# The Relational Species Concept

Andrea Borghini
Department of Philosophy, Columbia University, New York

## 1. Introduction

What is a species? Until a few decades ago, if one were to ask this question to some biologist, the answer would have probably been something like the following:

(T) A species is a cluster of intrinsic properties, the possession of which by a given individual is a necessary and sufficient condition for belonging to the species.

Sure, some may have preferred to substitute "cluster" with "set" or "conjunction" and others may have also added that (T) defines the *ideal* member of the species, so that the existence of some *deviant* member was tolerated. But the core idea was common: a species is a certain number of properties that, when coexisting in a certain individual, are by themselves necessary and sufficient to collocate that individual within one *taxon* or another. Thus, according to (T), the world is divided into types of individuals, and species *taxa* aims at capturing such types. This means that each organism belongs to one and only one species, and it does so no matter how large or small the number of con-specific individuals is. This is, briefly, the typological species concept (cfr. Sober 1978, Ruse 1987 and Kitcher 1984).

Over the last few decades, especially because of the better understanding of the patterns of variation within populations, serious doubts were cast on the plausibility of the typological species concept. To cut a long story short, there simply seems to be no general method of specifying some common properties that all and only the organisms belonging to a certain species possess. Such a negative result, however, was not followed by the introduction of a new general picture of what species are, but by the proliferation of several different species concepts. If you open a biology book or you take a class in biology, you will be presented with several ways of classifying organisms, according also to what kind of properties one considers as relevant for classificatory purposes (morphological, phenotypical, or genotypical.) Roughly, there are as many different species concepts as there have been different goals in the classificatory activity of biologists, ecologists and genetists. Therefore, it seems that, after the failure of the typological species concept, no general picture can be provided.

Here I would like to question this claim. That is, I would like to question the idea that we do not have any general picture of what species are. As a matter of fact, I believe that fairly each of the classificatory schemas that have been proposed over the last decades serve some genuine scientific purposes. Therefore, it is our speculative duty to regard all of them as valid. However, at the same time, none of them succeeded in representing the elements they have in common, so to offer an alternative to the typological species concept. To fill this gap is the goal I have here. I will present a species concept that subsumes under itself the various ways of classifying individuals into species *taxa* proposed over the last decades. The label I reserved for my attempt is *the relational species concept*, and I define it this way:

(R) A species is a population of individuals tied together by a particular relation of similarity.

What is peculiar to (R) is the reference to a relation of similarity. However, even if such relation largely shapes the process of sorting out the population of a species, it is not the only element at play in this process. In fact, I hold that there are three elements characterizing the relational species concept. Besides (i) the relation of similarity, every classificatory schema works on the basis of both (ii) a division of biological history into relevant space-time regions and (iii) the specification of a method to group individuals inside and outside the different space-time regions. If one has classificatory purposes, then she has to make clear her mind on each of these points. In the sequel, I will consider them in order, and I will try to show the lines along which each classificatory schema could be cashed out on their basis. Finally, in the last section, I will briefly come back to the comparison between (T) and (R).

## 2. The Relation of Similarity

As it is well known, the relation of similarity can be a non-symmetric, non-transitive, vague and context-relative relation. However, in the case of biological species, one should prefer not to have such a liberal relation. In fact, since the relation of similarity basically cashes out the relation of inclusion into a species, it should reflect our opinions on the latter. Now, I take it that, when we come to inclusion in a species, one does not want to break symmetry: it cannot be the case that a bird *bib* is of the same species that a bird *bid*, and yet *bid* is not of the same species that *bib*. Also, I take it that one does not want and cannot break transitivity. To cope with the many puzzling cases, one can hold that species can have sub-species, so that two organisms within the same species can nonetheless belong to two different sub-species. But it is not the case that a species can branch, so that, to remain with our example, we have a bird *bib* which is of the same species that both *bid* and *bip*, while at the same time *bid* and *bip* do not belong to the same species. Therefore, we want our relation of similarity to be symmetric and transitive and, on this respect, to resemble the relation of inclusion of the typological species concept.

Where the typological and the relational species concept start to diverge is on vagueness and context-relativity. Often, it is vague whether a given organism belongs to one species or another. According to the typological account, there is always a fact of the matter as to whether an organism has or lacks the properties required to be included in a certain species. The vagueness, therefore, has to be attributed to the lack of some data, so that, once our knowledge of the organisms under consideration will be improved, we will be able to settle the question. The context-relativity of our classifications could be explained along the same lines. If an ecologist and a genetist diverge sensibly on the number of species they recognize this is because our knowledge of the issues still has to grow to the point in which we will be able to recognize the ‘hard-core’ species.

My problem with this reasoning is that it hides the assumption that our classifications are deemed to be provisory and it is this assumption that I regard as highly implausible. It is true that what we today consider as individuals belonging to the same species in some decades or centuries we may consider as belonging to different species. Each of our classification is open to revision. However, this does not imply that they are provisory. They are simply different. According to the relational species concept, species are groups of individuals tied together by a relation of similarity. One could take a privileged perspective, and pretend that what is *really* similar to what can be said only once all the pieces will be at place. But this claim starts losing its force once it is recognized that what is considered similar to what is the result of an intellectual abstraction. Sure, the pigeon in front of my window is similar to the one I have see yesterday at the museum *under certain respects*; but they are also very different under other respects that I may consider very important. For example, they are fed differently and live in different environments. And I take these last two facts to be true of them no less than the probability they have to interbreed within each other or no less than the fact that they have morphological traits they have. Therefore, insofar as the typological account is at place, one can have good reasons to believe that our classifications will eventually get rid of vagueness and context-relativity. But, once a judgement of similarity is introduced, reasons seem to suggest that there is no privileged perspective. Our present species *taxa* have to be considered at face value.

Unless we have a sophisticated theory of vagueness that allows us to do so (as, for example, the epistemic theory of vagueness) we have to accept that species are vague. No panic, though. What is vague is the degree of similarity and not the properties itself of the individuals; in other words, the nature of vagueness has not to be ontological, but can be just semantical. As for the context-relativity, it is important to specify what type of context is at issue. In fact, on the one hand, we surely want our classification to be enough solid. We do not want to change our *taxa* every time that a new organism falls under our consideration or to make them brutally dependent on one’s own moral or political trends. Also, unless we have specific reasons to do so, we do not want to consider a revision of our classifications as context-relative, so that both the classification that is settled aside and the one replacing it are considered valid *each from its own point of view*. What we want to allow for is the possibility of holding consistently that two alternative classifications, supported by different and coexistent research interests, are both true. For example, we want to allow that, given three different classifications of the same organisms, one ecologically oriented, another interested in the overall morphological traits and a third one grounded on genetics, we can conceive of the them as all valid at the same time.

Which type of properties is relevant to define the similarity relation? The choice can sensibly vary and, mainly, reduces to three different alternatives. The first gives priority to an overall comparison of the morphological traits of the organisms (e.g. Ehrlich and Raven 1969). The second is based on their genetic material (e.g. Hull 1978 and Ghiselin 1974). A third party, finally, regards as fundamental the probability of interbreeding (e.g. Mayr 1963). It is important to emphasize that the choice of a type of properties on which to tailor the similarity relationship is at place in *every* classificatory schema. Even proposals like the individual concept of species, whose main advocate is David Hull (e.g. Hull 1965, Hull 1978, Ghiselin 1974 and Kitcher 1989), have to assume some respect of similarity. In fact, even assuming Hull's point of view, we still need some criterion to cut the philogenetic tree into branches.

It is not the degree of similarity among its members to individuate a species. In fact, different species may be characterized by the same degree of similarity. What make the relation of similarity of a given species unique are the actual properties of its members. A certain species is a relation of similarity *of certain properties* among a group of individuals. As we shall see, judgments of similarity basically work at two different levels: within a region that we consider relevant; among group of individuals inhabiting different regions. It is hard to say to what extent the two types of levels involve different patterns of reasoning. Certain rules seem to be the same, others don't. What seem to be kept constant is that, within a given context of judgment, individuals are classified so as to preserve symmetry and transitivity. This is because the individuation of species is a holistic process, in which the single individual under classification is always put into the context of the whole range of individuals to be classified. There is no ideal type member of a species, instead there could be several *exempla* chosen among the whole *spectrum* of variation offered by a single context of judgment. (This is another main divergence from the typological approach to species.) The difference between the two levels of application of similarity is the degree of abstraction. Comparing properties of individuals is different from comparing more abstractly sorted out features of groups of individuals. The second task is, in fact, the one that can more easily comport paradoxes, because the criteria employed within two or three regions taken separately may result in a bad choice once we compare the whole individuals (cfr. Kitcher 1989. More on this later). For example, we may be unclear whether a certain type of bird, lived a hundred millions of years ago, belongs to the same species that a type of bird of which there are still living exemplars. If we were to classify all the birds under consideration at once it could have been clearer to come up with a general criterion of similarity. But, since we have to judge starting from independently led classifications, things are deeply and, in a way, irritatingly vague.

## 3. The Relevant Regions

The second element characterizing the relational species concept is the division of biological history into space-time regions. Several alternative criteria can do the job. A first one consists in giving priority to temporal distances (Hull 1978). Before considering the degree of similitude between two organisms, the first lived some millions of years ago and the second one still living, it is preferable – one could hold – to put each of them into the context of their "biological era" and look at the similarities that each of them has with organisms lived in their periods. In fact, it is unlikely that two organisms lived at great temporal distance belong to the same species. Another plausible subdivision is grounded on similarity of environments (Van Valen 1976). Carve out the space-time of biological history into environments, and compare first individuals inhabiting the similar ones. In fact, an environment imposes a certain degree of adaptation to the organisms inhabiting it, so that it is likely that two individuals inhabiting different environments belong to different species. One can also combine these two ways of dividing biological history into relevant parcels and give priority to the types of environments within a certain temporal extension.

The actual individuation of the relevant regions is, however, a more complicated affair. As we know, different organisms can live in different environments. For example, the spatial extension of the environment of a worm is quite smaller than the one of a migratory bird. As for the temporal extension, some organisms live just for few days, so that, within a relatively short time, it is possible to appreciate sensible variations within a species and even some speciation phenomena; on the other hand, some organisms live for centuries, so that speciation events will occur at a much lower rate in time. Clearly, the classificatory activity will take these facts into account, requiring a more and more fine-grained choice of the relevant regions the more information about the organisms under consideration is available. The three way of carving out regions out of the biological history of organisms should therefore be considered as schemas that, from time to time, are integrated with the available knowledge of the environments and the relative times of speciation of the different organisms to be classified.

In general, I take it that a prejudice toward certain space-time regions is always at play in the classificatory activity. A species population can comprehend a large number of individuals. It is unlikely that our similarity judgments will come all at once. One will focus her attention first where it is more likely to find similarities and will try to spell them out just within that region. Only once that this first-level of classification is at place she will be able to consider higher-order similarities.

## 4. Populations

Once that both a division of the space-time and a type of properties on the basis of which to tailor the similarity relation are at place, we need to specify the criteria by means of which species populations are put together. Fundamentally, this is a two-steps process. First of all, the individuals within a same region are grouped together, on the basis of the type of properties regarded as relevant for classificatory purposes. As I said before, this is a holistic process carried on (ideally) preserving symmetry and transitivity, but tolerating vagueness and context-relativity. It is important to stress that this first-level of classification clearly puts into the whole classificatory process some level of organization. What organisms will be considered as belonging to the same species will be biased by what regions are considered relevant and by how individuals have been grouped within such regions.

The second stage consists in matching up the individuals within different regions so to finally obtain the populations of the different species. In order to do it, besides adopting the relation of similarity, some wants also to put constraints on the temporal or spatial distance of the relevant regions. Thus, for example, according to the individual species concept, the population of a species must be temporally continuous. This means that species, once disappeared, cannot reappear. Under this respect, they are like any other individual organism that, once dead, cannot come back to life. A second common constraint, at work in the ecological species concept (e.g. Van Valen 1976), is a spatial one. Individuals inhabiting different environments (usually developing different abilities and different morphological traits) cannot count as the same species. Spatial and temporal continuity might, therefore, be required in order for a population of individuals to count as the population of a *species*.

The matching-constraints of individuals across regions prepare the field for comparing such individuals and devise the species populations. The respects of similarity will be the same one employed within each relevant region. To some extent, though, the way it is applied could vary, as the comparison process is carried out at a higher level of abstraction and is dependent on previous choices.

In this way, the relational species concept ends up subsuming under itself the various alternatives to the typological species concept, at the same time making explicit certain of their tacit assumptions. For example, if you favor the biological species concept (e.g. Mayr 1963), then you will employ the probability of interbreeding as the relevant type of properties to judge similarity; however, you will also have to make clear your mind about which spatio-temporal regions you are going to consider more relevant for your classificatory purposes. If you believe in the ecological species concept, you may have some model on how to determine the relevant regions; however, you will also be required to specify the relevant properties on the basis of which to group individuals within each environment. If you believe in the individual species concept, then you will put a constraint on how to group individuals within different regions, but at the same time you will need to specify both the relevant similarity relationship and the relevant regions. Saying that species are individuals is just one third of the story.

## 5. Typological *vs* Relational Species Concept

The relational species concept proposes itself as an alternative picture to the typological concept. In the same way in which the latter was susceptible of several quite different interpretations, so the former subsumes under itself many other different proposals. This resemblance, however, is not enough to justify the claim that the relational species concept is a general picture of what species are. One could point out that the typological concept has some theoretical import. For example, it is strongly suggesting (if not implying) that to each species *taxon* corresponds a natural kind. Not to talk about how it influences what biologists consider as the goal of their activity and, more broadly, how society in general perceives it. On the other side, what is the theoretical import of the relational species concept? What I hope to have shown so far is that it specifies what is required in order to provide a classification of organisms into species *taxa*. This result has some bearing at several levels of the discussion about the status of species. First of all, it states more clearly the duties of the particular species concepts proposed in the last decades and still used by scientists. To recall an example used before, the analysis revealed that Hull's account of species is not a full account.

More importantly, the relational account is capable of helping us discussing, from a general perspective, puzzles about species. Take, for example, the following paradox concerning speciation, put forward by Philip Kitcher (Kitcher 1989: par. 4). Consider a case of speciation in which there happen to be three groups of organisms, $Gn$, $G1$ and $G2$ such that, $Gn$ exists at time $t_n$, while $G1$ and $G2$ co-exist at time $t_{n + m}$. Also, suppose that, even if both $G1$ and $G2$ resemble $G_n$ to the same close degree $s$, $G1$ differs from $G2$ within a quite greater degree than *s*. Accordingly, one should classify *G1* and *G2* as belonging to two different species. But what to say about the individuals in *Gn* and *G1*? It could seem reasonable to consider them as belonging to the same species. And so for the individual in *Gn* and *G2*. However, if we accept this whole classification, then we break the transitivity of the relation of inclusion in a species. So, do we want to appreciate similarities at the cost of breaking transitivity? First of all, a bolster of the relational account could protest that, by assuming which are the relevant regions, the puzzle is, in a certain sense, assuming its conclusion. In fact, in order to have the three sub-populations described, priority to temporal extent of regions must have been given. If so, then the answer is that, whenever there is a branching in the philogenetic tree, two new species come to exist, as it happens in any case of both sympatric and allopatric speciation. However, the relevant regions could have been individuated in a different way. One could have considered just one big region, occupied by the individuals in *Gn*, *G1* and *G2*. At this point, having the possibility of revising the first level of classification, the judgment of comparison could have taken care of the whole range of variation among individuals and be sensitive to it.

To show that our judgments are and *should be* context-sensitive, consider also this variant. Suppose that after few generations, individuals in *G2* were exterminated by a catastrophe. Then, it seems plausible to say, individuals in *Gn*, *G1* and *G2* would have belong to the same species, with the proviso that the ones in *G2* compose a sub-species. For a bolster of the relational species account, this consideration is non-problematic. We know that our similarity judgments, since they are holistic, are context-relative. On the other hand, a bolster of the typological species account will find puzzling the fact that a certain group of individuals could be classified under different species without any change in their intrinsic properties. One of the two classifications - she will conclude - must get something wrong. I take this difference to be an advantage of the relational account over the typological account. The relational account can make better sense of our actual classificatory criteria.

Finally, I would like to briefly consider the import of the relational species concept on the issue of natural kinds. If the typological concept suggested the existence of natural kinds, the relational one seems to move in the opposite direction. In fact, provided that the properties on which we base the similarity judgments are 'real', the relational species concept considers all the different ways of classifying organisms as equally 'real'. And it does not seem to be the case that each of such classificatory schemas picks out natural kinds. This is because one of the relevant type of properties available for classificatory purposes is the probability of interbreeding, that is a relation among individuals. Now, the status of natural kinds is not less controversial than the one of species; but it is quite uncontroversial that natural kinds are not relations of the sort of the probability of interbreeding. Therefore, I conclude, the relational species concept suggests that species are not natural kinds; they are just different, compatible and definitive ways of classifying individuals.[1]

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