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Vague Kinds and Biological Nominalism

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Abstract

Among biological kinds the most important are species. But species, however defined, have vague boundaries, both synchronically owing to hybridization and ongoing speciation, and diachronically owing to genetic drift and genealogical continuity despite speciation. It is argued that the solution to the problems of species and their vague boundaries is to adopt a thoroughgoing nominalism in regard to all biological taxa, from species to domains. The base entities are individual organisms: populations of these compose species and higher taxa. This accommodates all the important biological facts while avoiding the legacy problems of pre-evolutionary typological taxonomy, which saw species and other taxa as prior to their members. Species are however not individuals: they are spatiotemporally bounded collections, which are plural particulars.

Keywords

vagueness, nominalism, biological species, taxonomy

1 Introduction

Vagueness, in whatever context, typically manifests itself in two characteristics: (1) the existence of obvious borderline cases, and (2) susceptibility to uncontrolled slides or sorites from one case to another incompatible case. Considering biological kinds, that is, species, genera, and other higher taxa, obvious borderline cases include hybrids, symbiotic communities, some products of genetic experiments, transitional and ambivalent forms, and cases of limited cross-fertilization. A disturbing soritic slide can be generated by the following valid sequent: each individual organism belongs to the same species as its parent or parents; chimps and humans had a common ape ancestor species; therefore chimps and humans belong to the same species. So there is vagueness in biological taxonomy. The point is not to wish it away, but how we should we understand it and what (if anything) we should do about it.

2 Biological Taxonomy

A major part of biological systematics consists in the classification of organisms. Originally practised on the basis of morphological and other readily observable characters, this has expanded its field of data in two directions. The first expansion is in time. With the recognition of the great age of life on earth and the explanation of its variety and change over millions of years through theories of natural evolution, taxonomy acquired an indelible historical dimension. Since Darwin it has gradually become undisputed practice to classify organisms primarily according to their genealogy. The second expansion is through genetics and the investigation of biochemistry. The ability to identify genes, to sequence the genomes of organisms and to recognize similarities and differences in genetic code has immeasurably expanded the field of data on which comparisons and judgements regarding genealogical relationships, past and present, synchronic and diachronic, can be made.

Before continuing, I wish to import some terminological clarifications from biological best practice. In everyday situations we sometimes use the term ‘classify’ for the following activity: we see or otherwise come across an individual organism or group of like organisms, and on whatever evidential basis place these in a particular biological class. For example I see a bird in my garden and judge it to be a song thrush, *Turdus philomelos*. Biologists do not call that ‘classifying’, they call it ‘identifying’, and I shall follow their usage. Anyone can engage in identification: only some people engage in classification, which is deciding on the arrangement of biological classes. These people either discover a new kind of organism and propose how to interpolate it into an existing classification scheme, or they propose, for whatever reason, a restructuring of such a scheme. For example in the 1980s Carl Woese et al. proposed on the basis of genetic and chemical characters to add a new taxonomic rank of DOMAIN above Linnæus's highest rank of KINGDOM, resulting in the division of bacteria into two domains and the placing of animals, plants, fungi and all other eukaryotes into a single domain.[1]

Secondly I adopt the clarificatory distinction made by George Gaylord Simpson between taxa and categories in biology.[2] A taxon is a group of organisms figuring in a classification: it may be a species like the domestic cat, or a genus like the thrushes, or a more inclusive taxon such as the carnivores, mammals or animals. A category is a group of taxa at the same level, such as the species, the genera, the families, the orders, etc. The two are often confused, not helped by biologists' prevalent practice of using the grammatical singular for kinds.

3 The Species Problem

In the philosophy of biology, and in biology itself, one of the outstanding theoretical issues is what is called the Species Problem. This can be simply stated: What is it to be a species? There have been many answers down the centuries, from Aristotle to the present day. Current consensus is that there is no single answer that works for all kinds of organisms, from humans to bacteria. How many different accounts or definitions of the species category are required is hotly debated and we here deliberately avoid that debate. The most famous and (apart from its known lack of universality) most widely applicable is the so-called biological species definition: a species is a group consisting of one or more populations of organisms that interbreed and that are reproductively isolated from other such groups.[3] This does not work for asexual organisms and various other forms of life but it mostly works well enough synchronically, for most of the eucaryotes including ourselves.

It is no aim of this paper to investigate let alone solve the species problem. Rather the point is twofold: firstly, that however species are delimited, whether by Dobzhansky–Mayr or another way, vagueness intrudes; and secondly, for later reference we note from that

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[1] Woese et al (1990).

[2] Simpson (1961), 19.

[3] Dobzhansky (1935), Mayr (1942).

definition the term ‘population’, which refers to a suitably delimited plurality of individual organisms.

4 Vagueness in regard to Species

Membership of species is in certain cases vague. This means that for some individual organisms it is for whatever reason unclear or indeterminate whether or not they belong to a certain species. There can be several reasons for this. One is hybridization: hybrid offspring of parents from different species may, if the species are sufficiently distinct, be of neither species: this applies to mules, tigons and ligers for instance. But where species are closely related and sufficiently similar, hybrids seem to hover between them. The European carrion crow *Corvus corone* and the closely related hooded crow *C. cornix* hybridize fertilely along their zone of overlap in West Central Europe and this was long regarded as sufficient to warrant treating *C. cornix* as a subspecies, *C. corone cornix*, of the former, but the relative paucity of interbreeding and the lower viability of the hybrids led to ornithologists in 2002 separating *C. cornix* as a new species. The hybrids are not clearly of either species. Speciation is not usually an instantaneous process and where species are splitting due to geographical separation and/or genetic drift there may be viable intermediate cases at a time. *C. corone* and *C. cornix*, assuming they speciated from a single common ancestor, are an instance of paripatric speciation (speciation in adjoining locations).

The blurred boundaries of species become much more evident in the diachronic dimension however. At the end of an evolutionary process involving speciation, the new species may be clearly separate from its ancestor and its co-generic sister species, but there is no sharp cut-off between the old and the new. In some cases, as with Darwin’s Galapagos finches, the ancestral species may continue to exist on the continental mainland synchronously with its daughters. *Homo sapiens* is distinct from its assumed ancestor *H. erectus* and its assumed sister *H. neanderthalis* but there were once individuals who straddled the boundaries we draw today. The reasons those boundaries appear clear to us are that either the species are clearly distinguished at present, as in this case because only one survives, or are separated by reproductive barriers in coeval species, or else because the gaps in the fossil record do not present us with awkward transitional cases. Palaeontologists may avail of these gaps but they are essentially fudging and ducking the problem. Sudden stable mutation or hybridization apart, there are no clear discontinuities in the genealogy of species.

What applies to species applies to all higher taxa, since divergence and speciation occur at the lowest level. The class *Aves*, birds, evolved from some group of dinosaurs. But there was no first bird which hatched from a dinosaur egg and no dinosaur whose offpring were birds.

The distinction and delimitation of species even at a time is not always possible. There are several cases of *ring species*. These are groups of populations *A*, *B*, *C*, … *M*, *N* such that *A* and *B* overlap in location and interbreed, so do *B* and *C*, …, so do *M* and *N*, but while *A* and *N* are collocated they do not and perhaps can not interbreed. The most famous case are a complex of palaearctic gulls of the genus *Larus*, including the Herring Gull, *L. argentatus*, though recent research suggests they are not in fact an example.[4] However there are a few other cases, such as Asian complex of Greenish Warblers, *Phylloscopus trochiloides*.[5]

5 Types, Sets and Collections

Modern evolutionary biology is based on populations of organisms. In this respect it is bottom–up or nominalistic, since populations are particular, not universal. It constitutes a definitive rejection of the platonistic conception of biological kinds as ideal archetypes initiated by Plato, retained in modified form by Aristotle, and perpetuated by scholasticism, Linnaeus, Goethe, Cuvier and Owen. The gradual acceptance of evolution following Lamarck and the subsequent explanation of its mechanism by Darwin and Wallace mean that biologists can no longer sustain a top–down or *typological* conception of what constitutes a species. As to what species are, even under a single conception, theorists differ. The commonsense idea is that they are certain pluralities or collections of organisms, delimited by their interrelations, as in the biological species concept, which however only gains traction synchronically and then not always. One philosopher of biology, Philip Kitcher, took species to be sets, albeit with suitable restrictions to eliminate arbitrary sets.[6] But sets are abstract entities (outwith space and time) and have essentially extensional membership conditions, whereas species are in space and time, and have many or all of their members contingently. This particularity and locatedness led philosophers of biology Michael Ghiselin and David Hull to propose instead that species are spatiotemporal individuals and individual organisms

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[4] Liebers et al (2004).

[5] Alström (2006).

[6] Kitcher (1984).

are their parts.[7] This was not new. As early as 1866 Darwin's German adherent Ernst Haeckel declared "die Art ist ein Individuum".[8] But there are more categories of particular than just individuals and sets. Concrete collections or pluralities of individuals, some with extensional membership conditions, most not, are just as particular. This allows us to maintain that species are spatiotemporally localized particulars, neither abstract sets nor single individuals.[9] It is also a welcome return to common sense. A general ontology of collectives is work in progress, but the increasingly widespread acceptance of pluralities in logic lends some lateral support to the view.[10]

It should be noted for the sake of philosophical readers that biological systematists nowadays use the term 'type' to refer not to a kind or an archetype but to an actual individual, a specimen of the species or higher taxon in question[11] that serves as a reference point for subsequent taxonomic investigation. Another organism counts as being of the relevant species or higher taxon when it is relevantly similar to the type specimen. In the classical case this will be an actual organism captured, preserved and maintained, usually dead, often but not always by the discoverer of the "new" species, who has naming rights. Sometimes when preservation is difficult or the original type degenerates, one or more substitute types are allowed, and in palaeontology fossils and fossil fragments, sometimes even tracks or other indirect traces, count as types. Systematists have a bewildering array of terms and rules governing the use of types which are not relevant here. The other theoretically important point is that the type need not be "typical". It might be a juvenile or anomalous individual some of whose features vary notably from statistical means. Often there is little or no telling how "typical" the type is, for paucity of conspecific specimens. All that matters is that the type be of the right – "type" – and this is established by fiat, once it is determined that it is *not* a member of a previously identified species.

6 Nominalism, What

In this context I understand the term 'nominalism' to encompass the rejection of two categories of entity: universals and abstract (non-spatiotemporal) objects. These are two distinct rejections but they are linked in that the biological nominalism I am proposing says

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[7] Ghiselin (1974), Hull (1975).

[8] Mayr (1996): 275.

[9] I proposed this in a letter to Ernst Mayr and he did agree that the idea of a highly scattered individual was strained.

[10] I have been advocating concrete pluralities since Simons (1980).

[11] The type of a genus or higher taxon is a type of one of the species subordinate to it.

that biological kinds are neither universals nor abstract entities. Nominalism has traditionally had a bad name in biological systematics, for historical reasons. In the early modern era some taxonomists proposed in opposition to scholastic notions that taxonomic boundaries are arbitrary and conventional. This flies so blatantly in the face of the evidence from nature that it is surprising not that was almost universally rejected but that it was entertained in the first place. Nature does group organisms, both by objective similarities and by descent, and these groupings ground our classifications, both folk and scientific. The scope for convention is restricted mainly to nomenclature and does not impinge on the ontology. But this absurdly extreme form of nominalism should not be assumed to infect all views bearing the name. If the ontological basis of taxa is individuals and taxa are collections of these, and collections of concrete non-repeatables are concrete and non-repeatable, then taxa are concrete non-repeatables and we have nominalism.

7 Vagueness, like the Poor, is Always with Us

Treating species and other taxa as collections does not remove the issue of vagueness: it merely focuses it in a certain place. If species are individuals and species are vague then there are vague individuals and we have ontic vagueness. But if species are collections and are vague then we have vague collections. This *may* be a form of ontic vagueness, but I am inclined to think it is not and that we should account for this vagueness semantically. Importantly, vague collections are consistent with there being no vague individuals. Suppose for the sake of argument that every human being has a precise height at any time. This is compatible with the predicate ‘tall’ being vague for non-ontological reasons, whether these are epistemic or semantic. Likewise the biological characteristics of individual organisms at a time and over time may be completely determinate and yet a species term such as ‘*Homo sapiens*’ or a higher taxon term such as ‘*Aves*’ does not delimit a determinate collection. A determinate collection D is a plurality of objects such that for every individual x it is either true or false that x is a member of D. An indeterminate collection I is one such that there is at least one individual x for which it is neither (determinately) true nor (determinately) false that x is a member of I. Species and other taxa are vague. If they are determinate collections this vagueness is epistemic. If they are, as I think, indeterminate collections, then the vagueness is not epistemic.

8 How to Deal with Vagueness of Biological Kinds

There are vague individuals, at least in the following sense. Things we denote by singular terms and understand to be individuals, such as ourselves, Lake Constance, Europe, the Earth, and the Sun, are such that there are individuals *x* such that it is neither determinately true nor determinately false that *x* is a part of one of these individuals at a given time, e.g. whether this small portion of hydrogen gas is part of the sun, this hydrocarbon molecule is part of me, this small portion of water part of Lake Constance. To accommodate such cases we should accept, with a light touch, degrees of truth between 0 and 1. To cope with what Kit Fine calls penumbral connections among predicates[12] we should deal with logically complex predicates of such individuals not truth-functionally as in fuzzy logic but supervaluationally, with a numerical component obtained by summing weighted products of truth-values, the result being a theory I call supernumeration.[13] This offers a good fit with actual linguistic practice, it incorporates the virtues of supervaluation, and it accommodates the practical advantages of numerically tractable data, which result in there being thousands of computer applications using fuzzy logic and none at all using the philosophically preferable theory of supervaluation. This method is transferrable to collections, the intermediate truth-values affecting not the part-relation but the membership relation (the two are similar but distinct).

Now here is where the two applications of the approach differ. In the case of many (not all) disputedly vague individuals there are fairly clear data and a strong consensus as to the desired outcome. For example we want there to be only one me and not none or very many, likewise Lake Constance and the Sun are to be unique. Incidentally the territorial status of Lake Constance shows that the three countries that border it, namely Austria, Germany and Switzerland, are not determinate territories, as there is no treaty agreement as to where the boundaries lie between them where they meet in the lake.

In the case of vague species, most especially in the diachronic dimension, the gradualness of change and speciation strongly suggests that there are fewer ontologically compelling indicators of the extent to which an individual is a member of a given collection. There is thus greater scope for linguistic decision and convention than in the case of individuals. It is in other words, partly a matter of convention, assisted by convenient ignorance, as to when the birds or *H. sapiens* came into existence. Also because the issue of vagueness essentially turns on a single predicate, that of membership or 'is one of', the scope

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[12] Fine (1975).

[13] Simons (2010).

for unforeseen penumbral connections is somewhat reduced by comparison with more multidimensional cases of predicate vagueness. Thus, assuming for the sake of example that *H. erectus* was the immediate ancestor of *H. sapiens*, for a penumbral individual of which it say 50% true it is *erectus* and also 50% true it is *sapiens*, 100% true it is either *erectus* or *sapiens*, much less than 50% true it is *neanderthalis*, and 0% true it is a chimp, *Pan*.

This combination does not eliminate the problems of vagueness, but it puts them where reasonable tools can be developed to cope with them. The upshot of the suggested solution is that we may continue to use the standard scientific terms for biological taxa, but acknowledge that they are not and never will be exact in extension and that a measure of arbitrariness and convention may attach to them, though the arbitrariness is revisable in the light of empirical discoveries. To confirm the ontologically shallow nature of the border-drawing in many cases it suffices to examine actual debates about placement and delimitation of species among biologists, where the very heatedness of some debates suggests that, as in much university administration, little of substance is in dispute.

9 Other Biologically Relevant Kinds

Not all of biology is about the taxonomy of organisms. There are the parts of organisms, from the subatomic level through atoms and molecules to genes, cells, organs and systems. There are non-taxonomic collectives such as families, herds, ecosystems, predator–prey complexes and more. There are the processes within and among organisms: the physical and chemical vital processes of energy capture and production in metabolism, the assembly and maintenance of bodies and their parts, the reproductive cycle, behaviours and much more. All of these are particular: individuals, masses, collections. That there are many similar ones leads us here as elsewhere efficiently to abstract and speak of *the* eucaryotic cell, *the* FOXP2 gene and so on, just as we speak of *the* Grey Wolf, *the* Herring Gull, and so on. In many cases the problems are less severe than they are for biological taxa because vagueness is much less of an issue. So while this is not the main thrust of the paper, the implication is that if nominalism works for taxa, it will work for other biologically relevant kinds, including DNA.[14]

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[14] In unpublished work with Yu Lin we propose a nominalist account of DNA sequences, using mereology and a nominalistic account of sequences (strings).

10 Conclusion

The biological facts support nominalism. Species and other biological taxa, as these are understood in biological systematics, are concrete collections of concrete individuals,[15] where co-membership of several individuals in the collection depends on the relationships among these individuals. The membership relation in some cases is not sharp or semantically bivalent, but sustains degrees between full membership and complete non-membership. This in turn depends in part on objective relations among the individuals, for example the fact that the interbreeding relation is not transitive (obvious diachronically, very occasionally true synchronically for ring species), but it also harbours a modest element of decision or convention that is dependent on our choices and interests, not all of which are constrained by the biological facts.

Glossaryette

category: a class the members of which are all the taxa placed at a given level in a hierarchic classification.[16]
liger: offspring of a male lion and a tigress
taxon: a group of real organisms recognized as a formal unit at any level in a hierarchic classification.[17]
tigon: offpring of a male tiger and a lioness

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[15] Cf. Vrana and Wheeler (1992).
[16] Simpson (1961): 19.
[17] Ibid.

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