Biometaphysics

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1. Historical Background

1.1 Aristotelian Realism

While biology has spawned many of the problems that have shaped the discipline of metaphysics since its inception, current advances in the biological sciences are disclosing hitherto unimagined dimensions of complexity in the processes of life, to a degree which poses challenges to standard metaphysical ways of thinking. In what follows, I shall show how metaphysical ideas nonetheless continue to play a role in biological science, focusing my attentions in particular on problems of biological classification.

In the time of Linnaeus, familiarly, biology was still rooted in a recognizably Aristotelian view of classification. Before articulating this view, it will be useful to begin by distinguishing two meanings of 'classification': 1. as a division or subgrouping of the entities in reality; and 2. as an artifact created by humans. The common Aristotelian-Linnaean view of the classification of organisms can be summarized in these terms as follows:

a. There is a fixed division of the totality of organisms into subgroups called *species* (sense 1), which obtains independently of the activities of scientists. This division is permanent in virtue of the fact that to each species there corresponds an ahistorical essence, a property or group of properties severally necessary and jointly sufficient for an organism to belong to that species. (An assumption of this sort still prevails today in many areas of physics and chemisty, for example in the classification of quarks, or of the chemical elements.)

b. This division forms one level in a hierarchy, which has the structure of a directed acyclical graph (the 'tree of life'), whose nodes (*taxa*) are ordered by the relation of inclusion culminating in a single maximal root node (*organism* or *living thing*). All taxa on any given level in the hierarchy are disjoint (they share no common instances and also no common subtaxa). All instances of taxa on lower levels inherit those properties which hold of all instances of the including taxa above them. Each node in the hierarchy below the root has exactly one including node on the next higher level (the principle of *single inheritance*).

c. There exists a single classification (sense 1) of the biological realm, which scientists attempt to reproduce in the form of a single, correct representation (sense 2). To achieve this goal, they seek to identify organisms that are exemplary or prototypical for each given species. Differences between and

changes in organisms of a single species are noted, but they are regarded as being of secondary significance.

1.2 Darwin and Beyond

Already in the 18th century, biologists had begun to move away from the essentialist idea of fixed species, and Darwin's decisive achievement consisted in establishing a framework for understanding how new species can come into existence (have *origins*) in time. As mutation and the non-prototypical thereby come to occupy roles at the centre of biological science, all of the other mentioned aspects of the traditional approach to classification are to different degrees called into question. Already (though not consistently) Darwin saw the notion of species as a matter of mere fiat determination on the part of biological theorists:

> I look at the term species as one arbitrarily given for the sake of convenience to a set of individuals closely resembling each other. (Darwin, 1988, p. 39; contrast Stamos, 2007)

More recently, competing approaches to biological science on the part of taxonomists, evolutionary biologists and molecular biologists have brought competing conceptions of the goal of species classification and of the nature and status of species, and some have embraced pluralist views according to which there is no single division on the side of reality to be reflected in our classifications.

The impact of the mentioned changes should not be overestimated. The tree of life conception still serves as overarching framework for the understanding of evolutionary history, and even though the simple branching tree conception breaks down for bacteria and other microorganisms because of the prevalence of lateral gene transfer, most taxonomists still see the totality of organisms as susceptible to a division into taxa that look very much like traditional species, even if the rationale (or rationales) for division is nowadays quite differently conceived. The major competing species concepts still broadly agree in the classifications of organisms they dictate in areas of overlap (though what is, for example, subspecies in one may be species in another).

Moreover, while most philosophical attention to biological classification has been focused on the classification of organisms, the classificatory concerns of contemporary biologists extend much further. Already Linnaeus had proposed a classification of diseases (Linnaeus, 1763), and efforts are, as we shall see, increasingly directed towards the creation of standardized classifications (called 'ontologies') of entities such as genes, proteins, cells, anatomical structures, or biochemical networks and pathways.

2. The Species Problem

2.1 What is a Species?

A large number of different conceptions of species have been advanced in recent years (Ereshefsky 1992), including for example definitions based on shared environments, on cohesion, or on intraspecies recognition. Three families of definitions are of particular importance:

On *similarity-based (phenetic) species definitions* a species is a totality of organisms possessing certain predefined properties. Traditionally all species definitions were of this type. For Linnaeus organisms were classified according to differences in the form (shape) of their reproductive apparatus. Currently, similarity-based definitions often include the factor of similarity of DNA of individuals or populations.

On *phylogenetic species definitions* a species is a lineage of one or other sort, which is to say a totality of organisms extended over time and linked by parenthood relations to a common ancestor.

On *biological species definitions* a species is a totality (a population or aggregate of populations) of interbreeding organisms. It is a persisting material object that is delineated by the ability of its constituent organisms to reproduce naturally in such a way as to yield fertile offspring.

2.2 Particulars, Collections and Classes

The above provides us with some examples of how species are conceived by influential communities of biologists. But it does not yet tell us how species, on such conceptions, are to be understood metaphysically. In answering this question we shall adopt the following terminological conventions:

A *particular* is an entity which exists in space and time and which is involved in causal relations. Particulars are divided into *continuants,* entities (things, objects) which endure through time, and *occurrents*, entities (processes, changes) which occur or take place in time. An organism is a particular continuant; an organism's life is a particular occurrent. In the course of its life each organism undergoes changes of various sorts, including gaining and losing parts.

A *collection* is a continuant particular comprehending at any given time a number of simultaneously existing continuant particulars as its parts and linked together via certain relations, for example of spatial proximity. A collection – for example the collection of stickleback fish in this pond – is a concrete, historical entity, similar in this respect to a single organism. And just as a single organism may survive the gain and loss of cells, so a collection of organisms may survive the gain and loss of members.

A *class* (for our purposes here) is an entity that results from the grouping of other entities, whereby the latter are not required to be entities that exist simultaneously. The class of tiger beetles, for example, is the grouping of all tiger beetles which exist, have existed and will exist in the future. Classes as thus conceived do not endure through time while gaining and losing members. Their

members may exist in time and undergo changes of various sorts, but the class abstracts away from all such temporal differences. Thus the members of the class of beetles are indeterminately eggs, larvae, pupae and adults.

3. The Biological Approach to Species

3.1 Species as Classes and as Collections

All three families of species-definitions are in one or other form compatible with both collection- and class-based views of species. However, both similarity-based and phylogenetic definitions have tended to go hand in hand with a view of species as classes.

Because of the growth in predominance of population-based approaches to the study of biological phenomena, it is the biological approach to species as articulated by Ernst Mayr (1942) that comes closest to enjoying consensus status among contemporary biologists, and it is this approach that will occupy us in what follows. Species are seen as collections; thus they are continuant particulars made up of organisms as parts. Each species is a cohesive population (aggregate of populations) that maintains its integrity over time in virtue of highly sensitive intra-species recognition systems which promote actual gene flow within the species and inhibit gene flow without. Species on this view are not lineages (any more than do individual organisms); rather, they form lineages when viewed in terms of their development over term.

3.2 Species and Particulars

The most crucial element of the biological approach from our present perspective is the thesis to the effect that species are particulars, a thesis first advanced by Ghiselin (1974) and then by Hull (1976). Mayr accepts this thesis, though he objects to the specific formulation given to it by Ghiselin and Hull:

> There is no doubt that there is a real difference between a spatio-temporally unrestricted   class characterized by its definition (its essence), and a spatio-temporally restricted item with internal cohesion. It is only that the designation 'individual', chosen by Ghiselin and Hull, is rather unfortunate. I refer to such items as 'particulars' or, when involving living organisms as 'populations'. They have, indeed, all the characteristics ascribed to them by Ghiselin, except that the use of the name 'an individual' for 5 billion humans is rather absurd. (Letter to Peter Simons, dated 15 January 1993)

The thesis that species are *cohesive scattered continuant particulars* represents a radical departure from traditional views according to which species are *natural kinds* (like *oxygen*, or *gold*) with organisms as particular instances. If each species is a particular, then it does not make sense to speak of species terms as

figuring in statements of natural laws, any more than it would make sense to speak of 'Arnold Schwarzenegger' or 'Belgium' as figuring in such statements.

But just as the *class* of organisms – like the class of cells, or the class of proteins – forms a natural kind, so also does the *class* of species. For just as there are natural laws governing the class of organisms, so also there are natural laws governing the class of species.

Such laws are typically statistical. One example is: *species formation typically requires antecedent geographical isolation*. A statistically typical speciation event occurs when a species is divided into two separate sub-collections which over time develop into two reproductively isolated populations. One species is replaced by two, in a process analogous to the splitting of an amoeba. The totality of organisms after species separation is then like the totality of living material in the two amoebae that result from splitting: each is a purely historical entity that forms no biologically significant unity. On the view of Ghiselin, something similar applies to all higher taxa – all are purely historical entities that do not function as cohesive units. This suggests also one potential resolution of what some see as a fatal flaw in the biological approach, namely that it can be applied only to organisms which reproduce sexually. The solution is to treat asexual taxa, too, as purely historical entities (Ghiselin, 2002, p. 157). Thus where some would argue that a mix-and-match of different species views is needed in order to cope with the peculiarities of organisms of different types (a phylogenetic view, for example, to cope with bacteria), Ghiselin can maintain a unitary view, and thus preserve the capacity of species to figure in natural laws (Ghiselin, 1997).

4. Mereology and Set Theory

4.1 Species as Sets

Species are, on the biological approach, like cells and organisms. They exist in time and undergo changes in the course of time. They are cohesive material actors firmly rooted in the nexus of cause and effect. In spite of this, there are some, such as Kitcher (1984) and Guenin (2008), who have defended a view of biological species as sets. This view is in line with assertions often found in introductory textbooks of set theory according to which collections such as 'a pack of wolves, a bunch of grapes, or a flock of pigeons are all examples of sets of things' (Halmos 1960, p. 1). As Simons has noted, such remarks imply that 'one can be chased, attacked and even eaten by a set, oneself eat a set and absorb vitamins from it, press a set and make wine out of it.' (Simons, 2005) The cognitive dissonance sparked by such implications rests on the fact that all standard attempts to specify axioms for the theory of sets rest on a view of sets as entities which exist outside the realm of time and change. Sets, as defined by these axioms, cannot evolve. Species evolve. Hence species are not sets.

Kitcher's response is to argue that there is committed here what he calls 'the fallacy of incomplete translation' (Kitcher 1984, pp. 310-311). This is because 'a

species evolves' is left untranslated. To complete the translation we need to bear in mind that each set-theoretically conceived species is a union of subsets – call them 'time slices' – comprising, for each given time, all the organisms belonging to the species which are alive at that time. On Kitcher's view, 'a species evolves' is then shorthand for:

> the frequency distribution of properties across one time slice will differ from the frequency distribution of properties across a later time slice,

and similarly for other assertions involving apparent reference to species changing over time such as 'this species branched into two species' or 'that species became extinct.' (Guenin, 2008, p. 107)

Note that Kitcher is not here telling us what species (entities which, on standard views, evolve, speciate, become extinct, etc.) *are.* Rather, he is offering a proposal to replace the familiar species notion with another, different notion. As Guenin puts it: 'expressions in terms of sets more accurately describe selection than does talk of species changing.'

One advantage of the language of set theory is that it provides us with a well-understood common logical framework within which we can clearly and rigorously formulate what might otherwise be opaque claims pertaining to species and their instances, as well as to biological entities of other sorts. Against this, however, is the fact that the conception of species themselves as sets cannot do justice to those aspects of the biological approach which rest on the view of species as particulars, entities which not only evolve, but also do a variety of other things, including crossing mountains, replenishing the earth, and so forth. This requires a view according to which species have organisms not as *members* in the set-theoretic sense but as *parts* in the sense of mereology (Simons, 1987). Can we, then, formulate a compromise framework in which we can enjoy the advantages of both the set-theoretic and the mereological approaches?

4.2 Species, Sets and Biological Classification

A framework along these lines has been most prominently advocated by John Dupré, who argues that two distinct approaches to species are required, one for the study of evolution – which demands a view of species as particulars exactly as adumbrated by Ghiselin – and one for classification – where in addition, as Dupré sees it, a pluralistic view is required, which allows for a mixing and matching of species concepts (Dupré, 2001).

Understandably, given his interest in biology as a science, and in natural laws, Ghiselin responds in negative tones to Dupré's proposal:

> The idea here is that there should be one way of ordering nature for evolutionary research, another for classification, perhaps with classification adapted to the needs of the aquarium trade. (Ghiselin, 2002, p. 159)

We should beware, however, of assuming that every supplementation of the strictly mereological approach to species must involve an avowedly promiscuous pluralism of the sort defended by Dupré. A more acceptable strategy is to see set theory not as an ontological alternative or supplement to mereology-based particularism, but rather as an ontologically neutral linguistic framework within which to formulate the classificatory implications of biological research in a rigorous and consistent way.

It can provide us, for example, with the means to enhance the strictly mereological formulation of the particularist view of species by allowing us to capture the sense in which species are totalities of *organisms* rather than of *cells* or of *molecules* – the sense in which species, on the biological approach, are thus properly referred to in terms of *populations*. The problem here is that, in contrast to set-membership, parthood is transitive – so that there is a sense in which mereology washes away the differences between parts at different levels of granularity. Every part of me – my cells, my teeth, my digestive tract – is also a part of the species of which I am a part. Yet my teeth are not human beings*.*

The language of set theory provides us with a means of resolving this problem in a way that leaves the underlying ontology unchanged. Briefly, we can define for each non-empty set A a corresponding *mereological fusion*, which is what results when we imagine the members of A as being put together to form a whole. In symbols: the fusion σ(A) is the maximal whole all of whose parts overlap with some member of A. For any species S as conceived on the biological approach we can then create a series of designations of such mereological fusions, each of which recognizes the parts of S at a certain specified level of granularity. Most prominently, these include:

i. σ({x │ *part_of*($x,$ S) & *instance_of* ($x, organism$)})

ii. σ({x │ *part_of*($x,$ S) & *instance_of* ($x, cell$)})

iii. σ({x │ *part_of*($x,$ S) & *instance_of*($x, molecule$)})

where the terms '*organism*', '*cell*' and '*molecule*' refer to the corresponding natural kinds. Only i., it seems (or better: some modified version of i., in which account is taken of time), represents a generally applicable candidate to *be* the species S; for only i. does not leave mereological gaps. (ii. leaves out bones, hair and other parts of organisms of higher species which are not made of cells; iii. leaves out parts, such as the cavity of the bladder, not made of molecules.)

5.   The Future of Biometaphysics

We referred earlier to attempts by contemporary biologists to create standardized classifications of entities such as proteins, cells, or pathways. Such work is playing a crucial role in helping to organize the massive quantities of data now being made available through high-throughput experimentation techniques in functional genomics and related areas, to the degree that the activity of

classification is itself enjoying something of a renaissance in biological science. The most successful example in this regard is the Gene Ontology (GO), a collection of three cross-species classifications (of *molecular functions*, *biological processes* and *cell components*) now applied in many areas of biological and biomedical research to promote the integration and comparison of data deriving from the study of genes and gene products in organisms of different species. The GO has proven useful especially in research on so-called 'model organisms', which are studied experimentally for purposes of drawing implications for our understanding of human health and disease (Gene Ontology Consortium, 2006). The GO is now supporting efforts (a) to establish for each type of biological entity that mode of classification which best conforms to our current scientific understanding, and (b) to create on this basis an orthogonal suite of interoperable representations of biological reality employing a common formal framework. Interestingly, these efforts are drawing on both biological and philosophico-ontological expertise (Smith *et al.*, 2007). Their goal is to ensure that we will be able to harvest maximal benefit from the biological information resources of the future.

We already face enormous challenges in assimilating the huge amounts of life science data being made available to researchers, and there is an increasingly urgent need to ensure that these data work well together. The language of set theory – or better: one or other modified language honed to possess more useful computational properties (Rubin, *et al.*, 2008) – is beginning to provide the framework within which classifications of organisms, diseases and molecular functions can be made to work together in ways useful for research. The need for such a framework creates at the same time, however, a strong practical argument against pluralistic approaches of the sort favoured by Dupré. For the mentioned challenges would become even more intractable were different research groups addressing the same biological phenomena each encouraged to employ their own classifications in a spirit of tolerance and diversity.

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