

Chapter 9: The Classification of Living Beings

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Biomedical ontology is the study of entities in the domain of biomedicine, specifically of the general kinds and properties which these entities instantiate. Living beings are among the key entities in this domain. No ontology of the biomedical domain would be complete which does not take into account the fact that living beings are subject to division into species and genera. One reason is that this is a fact about living beings, and the best ontology is the one that is most accurate to reality. Another reason, specific to *biomedical* ontology, is that health is species-relative; hence, it is important to understand the way in which living beings are classified and divided into species. Further, living beings are composed of parts, such as organs, many of which have specific functions. Insofar as biomedical ontology aids in the practice of medicine and clinical research, it is crucial to know which specific function to attribute to which part. But a part of a living being can be said to function or malfunction only against a background of knowledge about the features that are characteristic of the species to which this living being belongs.

This chapter proceeds in five steps. First, we will describe and justify the structure of the traditional system of species classification. Second, we will discuss three formal principles governing the development of taxonomies in general. It will emerge that, in addition to these formal principles, a division of living beings must meet certain empirical constraints. In the third section, we will show that the traditional division of living beings into species best meets these constraints. Fourth, we will argue that a taxonomic system based on this notion of species provides a more natural alternative to the many arbitrary classifications that are possible. Hence, the traditional classificatory system is also the most natural one. Finally, we will discuss and reject an alternative account that suggests defining species solely with a view to their evolutionary history. We will argue that taxonomic trees do not depict hereditary connections but, rather, something else.

1. *The Structure of the Traditional System*

The purpose of a taxonomic system is to systematize the names of, and our knowledge about, kinds of entities. In the taxonomy that is in use in present-day biology, the European domestic cat is classified as follows:

Domain	<i>Eukaryota</i>
Kingdom	<i>Animalia</i>
Subkingdom	<i>Bilateria</i>
Phylum	<i>Chordata</i>
Class	<i>Mammalia</i>
Legion	<i>Cladotheria</i>
Cohort	<i>Placentalia</i>
Order	<i>Carnivora</i>
Family	<i>Felidae</i>
Genus	<i>Felis</i>
Species	<i>Felis sylvestris</i>
Subspecies	<i>Felis sylvestris sylvestris</i> ⁴³

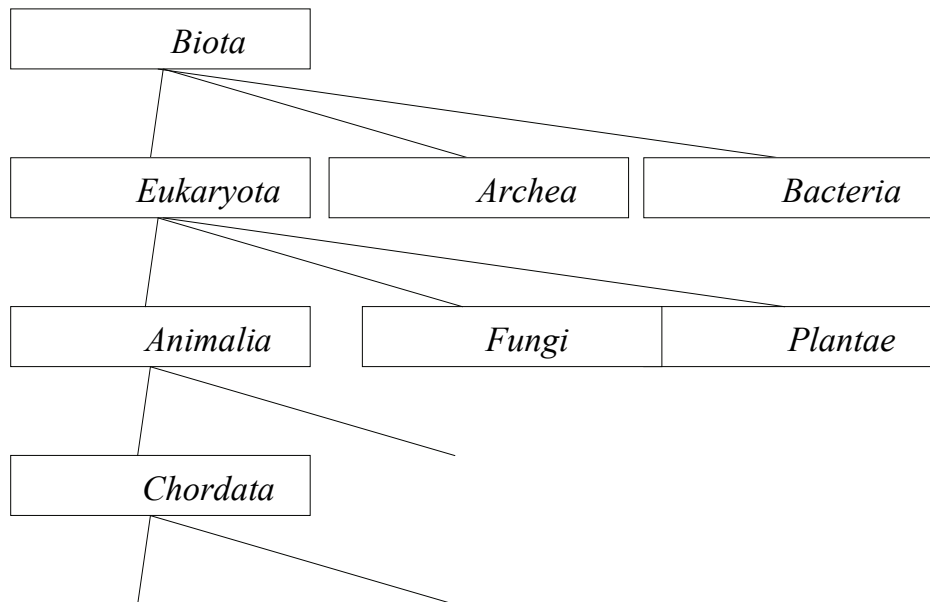
Felis sylvestris sylvestris is located at the bottom level of a series of distinctions. The domain *Eukaryota* is distinguished from other domains such as *Bacteria* and *Archaea*; the kingdom *Animalia* is distinguished from other kingdoms such as *Plantae* and *Fungi*; and so forth. As a whole, these distinctions constitute a tree-like structure; that is, a structure with one top-level node that divides into several child branches, which in turn divide into further branches. The branches at the bottom of the tree, which do not divide into further branches, are called *leaves*. The initial segment of the series of distinctions by which *Felis sylvestris sylvestris* is classified may be depicted as in Figure 1. The nodes here are called *taxa* (singular: *taxon*). All taxa above the level of Species are called *higher taxa*. The purpose of situating individual species into such a tree can be explained best by considering both technical and empirical constraints.

First, tree structures can be browsed much more efficiently than lists of items. For instance, suppose that the question is ‘To what species does a given insect belong?’ and this is to be decided by matching that insect’s features against a complete list of species descriptions. Since the class *Insecta* includes more than 750,000 known species, this will take a long

⁴³ See *Taxonomicon*. We leave out several intermediate taxa such as infrakingdom, branch etc.

time; in the worst case, it will involve 750,000 steps. By contrast, in the worst case scenario searching a tree structure with two branches at each level and 750,000 leaf nodes would only take approximately 20 steps.

Figure 1: *Fragment of a Taxonomic Tree*



Taxonomic trees have the further advantage that information associated with their leaf nodes can be stored and retrieved very efficiently. For instance, a knowledge representation that contains information pertaining to all chordata alike, at the lowest level, would contain much repeated information. It would tell us that cats have a spine, dogs have a spine, horses have a spine, and so on. It is clearly more efficient to associate information that holds true of all these species alike with a higher level node, namely *Chordata*, so that it needs to be stored only in one place. (Compare Aristotle, *Parts of Animals* 639a15–30.) Such information, then, would be inherited by the nodes lower down the tree. In this way, one may gather all information about cats by traversing the tree upwards and adding more and more general knowledge about mammals, vertebrates, chordates, etc. As a result, one may conclude from the fact that a given living being is a cat, and cats are chordates, that this living being has a spine. This only works, however, in systems where no taxon has more than one immediate parent group (as we see in Chapter 8); that is, it works only in tree structures.

It is also easy to see why a taxonomic system must have highest and lowest elements in order to be effectively browsed; that is, a root node and

leaf nodes. First, a search within a taxonomic tree must proceed in only one direction, and it must begin from a point from which all taxa may be reached. Therefore, there must be a highest taxon; otherwise, the search could not begin. If there were two highest-level genera, there would also have to be a procedure to decide where to start looking, and this would amount to the introduction of one highest order taxon. Further, any process of traversing the tree downwards must be guaranteed to terminate at some point. A system that endlessly divides every taxon into further subtaxa would not be of much use.

It should be clear that a system for classifying biological kinds or species can only be established on the basis of knowledge about the *particular* living beings which instantiate them. In order to locate a species in the taxonomic tree, one must already possess extensive knowledge about the features of its instances. Further, many of the terms that are used in a scientific taxonomy are also used in everyday life and, hence, have a meaning of their own. The mere labels already encode empirical knowledge. It is not always possible to introduce higher-level taxa by focusing on one feature, as in the case of *Mammalia* (which are defined, through the presence of mammary glands in females). For instance, the division of living beings into plants and animals is used in everyday life and, hence, has a meaning of its own; but there is no single feature that all plants share and all animals lack. We will show that the traditional classificatory system is also the most *natural* one.

It is a remarkable fact about living beings that they admit of a classification in a tree structure. There may be cases that are difficult to accommodate, but it is still possible to amend the tree structure to make it fit. For instance, the platypus has features of typical mammals but also lays eggs. In order to fit it into the system, the class *Mammalia* was divided into the subclasses *Prototheria*, *Metatheria* (including marsupials), and *Eutheria* (higher mammals). The platypus is classified under *Prototheria*. This is only one instance in which an empirical discovery has led to a change in the taxonomic system.

2. Three Regulative Principles

The last section emphasized the practical advantages of taxonomic trees. Following Kant, we will now consider three formal principles governing the construction of any such tree. It will emerge that, in addition to these logical constraints, a good taxonomy of living beings must be based on an

empirically founded basic division which will turn out to be the division of living beings into biological species.

Kant postulates what he calls three formal principles of reason, which are necessary for systematizing any domain, namely, (1) the principle of specification (*Critique of Pure Reason*, B 682), (2) the principle of unity (B 680), and (3) the principle of homogeneity (B 685). These principles are merely regulative (B672). This means that they are not aspects of reality, but only guide our inquiry into the nature of real objects. Since they direct the acquisition of knowledge and are not derived from this knowledge, they may be called *a priori*.⁴⁴

The *principle of specification* demands that, for every taxon, one should ask whether it may be divided into further subtaxa. Since the same question is to be raised concerning the subtaxa, the process of division does not come to a natural end. Every species may, and should, be divided into subspecies, and these subspecies should be further divided. As a consequence, Kant claims that there is no lowest species. In his *Logic*, Kant writes:

Even though we may have a notion that we apply immediately to individuals, there may still be specific differences regarding this notion, which we either do not notice, or neglect. It is only comparatively, as a matter of convenience, that there are lowest level notions, which receive their meaning as it were by convention, as it were, when one agrees not to proceed further down. (*Logik* §11, *Akademie-Ausgabe* vol. IX, p. 97; our translation)

Note that, although the division of taxa into further subtaxa can go on indefinitely, it will never reach the level of individuals. It is possible to distinguish species in such a fine-grained manner that every individual is taken to be an instance of its own kind, but even then, the individuals will not coincide with the species to which they belong. Kant writes, metaphorically, that ‘the logical horizon consists of smaller horizons (subspecies), but not of points (individuals), which possess no extent’ (B686). Just as we can always further divide a geometrical line without reaching the level of geometrical points, so too, we can always divide a taxon into further subtaxa without reaching the level of individuals.

The converse of the principle of specification is the *principle of unity*, which Kant also calls the principle of genera. It requires that we always try

⁴⁴ For a discussion of the role of *a priori* knowledge in formal ontology, see Chapter 2, Section 4.

to bring different taxa under a common higher-level taxon, and ask further under what higher-level taxon this latter taxon may be brought. Kant writes: ‘There is a genus that cannot be a species [i.e. a subtaxon], but there is no species that could not be a genus [i.e. have subtaxa]’ (*Logik* §11, 97). The principle of unity instructs us to always proceed to higher and more general taxa, and again, it does not seem to tell us where to stop. As a matter of fact, however, there must be some point where the application of this principle comes to a halt. The reason is that if we only allow one parent node per child node, we will eventually reach a highest parent.

To these two principles, Kant adds a third, the *principle of homogeneity*. This principle demands that, whenever we draw a clear distinction between species, we should be aware of the possibility of borderline, intermediate, or mixed cases. We should always keep in mind that, as a rule, the universe is continuous: between any two distinct entities, there can be an intermediate one (B687). The principle of homogeneity counteracts the principle of specification by postulating a certain affinity between instances of different species. It does this in two ways.

First, for every two taxa, some common higher-level taxon can be found, however remote. Hence, the instances of every pair of different species are also alike in some sense. This follows from the principle of unity. Second, for all taxonomic divisions, there may be intermediate stages or forms. Following the 18th century biologist, Charles Bonnet, this may be dubbed the principle of continuity (Bonnet, 1766).

The principle of continuity, itself, can be understood in two different ways. First, it may be taken to postulate that, between every taxon and its higher-level taxon, further taxa may be introduced. An application of this principle has already been mentioned: the insertion of subclasses of *Mammalia* in order to accommodate for the features of *Platypus*. This procedure is quite common; for instance, in the complete classification of *Felis sylvestris sylvestris*, three taxa have been inserted between cohort and order – magnorder, superorder, and grandorder – and more still could be inserted.

A second way of understanding the principle of continuity is that, for every division of taxa into separate subtaxa, there will be certain items that fall between the cracks. In general, wherever we draw distinctions, there may be borderline cases. However, the existence of borderline cases does not prove that there are no distinctions to be drawn. Further, it will become

apparent that there are real distinctions in nature between different biological species.

Kant emphasizes that all three principles are only of heuristic value. They direct our empirical research in that they tell us where to look for further evidence. They do not directly apply to the world we experience; that is, they do not tell us that there must in fact always be a common genus, a further species, or a borderline case. The principles only encourage us always to look and see whether there are common genera, further species, or borderline cases. When Kant writes that there can be no lowest species he can only mean that there can be no *logical* reason to stop subdividing a taxon. In principle, it is always possible to insert an intermediate taxon between a given taxon and its subtaxa. However, Kant does not tell us when to stop looking. Further, since all biological individuals possess their own unique features and, since as long as there are living beings new living beings may be born, there is no limit to the possibility of dividing species into further subspecies, and no limit to the possibility of borderline cases.

Of course, there are practical and theoretical reasons why we should stop adhering to the Kantian principles after a certain point. Consider the principle of unity. It demands that we should try to bring every taxon under a higher-level taxon. This process must come to a halt, at least when the highest possible genus, ‘being’ or ‘entity’, is reached. But there are also reasons to stop applying it well before the highest possible genus. The most general set of beings relevant to biology is the set of living beings (*Biota*). To be sure, it is possible to subsume living beings, artifacts, and other physical objects under one common header; but this is of no practical value. Moreover, it tends to blur essential differences, which is an important theoretical consideration for anyone interested in an ontology of the biological domain that is accurate to biological reality.

For instance, there are no criteria of identity that apply to material things in general. Living beings remain the same entity as long as they stay alive, and they need to exchange matter in order to do so. By contrast, lifeless objects may be identified, simply, in terms of their matter. Further, although (most?) artifacts are lifeless objects, an identification of artifacts in terms of their matter leads to certain problems: a ship arguably does not cease to be the same ship when all its planks are replaced.⁴⁵ Hence, living beings, artifacts, and other physical objects should be distinguished, not in

⁴⁵ This is known as the ‘Ship of Theseus Problem’ (Hobbes, *De Corpore* XI). See, for instance, Rea, 1995.

terms of specific differences regarding their features and qualities, but in terms of the principles according to which they may reasonably be identified as the same things over a certain period of time (Schark, 2005). This means that an ontology of the biological domain does not have much use for a common genus that embraces these different kinds of beings, although such a genus is required for an upper-level ontology such as BFO (see Grenon, *et al.*, 2004; Grenon and Smith, 2004; Grenon, 2003).

We conclude that the three principles put forward by Kant apply to all taxonomic systems but that, in each case, they need to be complemented by empirical constraints. In biology, there is a particular highest taxon (*Biota*) and a basic level of division on which the whole taxonomy of living beings is founded. It is important to keep logical and empirical constraints distinct from one another. It is an empirical fact that all living beings have something in common, so that they constitute a realm that admits of a taxonomic classification. It is also an empirical fact that there is a point where the division of taxa of living beings into further subtaxa comes to a natural end. That such a basic division exists is not a logical requirement. It is a logical requirement, however, that taxa divide into further subtaxa such that a tree structure results.

In accordance with the three principles of classification named by Kant, one may establish this structure by proceeding both upwards and downwards: upwards by grouping species together in higher taxa and by bringing the higher taxa under taxa that are still more general; and downwards by dividing the realm of living beings into domains and subtaxa. The most general distinction we make within the realm of biology is the one among *Bacteria*, *Archaea*, and *Eukaryota*. From this point on, one may develop the system by introducing a series of distinctions. At the same time, however, the system is supposed to capture the known species of living beings. To this end, one should look at the accounts and descriptions of different biological species such as *yarrow*, *cat*, and *sparrow*, and consider how they are best grouped together under more general labels. The task is to unify and merge different groups into higher order groups.

As has already been noted, the advantage of this bottom-up procedure is that we may associate certain bits of knowledge with the higher order groups instead of redundantly associating them with several lower level groups alike. This procedure facilitates the learning and teaching of facts about kinds of living beings. The purpose of a classification of living beings is to provide a basis for the storage and acquisition of knowledge

about living beings, not to merely impose order. This is even more important in contexts where knowledge is processed automatically, and where vast amounts of knowledge are maintained. It can cause a great deal of trouble to maintain and update a system containing redundant information. For instance when new information concerning all insects comes to light, data would need to be changed in almost a million different places in the same way. But if the information is stored only in one place, namely under the label *Insecta*, such a change is easily made in one step.

Though the classification of kinds into higher order kinds has such a practical purpose, it must not be arbitrary. Indeed, the best classification will always be one that refers to features that are, in fact, typical for the respective range of living beings. The class of mammals is a group of items that belong together in more than one respect, whereas the introduction of a class of two-legged animals would soon cause trouble (since it would include birds and humans alike). Which divisions are appropriate can only be seen by simultaneously pursuing the downward movement of division and the upward movement of unification.

3. *Biological Species*

We will now argue that a system for classifying living beings must be based on a division into biological species. This gives rise to the question of what a biological species is. This section will provide an answer to this question.

In a logical sense, every group that may be divided into subgroups is a genus, and every group that may be brought under a higher order group is a species (Kant uses the terms in this sense in the second passage quoted above). The biologist, however, uses ‘species’ in a much narrower sense. Biological species constitute only one level within biological taxonomy.

Below the level of biological species, one may distinguish populations, varieties, races, and forms; but these distinctions are always, to some extent, arbitrary in that they involve merely geographical and phenomenal differences. The taxa above the species level differ from species in that they are only associated with a fragmentary or ambiguous description. There are instances that satisfy all and only the criteria that apply to the species *Felis Sylvestris*, but there are no instances that would satisfy only the criteria that apply to the class *Mammalia* in general. *Mammalia* is an abstract taxon in two respects. First, there are different kinds of mammals; some have fur, long tails, exposed genitals, and some do not. The

description of the class *Mammalia* is incomplete in this regard. Second, every mammal is necessarily an instance of some species, whose description can be made complete to an arbitrarily detailed degree. This does not mean that the class *Mammalia* does not really exist, let alone that there are no mammals. It means, however, that there are no mammals over and above the instances of particular species of mammals.

In this respect, class names are like mass terms. Mass terms such as ‘milk’ apply to real things, but they do not refer to countable items. In reality, however, everything that exists can also be counted: every instance of milk is an instance of so and so many centiliters of milk, and centiliters of milk can be counted. Nonetheless, it makes perfect sense to speak of *milk*, in contrast to definite portions of milk. When we do so, we abstract from the countability (portioned nature) of all real milk. Likewise, class terms such as ‘mammal’ apply to real things, although in fact, every mammal is also an instance of some more specific species. When we use such terms, we abstract from certain specific features of a living being.

Species provide the units of biological reality, and taxa below and above the species level can only be introduced against the background of a species division. Therefore, it is of the utmost importance to be clear about the precise circumstances under which a taxon constitutes a species. That the discovery of a new species is something biologists tend to be proud of shows this is important as well. In some cases, species bear the name of their discoverer, as for instance the *Ophrys regis fernandii* or the *Epipactis mülleri*, named after their respective discoverers, King Ferdinand and Müller. To discover a new biological species is regarded as a lasting achievement. However, since it is always possible to introduce further distinctions, it is logically possible to divide every known group of living beings into further subgroups. The question is, under what conditions is such a division, in fact, a division into different biological species, rather than a division into arbitrary sets, higher taxa, or parts of the same species. For instance, many plants differ from others merely because of the quality of the soil, or only because of their geographic location; but such differences should not license a species distinction. There should be a limit to making divisions since, after all, biological species have to be registered, described, learned, and taught. In order to avoid proliferation of species divisions, one needs non-arbitrary and ontologically sound criteria for what biological species are. Ideally, what we need is a basic division of living beings into species that carves reality at its joints (Plato, *Phaedrus* 265e).

Yet the question of what biological species are is subject to considerable dispute.⁴⁶

A perusal of the history of philosophy and science shows that the notion of a biological species was uncontroversial until, roughly, the 1850s. With the advent of Darwin's theory of evolution, according to which forms of life are subject to constant change, the claim that biological species are part of a natural order becomes problematic. All clear distinctions between species seem to be temporary, and the criteria according to which they are drawn begin to appear arbitrary. It is no wonder that, as a consequence, there are divergent opinions as to what counts as a biological species and a good classificatory system.

As we will see, however, a closer look reveals that many of the different accounts of what biological species are, in fact, do not contradict each other. They are not all of equal importance, and they are systematically related in such a way as to complement one another. In order to determine what biological species are, we need to consider two things. First, living beings maintain and reproduce themselves. Therefore, it is quite natural to assume that a species is a group of individuals that is engaged in generating and breeding further members of this group. The idea that species are basically reproductive communities has been put forward by Ernst Mayr (Mayr, 1996).

Second, reproduction and self-maintenance can be successful or not and, where they occur, there must be certain standards according to which their success may be measured. When one spells out these standards, one ends up with a description of a prototypical and idealized (canonical) instance of the respective species. A cat reproduces successfully if the result of what it does is something that satisfies all criteria that apply to healthy and typical cats. This motivates the account of biological species suggested by Plato and Aristotle. Species are associated with standards of typicality, and to describe a species is really to describe its ideal case: the idea (*eidos*) or essence of its instances.

One can bring together both strands in the following characterization: *Biological species are universals instantiated by members of reproductive communities that secure the (at least relative) permanence of a form of life that is characteristic of members of this community, by passing it on to their offspring.*

⁴⁶ See e.g. Ghiselin, 1974; Hull, 1997; Mayden, 1997; Ereshefky, 2002; Reydon, 2005.

Species are not sets of living beings; therefore, some biologists like Ghiselin (1974), Caplan (1981), and Hull (1997) have claimed that species must be individuals. This claim, however, rests on the assumption that the alternative between sets and individuals is exhaustive, which holds true only in an ontology such as the one suggested by Quine. Quine's ontology, however, is suitable for mathematical and physical entities only, and not for living beings. Species are neither individuals nor sets, but universals.

More specifically, to instantiate a species is not only to exemplify a set of characteristic features, but also to lead a certain life. For example, the instances of *Felis sylvestris* are born in a certain way, develop in a certain way, and perform certain characteristic activities during their lives. What they typically do in the course of their lives does not only contribute to their life; rather it *constitutes* their typical life. A description of what is characteristic of cats cannot consist in mere a list of features, but only in a story about the typical life of a cat (Thompson, 1995).

It is important to note that individual instances of a species may transmit their characteristic features to their offspring even if, for some contingent reason, they do not possess them. For instance, a cat with three legs, in most cases, will generate offspring that has four legs. In reproducing, instances of biological species do not just copy their own particular makeup, but transmit a form of life that is characteristic of instances of their species. Therefore, a species is constituted by all individuals that may successfully reproduce, such that instances of the same form of life result.

That species are instantiated by reproductive communities does not imply that all instances of a species can actually mate with all other instances of this species. First of all, it is not necessary that all instances of a species do, in fact, successfully mate with all other instances. Two male individuals of the same species cannot mate and generate offspring, but they both can in principle generate offspring by mating a female instance of the same species. Second, individual instances of a species may be entirely infertile, raising the question of whether they belong to the same reproductive community. But all that follows from our understanding of species is that, for all instances of a species, not to be able to generate further individuals with certain characteristic features constitutes a *defect*. If an individual is infertile, it thereby fails to belong to the species only if its infertility does not constitute a defect; and whether infertility is normal or pathological can usually be ascertained by independent means. It is also a matter of dispute whether two populations that cannot interbreed because

of geographical barriers constitute a species or not. In such a case, it is not clear whether both populations actually belong to the same species until it can be shown whether, in principle, they are able to interbreed.

These details do not alter the general idea that species are instantiated by reproductive communities of individuals. In order to flesh out this idea, one may describe what conditions must be fulfilled for individuals to successfully reproduce and preserve their characteristic form in more detail. This can be done by further discussing how a population manages to ward off distorting influences, and how reproduction works; for instance, by providing a detailed account of how genetic codes are merged and copied. Knowledge about genetic processes may be adduced in order to explain how living beings actually manage to transmit a characteristic form of life to their offspring. Such an explanation of how reproduction works complements the account developed so far; it does not lead to a different account of what species are.

However, the suggestion to define species *merely* in terms of evolution is problematic in certain respects. Species of higher forms of life are not rigid but, instead, provide for a certain range of differences concerning the features, form of life, and behavior of their instances. Thereby, they also allow for the development of new features that may be distinctive of certain races, forms, or varieties. But the emergence of a race should be distinguished from the development of a new species. Races are only possible within the range that is left open by the proper description of a biological species. For instance, the proper description of *Felis sylvestris* leaves open whether its instances have black or white fur. The coming into being of races, forms, and varieties is not an instance of evolution but, rather, the realization of features or forms of life that instances of some already existing species can exhibit. Races may remain stable for contingent reasons, but they tend to disappear when their instances interbreed with other instances of the same species.

The development of races can explain the emergence of new species only if additional conditions hold; for instance, that the members of a race have been isolated and have changed because of inbreeding. Considering that long isolation might lead to a radical change in reproductive behavior, so that interbreeding with other instances of the same species ceases to be possible. Such isolation, however, should be taken to abolish the unity of the original reproductive community and, where this unity is compromised, the permanence of the form of life characteristic for a species is not granted. As a matter of fact, species need the possibility of crossbreeding

between as many different populations and individuals as possible in order to retain their form of life. When a significant portion of a reproductive community ceases to contribute to the reproduction of the whole species and begins to constitute its own species, both parts of the original reproductive community come to instantiate a *new* species (although one of them may retain the old name), having evolved from the old one.

But this does not mean that species are changing things. They are universals. When something turns from red to green, the universal that it exemplifies does not change; that is, Red does not turn into Green. Rather, the thing changes by coming to exemplify another universal. Likewise, when a population comes to instantiate a new species, it is not the species itself that changes, but the population that ceases to instantiate one species and comes to instantiate another. Of course, we can say that a species changes in the same sense in which we can say that the color of an item changes when it turns from red to green. But this does not mean that the species itself undergoes a change, just as the change of color is not a change that the color Red undergoes.

Further, the process by which a population may come to instantiate a new species cannot be a continuous one. First, a *continual* evolutionary development could only take place where the evolving beings do not divide into biological species at all since, during this development, genetic changes are transmitted to the offspring without correction. There would be no difference between successful and failed reproduction and, hence, there would be no form of life that would be characteristic of the living beings in question. Second, even where evolutionary change does not occur continually but only temporarily, the criteria of successful reproduction are suspended as long as the change is taking place. As long as a species evolves, no one could possibly tell whether its offspring is as it should be; since by assumption, this offspring exhibits a new form of life, and this new form of life might become characteristic of resulting populations.

This implies that there can be no purely evolutionary concept of a biological species.⁴⁷ Where there are species, there is no evolution, and where evolution takes place, there are no species. A species can be the result of evolution and the starting point of more evolution, but as long as evolution is taking place, there are no clear differences between features

⁴⁷ *Pace* Hennig, 1966; Kornet and McAllister, 2005; Griffiths, 1996; and Millikan, 1999.

that are characteristic for the evolving beings and features that are not, and hence there is no species.

The relevance of these considerations becomes obvious when we consider that the permanence of a biological species is the conceptual precondition for a taxonomic system such as the Linnaean one. The Linnaean taxonomy systematizes universals, not populations; and whereas populations can change with respect to the universals they instantiate, the universals themselves do not evolve. On the other hand, the existence of continuous change is one of the central assumptions of Darwinian evolutionary theory. Hence, there are conceptual reasons why Linnaeus denied the possibility of evolution, and why Darwinians, on the other hand, have problems with the concept of a biological species. This conflict, however, is only apparent. Evolutionary theory does not really describe how species undergo a change; it only describes how populations come to instantiate new species.

This does not at all diminish the importance of evolutionary theories to taxonomy. In particular, it does not mean that evolution could not explain *why* and *how* living beings divide into biological species. It only means that evolutionary theory cannot provide the whole and exclusive basis for a taxonomic division of living beings into species.

It should be clear that we need, at least, the concept of a *relatively* permanent species in order to do taxonomy. The process of dividing taxa into further subtaxa would be brought to a halt if we assume that there are biological species with *certain* stable characteristics. We can do so by admitting that species may change, but abstracting from this fact and only considering the results of these possible changes at one instant of time. In fact, this is all we need since we are only interested in a classification of the living beings and the results of evolutionary change at a certain instant of time.

4. *The Search for a Natural System*

A system is artificial if it distinguishes between different kinds of things according to criteria that provide a superficial overview of the various forms of life, in reflection of chosen purposes. In order to establish a natural system, we need to inquire into the natural and objective order of things, so that we may divide our domain by criteria that are founded on the nature of the things to be ordered and, thereby, provide a better alternative to the many arbitrary classifications that are possible.

To be sure, in several contexts it is useful to classify living beings according to criteria that refer to our own purposes. Such classifications are already found in the Old Testament, where animals are distinguished into pure and impure ones, and members of the religious community can only eat the pure ones. One may also classify animals according to where they may be hunted, and what side dishes or kinds of wine fit with them. Such classifications, however, are valid only relative to certain human communities; they refer to things that are of more or less value to the members of specific groups of humans. Where a unified and scientific classification is in order, it does not make much sense to choose criteria that may vary from one set of scientists to the next.

One might object that a natural system is not needed, since it would be enough if scientists agreed to use some fixed set of arbitrary criteria. These criteria should not vary; but they need not be natural. Why do we need a natural system for classifying living beings? The answer is that an arbitrary set of criteria may become obsolete for irrelevant reasons. If the agreement of all scientists to use given criteria is itself arbitrary and not founded on objective facts, all scientists might as well decide to change the criteria for arbitrary and contingent reasons. Natural systems can only fail for relevant reasons, that is, only when reality changes, or if they were inadequate (that is, not truly natural) in the first place. Moreover, it is unlikely that all biologists would agree on a common set of arbitrary criteria, since different biologists (botanists, geneticists, physiologists, etc.) pursue different projects and take different views on biological reality. In fact, there have been a wide variety of different and even incompatible classificatory systems in biology before a natural system was established.

Further, it may be objected that every system of classification, including the biological one, is in some sense artificial. After all, science is an artifact, and so is every scientific taxonomy. There is some truth to this objection. Science is done and maintained by humans; however, this does not mean that the results of science are arbitrary. The traditional, Linnaean, biological taxonomy is based on a division into biological species that is found in nature, and is constrained by empirical facts. The task is to find out what is really essential to specific forms of life, and how different species actually differ from and are similar with one another.

Finally, one might object that the criterion of cross-fertility is as arbitrary as any pragmatic criterion that is used by scientists in order to suitably systematize their domain. After all, humans are especially interested in breeding plants and animals, and this may be why cross-

fertility is so important for them. It may also seem that, as Kant says, scientists assume the existence of species only as a matter of convenience, in order not to be forced to constantly divide all their taxa into further subtaxa. This view, however, would overlook the important fact that the instances of species themselves ensure the permanence of a certain form of life. Reproductive communities are engaged in generating offspring with certain characteristic features and, in this sense, they are engaged in perpetuating and stabilizing their own species. Put differently, there is an objective division of living beings into species because there are objective limits to reproduction; and there are species to be distinguished because reproduction occurs within these objective limits. Without limits to reproduction, instances of different species could mix and generate indefinitely many intermediate forms. In this case, it would be difficult to tell whether reproduction is successful or not. This, however, is not the case.

This is why the criterion of cross-fertility is more powerful than other criteria by which we distinguish kinds of things. It yields divisions that are probably only superseded in their clearness by the distinctions we draw between different individual objects. Individual objects may be distinguished from one another as long as they occupy a clearly limited location in space and are impenetrable in some sense, so that they do not merge with other objects, and do not move discontinuously. Similarly, particular species may be distinguished from other species (1) because their instances do not successfully interbreed with instances of other species, such that the boundaries between different species are impenetrable, and (2) because all instances of a species derive from ancestors that belong to the same species, such that there is a continuous path that leads from one instance to the next one. Most importantly, the existence of reproductive communities implies that the realm of living beings is not a continuum. There are real distinctions between different species because there are real reproductive barriers. Kant's principle of homogeneity does not apply.

The biological classificatory system is not natural in the sense that it may, as a system, be found in nature. It is natural because and insofar as humans have established it according to objective criteria that reflect the nature of things, and not according to arbitrary and artificial ones.

5. *Taxonomy and Ancestry*

In biology, attempts are being made to define species and higher taxa only by reference to the common ancestry of their elements. Some biologists have suggested that the evolutionary tree of descent directly mirrors the division of living beings into species. This has led to the idea that the tree of ancestors of biological species is also the best system for classifying them, and that it is evolutionary biologists and paleontologists, rather than taxonomists, who should lead the search for a natural system (see Mayr, 1969). But evolutionary theorists and paleontologists are concerned with establishing a family tree of biological species and, as we will argue, family trees and taxonomic systems are fundamentally distinct things.

Evolutionary biologists claim that the traditional classificatory system is not a natural one. We have already seen that for a classificatory system to be natural, it needs to be made according to non-arbitrary criteria which match the nature of things. A phylogenetic tree may seem to be more natural, in this sense. The question is thus whether, from a logical point of view, it makes sense to replace the traditional classificatory system with a new one based only on common ancestry.

This question already presupposes that we are able to give a reasonably complete family tree of biological species. Since such a tree cannot be based on direct observation of presently existing forms of life, the main method for establishing such a tree is a comparison between extant forms. However, similarities between living beings of different kinds, at best, indicate that they might have common ancestors. A method that allegedly serves to discover hereditary bonds was developed in the 1950s by Willi Hennig, who aimed at establishing a *cladistics*; that is, a classificatory system that is exclusively based on phylogenetic kinship (Hennig, 1966). To this end, particular features are singled out by way of comparison, and used in order to establish so-called *cladograms*. The comparison is carried out on the basis of morphological features, characteristics of the digestive system, and the DNA sequences of extant species.

In order to establish cladograms, derived features are distinguished from non-derived ones. Non-derived features are supposedly older in terms of evolution; they are also features of the ancestors of the species under consideration. For instance, it is a non-derived feature of mammals that they possess a spine, since instances of other and evolutionarily older classes also have spines. The derived features of a species, in contrast, are assumed to be younger in terms of evolution and occur only in this species

as we find it today. The totality of derived features constitutes the *principal form*, which is considered a possible candidate for an evolutionarily older and more original species. A derived feature of mammals is that they possess a placenta, and the assumption is that all mammals derive from a species that was marked by the possession of a placenta, among other features. Species that agree with respect to their derived features are taken to be cognate. In this way, one can establish trans-specific types similar to those suggested by 19th century biologist Georges Cuvier (Cuvier, 1827, *Introduction*). The assumption that the classification that is established by such means no longer rests on morphological criteria is, however, purely hypothetical.

Further, even if we were in possession of an adequate, complete, and empirically founded family tree of biological species, this tree would not depict the system of biological kinds. The reasons for this are conceptual ones. Genera, families, and other higher taxa cannot be ancestors of the extant forms at the same time, since the extant and the ancestry forms are all biological species. For instance, the *Archaeopteryx* is probably the ancestor of all kinds of birds known today, but *Archaeopteryx* is a species and not a genus, family, or class. In a family tree, the *Archaeopteryx* would be represented by a node whose child nodes include all extant kinds of birds. In a classificatory tree, the node representing the class *Aves* would occupy this position. It should be clear that the species *Archaeopteryx* cannot be identical to the class *Aves*, for it is also a species falling under this class. Just as an individual living being cannot at the same time be its own species, an individual species cannot at the same time be its own genus, family, or class. This is so even if a taxon contains exactly one species, since an individual that is the only instance of its kind is not thereby identical to its kind. This distinction between species and their instances, and classes and the respective subtaxa, may be less obvious when the taxonomic tree is read in set theoretic terms. In cases where a class only contains one species, the set of instances of the class is identical to the set of instances of the species. But this is *not* how one should understand the taxonomic tree (Buck and Hull, 1966).

Regarding morphological similarity, the *Archaeopteryx* is especially unsuitable as a primordial or paradigmatic form, because it lacks essential features of birds. Many of the generic statements about birds do not apply to the *Archaeopteryx*. For instance, it does not yet have the large sternum that is typical for all extant birds. Hennig seems to be aware of this

problem, since he explicitly neglects fossils and only compares extant species to each other.

We conclude that classes and species are related *conceptually*, rather than by way of ancestry. Evolutionary trees depict the historical sequence of generations of individual living beings; that is, the hereditary lines. Taxonomies bring living beings under general concepts according to their features, and their purpose is to provide an order that is as clear as possible, in order to systematize biological knowledge, so that certain propositions can be inferred in the way that has been described by Cuvier.

6. Conclusion

We have pointed out that an understanding of biological taxonomy is essential to biomedical ontology. The most appropriate account of the division of living beings into kinds, we have argued, is provided by the traditional, Linnaean system. First, the traditional classificatory system satisfies important logical and empirical conditions for any such system. It constitutes a tree, and can therefore be quickly and efficiently browsed by both humans and machines. Further, it embraces all known species and, thereby, provides a structure for systematizing and encoding our knowledge of all biological species. Finally, it serves to determine the species of individual living beings effectively. A mere list of forms of life, as suggested by Bonnet, does not allow for this; it would be extremely tedious to browse.

We have further argued that, in order to establish a classificatory system of living beings, it is not enough to adhere only to the logical principles that govern all possible taxonomies. Other conditions that have to be met are that (1) the taxonomic system must be founded on a basic division, such that the division of taxa does not go on indefinitely, and (2) the classificatory divisions within the system must be reliable and non-arbitrary. A classificatory system is a candidate for a possible taxonomy of living beings only if the basic and the higher-level divisions accord with the facts.

A division of living beings into biological species provides the basis of the traditional system. This division is well founded, since it mirrors the reproductive barriers between individual living beings. The boundaries between different species do in fact exist; they are the reproductive barriers that prevent the interbreeding of individuals from different species. In biology, the highest taxon is the group of living beings. No higher taxon is

needed. The classificatory divisions in between are also well-founded and non-arbitrary. For the higher taxa are intended to correspond to essential features that instances of certain species share, and by which they differ from instances of other species. In this way, a hierarchy of higher taxa is established. It is important not to restrict attention to only a few features or bodily parts of living beings in order to classify them; instead, one should always consider the living beings as wholes, taking into account their visible makeup as well as their inner structure. Even the DNA, however important it is in modern biology, should only be considered as one feature of a living being among others, which adds to the overall picture. Living beings that belong to different classes and differ widely with respect to their phenotype often possess surprisingly similar genotypes.

Further, we emphasized that family trees and taxonomic systems are fundamentally distinct things. Taxonomies systematize living beings according to shared and distinctive features, and their aim is to provide a clear and effectively usable system for describing and identifying living beings. Higher and lower taxa are related conceptually, and not in terms of ancestry. Evolutionary trees, in contrast, depict hereditary lines among different species, just as a family tree represents the pedigree of an individual. Taxonomic and hereditary relations have a different logical status, and neither can be reduced to the other.

We conclude that, in biomedical ontology, the traditional taxonomic system as developed by Aristotle and Linnaeus remains indispensable. Hereditary trees may be of help in establishing such a system, but they cannot replace it. To be sure, facts about the ancestry of a species should always be accounted for and acknowledged in taxonomy. A system that does not group species together – when, in fact, they have a common ancestry – would not be a natural one. But this does not mean that ancestry is the only relevant criterion, or even that evolutionary theories alone can do the job. It certainly does not imply that the genus of a species coincides with its ancestry.