pheneticist approach to species. Since at least some of the arguments for pheneticism are arguments against other genealogical approaches to taxonomy, arguments against pheneticism have also included counter-objections to pheneticists’ criticisms of these alternative approaches to biological classification. Ridley (1986), for example, has defended cladism against pheneticists’ objection that cladistic classifications are inevitably subjective because phylogenetic relations cannot be known. He has argued that, though our knowledge of phylogeny is incomplete, it is not for that matter inexistent, and he has also pointed out that cladistic techniques are clearly defined and in this sense are not subjective at

² Ironically, pheneticists (e.g., Sokal and Crovello 1970) sometimes assert that a theory-neutral approach using overall similarity better captures the results of evolution than do theoretically-driven approaches to biological classification.

³ As Ereshefsky points out, the similarities considered by pheneticists include “macrosimilarities—for example, morphological, physiological, behavioral and ecological similarities, as well as microsimilarities, such as DNA homologies and similarities in amino acid sequences” (2002, 86).

all.⁴ As one might expect, proponents of the genealogical approach to species equally argue that the pheneticist approach is simply wrong-headed, since the units of classification it produces are evolutionarily insignificant.

Pheneticism has also been criticized on the ground that it offers too little guidance concerning how to group organisms into taxa since it leaves undetermined the type of cluster statistic that should be used for this purpose. As I mentioned above, according to pheneticists, taxonomists should begin by recording all the measurements of the organisms they observe, and cluster statistics should then be deployed that average all the measurements to form clusters of units according to their similarity in all traits. But, as Ridley (1985, 1986) has argued, this strategy can in fact be carried out in various ways and can thus lead to diverse classifications, depending on which cluster statistic one deploys: “there is more than one cluster statistic, because there is more than one way to recognize the ‘nearest’ group” (1986, 79).

To take just two examples, the “nearest neighbor” statistic forms successfully more inclusive groups by combining the sub-groups with the nearest neighbor to each other, while the average neighbor statistic forms more inclusive groups not from those subgroups with the nearest nearest neighbor but from those with the nearest *average* neighbor. Since these two statistical techniques will not invariably produce the same taxa, and since pheneticism provides us with no principled way of choosing between these (as well as other possible) clustering techniques, the classifications it produces will inevitably be subjective, depending as they will on which of the possible clustering techniques the taxonomists carrying on the classification prefers. This is

⁴ Evolutionary taxonomy, by contrast, is somewhat subjective since there seems to be no principled answer to the question of when a divergence in a lineage is, from the perspective of evolutionary taxonomy, significant enough to mark the existence of a new taxon. I indeed agree with Ridley’s suggestion that since evolutionary taxonomy “brandishes a partially phenetic philosophy” it is plagued with some of the same problems as pheneticism (1986, 85). Although I believe there is reason to prefer cladism to evolutionary taxonomy, I will not defend the point here since such a defense is not crucial to my general argument against the essentialist conception of species.

especially troublesome given that one of the main advantages pheneticists first claimed for their theory relative to genealogical taxonomy was objectivity (Ridley 1986).

Another powerful objection to pheneticism concerns the phenetic species concept in particular, according to which species are those organisms that have the most overall similarity. This species concept has been criticized on the ground that it is empirically vacuous since, as Goodman (1955, 443) has shown, two things or organisms cannot be said to be more similar to each other than to another thing or organism *tout court*, since one can always single out respects of similarity according to which one of the members of the pair is more similar to the non-member than it is to the second member of the pair (on this view, all things can be said to be infinitively similar to each other). One can therefore only properly speak of two things being more similar to each other than a third *in certain respects*. What this analysis of the notion of similarity suggests is that the phenetic account of species membership is in fact no account at all, since it offers no guidance whatsoever as to how organisms should be grouped together into species. To put the point differently, the characterization of species as groups whose members are more similar to one another than to any non-members of the species is false to the extent that the notion of greater *overall* similarity is itself devoid of all empirical content. As Ridley (1986, 85) puts it, pheneticism fails as an account of the nature of species insofar as it appeals to something in classification “of which there is no natural measure: phenetic similarity.”

Pheneticists are in effect stuck between a rock and a hard place. Unless they come up with a finite list of characters according to which organisms should be compared to one another, they will not have provided a *bona fide* account of how organisms should

be grouped together into species. But if they do provide such a finite set of characteristics, they will end up violating their self-prescribed rule to the effect that the classification of organisms into species should be carried independently of any theoretical considerations.

Pheneticists can in fact be criticized on grounds of inconsistency, since they *are* in practice selective about the respects of similarity they consider in grouping organisms into taxa. For example, they never choose to classify the males and females of what would otherwise seem to be a single species into two distinct species merely on the grounds that they are less similar to each other than they are to members of other species. They equally exclude such trivial morphological “features” as exact number of hairs as relevant respects of phenotypic similarity. Moreover, the features pheneticists *do* make reference to in evaluating degrees of similarity are not themselves theory-free:

Pheneticists make reference to things like wings, antennae, anal gills, dorsal nerve cords, enzymes and nucleotides. These are hardly pure observation terms. They presuppose all sorts of previous knowledge of a purely theoretical kind (Hull 1984, 581).

In the face of these difficulties, pheneticists have come to acknowledge that the idea of a theoretically neutral classification is problematic, and have accordingly modified their position. They now accept that the practice of taxonomy be guided by *some* theoretical considerations, but persist in maintaining that it shouldn't be guided by considerations that spring from the theory of evolution itself (Hull 1984). This move is however questionable since it is difficult to see on what grounds pheneticists can permit the selection and weighting of certain respects of similarity on the basis of theoretical considerations and all the while maintain that theoretical considerations that ensue from evolutionary theory should be excluded from this process. In other terms, if pheneticists are willing to accept that theoretical considerations influence the

grouping of organisms into taxa, then there seems to be no reason for them to exclude evolutionary considerations in particular from their classificatory practices.

3. The Genetic Similarity Approach

Genetic similarity may intuitively seem to have better credentials than overall similarity as a potential candidate for the status of “statistical essence” of biological kinds. The notion of genotypic similarity at least comes with the relevant respect of similarity neatly identified. The genotypic similarity approach to taxa (Caplan 1981; Kitts and Kitts 1979; Ruse 1987) may also be deemed superior to strict genetic essentialism since it does not require that any particular gene occur in all and only the members of a taxonomic unit. But although it avoids some of the problems faced by both pheneticism and the strict essentialist conception of taxa, it does not overcome *all* the problems associated with these alternative conceptions. To begin with, the genetic similarity approach is subject to the same criticism Ridley directs against pheneticism, namely that it leaves greatly undetermined the question of how to group organisms into taxa since it leaves undetermined the type of cluster statistic that should be used for this purpose.

Moreover, the genetic similarity approach fares no better than genetic essentialism and pheneticism in picking out recognized species. Electrophoretic analyses have indeed shown that, in some cases, distinct species differ only slightly at the genetic level and, conversely, that the genetic distance between closely related species is sometimes considerable (Futuyma 1986, 222; Ridley 1985, 115). Ridley notes that the results of gel electrophoresis indicate that although the genetic differences between some species are large, between others they are small:

If the differences between species are only about the same as between two populations of a species, they can be counted as small . . . all degrees of distance, from this upwards, are found (Ridley 1985, 15).

In fact, on one estimate, while human beings differ from chimpanzees at only three percent of loci, in humans thirty percent of the genes at loci that code for structural genes are polymorphic, and in any one individual, roughly seven percent of the loci are heterozygous (Hull 1989, 17).

Objections to species essentialism that spring from the fact that currently recognized species do not invariably share any exclusive set of properties indirectly rest on the theoretical assumption that biological classification should reflect evolutionary processes since currently recognized species have been individuated with an eye to respecting known phylogenetic relations. As one might expect, the same is true of arguments against cluster theories that rest on the claim that currently recognized species are not invariably more genetically similar to each other than they are to members of other species. Although there is no consensus among genealogical taxonomists concerning the precise nature of the mechanisms leading to speciation, all agree that the development of irreversible reproductive isolating mechanisms between two populations is a sufficient condition for considering that these populations form two species. In other terms, if two populations of a species begin to diverge genetically in a way that impedes them from reproducing sexually, and if gene flow between both populations is never resumed, then the original species will be said to have speciated, and the two resulting populations will be considered different species. Speciation does not require a complete differentiation throughout the respective genomes of the two populations concerned, but can occur “by virtue of reproductive barriers that have the same kinds of genetic bases as characters that vary within populations” (Futuyma 1986, 247). What this implies is that, if genealogical taxonomists are right, the members of distinct species can resemble one another in almost all genetic respects, save those that are crucial to their reproductive success.

They may thus bear a greater resemblance to one another than they do to members of their own respective species.

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