

An argument for species as sets of organisms

According to the species-as-individuals view (SI), a particular species is a connected individual, having organisms as its parts. By saying that it is a *connected* sum of organisms, the defenders of the view emphasize that the individual is not simply a mereological sum, but a sum with certain relations between its parts, like spatiotemporal proximity, gene flow between con-specifics (the capacity for interbreeding), and a certain evolutionary continuity, or etiology. According to the species-as-sets view (SS), a particular species is a set of organisms. Ghiselin and Hull talk about SS as the view that species are “spatiotemporally unrestricted classes”, but as Kitcher repeatedly pointed out, SS does not in any way presuppose some old-fashioned, pre-Darwinian, essentialist view of species, according to which their members must share a common morphological property. SS is compatible with whatever species concept we take as the right one, because each such concept can generate a set of organisms.

The argument I want to put forward against SI is based on the idea, due to Saul Kripke, that an individual has its origins necessarily. Of course, the thesis, known as the necessity of origin, is far from being uncontroversial, and that is why I will also later offer a reformulation of my argument based on a much weaker and, I believe, uncontroversial premise: “the tenacity of origin”, proposed by Penelope Mackie. But let us focus now on the first version of the argument.

The thesis of the necessity of origin as applied to biological organisms would say that no actual organism could have been born from parents other than the actual ones. That is, in any possible world where the organism exists, it is born from parents that are transworld identical to the actual parents of that organism. It is important not to confuse this thesis with the somewhat similar looking one that no actual organism could have been born from parents that belong to other species than what the actual parents belong to. This latter thesis would be implied by the former only on the condition that an Aristotelian thesis is true, according to which an organism belongs to a species essentially. Wiggins’s thesis has received a simple and elegant refutation, based on evolutionary theory, from John LaPorte. Consider an actual species at time t that resulted from an ancestral species by allopatric speciation (geographical separation of a subpopulation). It is intuitively clear that the speciation event is contingent – it could have failed to take place. If there is a world in which the speciation event does not occur and the ancestor species continues to exist at time t , then there is an actual member of the new species at time t to who could have been a member of a different species.

If SI is true, then if we accept the necessity of origin for individuals, all actual species necessarily originate from what they actually originate from. Consider the first couple of mates that are, according to Mayr’s species concept, members of a different species S^* after the speciation event occurring in the original species S . If the necessity of origin thesis is true, then in all possible worlds S^* , taken as an individual, will have its origin in S . So far so good, but consider all possible worlds in which all and only the actual species are present. Since the origins of species are speciation events, the above conclusion will apply to all species in the worlds that we focus on; all species must come from the species they actually come from. But we assumed that all and only the actual species are present in the worlds we focus on, which entails a stronger

conclusion, namely, that for all species it is true that they come from species that are the same as the species they actually come from. This means that in all those worlds the actual evolutionary tree of life is duplicated with respect to the temporal order in which species evolve. The result is that the actual configuration of the evolutionary tree of life with respect to temporal order comes out as necessary in all worlds containing all and only the actual species. But it is intuitively clear that it is not necessary. There is no difficulty in imagining that, for instance, land animal species come first, then the amphibians.

Let's discuss the two points above: (i) that, indeed, it follows from the necessity of origin and SI that the actual temporal order of species on the phylogenetic tree is necessary in all worlds containing all and only the actual species, and (ii) that it is, indeed, possible for species to evolve in a different order.

In order to make (i) more apparent consider a simple model, depicted in Figure 1.

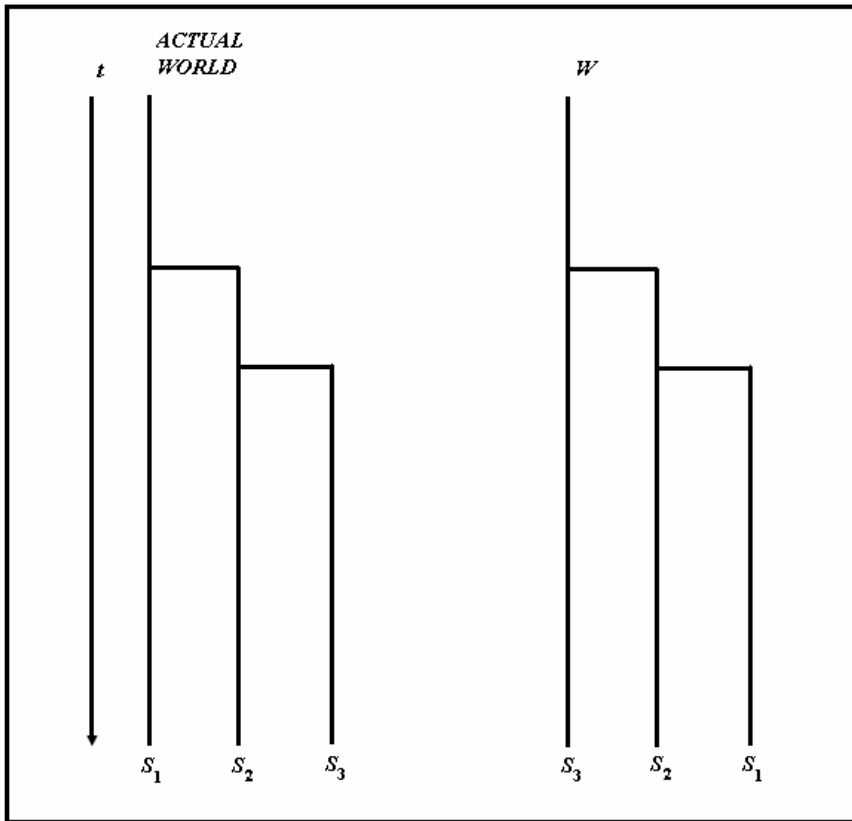


Figure 1.

Suppose there are three actual species – S_1 , S_2 , and S_3 – such that S_2 originates from S_1 , and S_3 originates from S_2 (none of them goes extinct). Suppose it is possible to reshuffle the temporal order of these species, as in world W in the figure. If species are individuals, then each of the species in W is transworld identical with the corresponding species in actuality. We observe in the figure that the individual organisms that are parts of S_2 in the actual world are transworld identical with the individuals that are parts of S_2 in W . In other words, they are both the same individuals as in the actual S_2 and are parts of S_2 , so belong to the same species as they actually belong to. We know, by the

necessity of origin, that the temporally first individual of S_2 has to have the same parents as it actually has. If that is the case, then those parents are members of S_3 in W and members of S_1 in actuality; they change their species membership from the actual world to W . By the repeated application of the necessity of origin thesis, we obtain the result that, in W , the parents of those parents, and the parents of the parents of those parents, and so on, have to be members of S_3 . This means that the first member of S_3 will be transworld identical with an individual that is a member of S_1 in actuality. But by the necessity of origin thesis, the first member of S_3 in W has to have the same parents as it actually has. In actuality the first member of S_3 has parents that are members of S_2 . Further, members of the actual S_2 , as we noted before, are transworld identical with members of S_2 in W . Therefore, the first member of S_3 in W has to have parents that are both the same as the actual ones and of the same species, that is, of S_2 . But that is inconsistent with the facts in W : all members of S_2 are *descendants* of members of S_3 ! So we have proven that a situation like the one depicted in Figure 1 is impossible, in other words, that the actual configuration of the phylogenetic tree with respect to temporal order is necessary in all worlds where all and only the actual species are present.

Let's move on to point (ii). If we show that the situation according to W in Figure 1 is consistent with the main species concepts that have been proposed, we will have shown that the situation is evolutionarily possible and, *a fortiori* that it is metaphysically possible.

I will consider four main categories of species concepts: phenetic, gene flow based, ecological, and phylogenetic.