



Cats are not necessarily animals

Margarida Hermida¹ 

Received: 4 November 2021 / Accepted: 17 June 2022 / Published online: 11 August 2022
© The Author(s) 2022

Abstract

Some plausibly necessary a posteriori theoretical claims include ‘water is H₂O’, ‘gold is the element with atomic number 79’, and ‘cats are animals’. In this paper I challenge the necessity of the third claim. I argue that there are possible worlds in which cats exist, but are not animals. Under any of the species concepts currently accepted in biology, organisms do not belong essentially to their species. This is equally true of their ancestors. In phylogenetic systematics, monophyletic clades such as the animal kingdom are composed of an ancestral stem species and all of its descendants. If the stem species had not existed, neither would the clade. Thus it could have been the case that all the organisms which actually belong to the animal kingdom might have existed yet not have been animals.

Keywords Essential membership · Natural kinds · Phylogenetic systematics

1 Introduction

Some plausibly necessary a posteriori claims include ‘water is H₂O’, ‘gold is the element with atomic number 79’, and ‘cats are animals’. In this paper, I challenge the necessity of a posteriori theoretical claims concerning biological taxa, in particular those concerning taxa higher than species. For example, although it is certainly true that, in the actual world, cats are animals, I argue that there are possible worlds in which cats exist, but are not animals; hence, ‘cats are animals’ is a contingent a posteriori claim.¹

¹In this paper, I adopt the convention that a proposition is metaphysically necessary if it is true in all possible worlds. By using the apparatus of ‘possible worlds’ I do not thereby intend to commit to the

✉ Margarida Hermida
margarida.hermida@bristol.ac.uk

¹ Department of Philosophy, University of Bristol, Cotham House, BS6 6JL Bristol, UK

Some of the problems facing the application of the Kripke-Putnam thesis of necessary a posteriori theoretical claims to biological cases have been recognised for some time. In particular, it is now widely accepted, as philosophers of biology have long defended, that biological taxa are not defined by intrinsic essences (Okasha, 2002; Leslie, 2013; Dennett, 2017). Biological taxa are not groups of organisms classified together according to similarity, but real units in nature which reflect relations of ancestry and descent. Species and higher taxa can be better thought of as historical individuals (Ghiselin, 1974; Hull 1976; Wiley & Lieberman, 2011) or, if they are natural kinds at all, then they are defined by extrinsic, relational essences (Okasha, 2002). There is no particular intrinsic property that all and only members of a biological taxon must have; instead, what matters is their position on the phylogenetic tree, i.e., how they are related to other organisms, and where they are located with regards to certain speciation events.

There is, however, a different problem which is not nearly as widely recognised: the question of essential membership, i.e. ‘do individual organisms belong essentially to the taxa they actually belong to?’. It is generally thought that organisms belong essentially to their taxa. Nevertheless, Hull (1978), LaPorte (1997), and Okasha (2002) have presented convincing arguments that organisms do not belong essentially to their species. The very same organisms might have existed while belonging to a different species, if the course of evolutionary history and, in particular, the occurrence of certain speciation events, had been different. In this paper, I argue that from the contingency of species membership, it follows that organisms also do not belong essentially to their higher taxa. Thus, statements such as ‘cats are animals’ or ‘tigers are mammals’, although being true a posteriori theoretical statements in the actual world, are not necessary.

The question of essential membership in higher taxa has previously been addressed by LaPorte. In his earlier work, LaPorte argued for the contingency of higher taxa membership (1997). Unfortunately, his arguments reflect an inadequate understanding of the principles of phylogenetics, and therefore cannot be used to support that thesis. In later work (2004), LaPorte has continued to defend the contingency of species membership but argues for the necessity of higher taxa membership. Here I argue that this position is inconsistent, because the former entails the latter, and I present a novel argument for the contingency of higher taxa membership.

The outline of the paper is as follows: in Sect. 2, I introduce Kripke’s and Putnam’s thesis of necessary a posteriori theoretical claims. In Sect. 3, I highlight two essentialist assumptions that are problematic for claims concerning biological taxa, and identify the second one, essential membership, as the one that is relevant for assessing the necessity of claims such as ‘cats are animals’. In Sect. 4, I explain in some detail how phylogenetic systematics works, and why it is the preferred classification in biology. In Sect. 5, I expound several arguments by Hull, LaPorte, and Okasha, to the effect that individual organisms do not belong essentially to their species. In Sect. 6 I present a critical assessment of LaPorte’s arguments concerning whether or not organisms belong essentially to the higher taxa they belong to, and in

existence of possible worlds. Rather, I take the statement ‘A is an animal in all possible worlds’ to be shorthand for ‘A could not simultaneously have existed, and not have been an animal’.

Sect. 7 I develop my own argument for the contingency of higher taxa membership as a consequence of the contingency of species membership. In Sect. 8 I examine three possible objections to this view, before concluding in Sect. 9.

2 Kripke and Putnam on necessary a posteriori theoretical statements

Beginning in the 1960s, Putnam and Kripke developed a cluster of views concerning natural kinds, natural kind terms, meaning, and necessity, which is broadly known as the Kripke-Putnam thesis, although Hacking (2007) rightly points out that the views of these two authors differ in a number of ways. In brief, science identifies natural kinds, and provides us with a posteriori necessary truths, i.e., claims which have to be discovered empirically, yet are true in all possible worlds.²

Putnam starts by proposing to analyse statements that ‘look necessary, but that are not analytic’, even though people often take them to be. He calls these sorts of statements ‘synthetic necessary truths’ (1962: 659). When discussing Donnellan’s (1962) example ‘all cats are animals’, Putnam claims that although the statements ‘all cats are animals’ and ‘all bachelors are unmarried’ are both necessary, the first is ‘less necessary’ than the second (Putnam, 1962: 660). While in the case of the meaning of ‘bachelor’ we need only consult a dictionary, in the case of cats we are required to look carefully at what the world is like, because we might be mistaken; they might be, for example, cleverly disguised Martian remote-controlled robots, Putnam argues.

But this, as Kripke observes, is just the distinction between a priori and a posteriori. Since we haven’t in fact discovered that cats are robots, or demons, or anything else – on the contrary, we have confirmed that they are animals – the truth ‘cats are animals’ is, according to Kripke, necessary (Kripke, 1980: 125). It is on a par with, and as necessary as, other scientific truths such as the theoretical identity statements ‘water is H₂O’ and ‘gold is the element with atomic number 79’. It might of course be possible that we are mistaken in any particular discovery, but if we are correct, then those statements are not contingent, but necessary.

Thus, if we came to discover that gold was not in fact yellow, but merely appeared so due to a pervasive optical illusion (Kripke, 1980: 118), we should have no inclination to say that we had discovered that this substance was not gold after all; but if we found a substance that resembled gold in all its macroscopic properties, but did not have atomic number 79, we should say it was not gold, but some other substance (as it happens, there is a mineral – pyrite – which has many of the same properties of gold, but is not gold). According to Kripke, natural kind terms such as ‘gold’ function

²Kripke and Putnam speak of ‘essence’ and ‘necessity’ almost interchangeably. In the wake of Fine (1994), it has become popular in metaphysics to explain necessity in terms of essence, where ‘essences’ are understood in a more substantive way than merely ‘essential properties’ (i.e. properties which a particular thing has necessarily, if it exists at all). This metaphysical trend coexists with the much celebrated elimination of the notion of ‘essence’ in philosophy of biology. In this paper I aim to steer clear of these particular debates. I will therefore confine my discussion to modal claims and ignore the question of whether modality is primitive or can admit of further reduction. I will, however, continue to refer to ‘essential membership’ in biological taxa when other authors do so.

as rigid designators, in the same way as proper names. Once it has been established empirically that gold is a chemical element which has 79 protons in its nucleus, the term ‘gold’ thereafter rigidly refers to any samples of the chemical element with atomic number 79, and does so in all possible worlds.

Something similar is true of biological species; the name ‘tiger’ (or, more scientifically, *Panthera tigris*) does not designate a description or a cluster of properties; it rigidly designates a species. Although tigers have many properties (e.g. black and yellow stripes, four legs, large canine teeth, etc.), any of these properties are such that any particular tiger might lack them. For instance, there might be three-legged tigers, and there are rare tigers born without stripes; not to mention tigers that die during development, before they acquire the relevant features (Hughes, 2004: 48, n. 71). And in fact, even if a particular morphological or genetic property was actually possessed by all, and only, the members of a species, it would still not be necessary – the property could at any moment be lost through random mutation, for example (Okasha, 2002). It could even be lost in all members of the species, if the new mutation became fixed. In that case, we would simply have to update our descriptions of tigers. In contrast, there is something ‘qualitatively different’, Putnam claims, about the feature ‘animal’; it would be much harder to revise the statement ‘all tigers are animals’ (Putnam, 1975: 188–189).

It is not impossible to imagine a situation where we might find out that what we thought were tigers were robots after all (Putnam, 1975), or that what we took for cats were actually demons (Kripke, 1980), but this would not be a situation in which tigers were robots, or cats were demons. It would be a situation in which there were no such things as cats or tigers. Just like pyrite looks like gold but is not gold, and is known as ‘fool’s gold’, if Kripke’s ‘demon cats’ existed, they would be ‘fool’s cats’, not actual cats. Kripke concludes: ‘given that cats are in fact animals, any cat-like being which is not an animal, in the actual world or in a counterfactual one, is not a cat’ (1980: 126). Although this seems plausible enough, I will argue that, counterintuitively, cats could in fact have existed and not have been animals; however, they could not have failed to be organisms.

It is essential, though, that we start by taking a closer look at the claims in question, since “cats are necessarily animals” can be read in three different ways:

- (1) $\Box \forall x (Cx \rightarrow Ax)$ [In every possible world, all cats are animals.]
- (2) $\forall x \Box (Cx \rightarrow Ax)$ [Every actual object is such that, in every possible world in which it exists, it is either an animal or it is not a cat.]
- (3) $\forall x (Cx \rightarrow \Box Ax)$ [Every actual object is such that either it is not a cat, or else it’s an animal in every possible world in which it exists.]

Claim (1) is *de dicto*. It excludes the possibility, in any possible world, of there being a cat which is not an animal, but leaves open the possibility that an actual cat exists in a possible world where it is neither a cat nor an animal. Claim (2) is *de re*, but it too leaves open the possibility that an actual cat exists in a possible world where it is neither a cat nor an animal. Claim (3) is a different *de re* claim, which excludes the possibility of an actual cat being a non-animal in any possible world, but leaves open the possibility of the existence of non-animal cats in other possible worlds.

Although it is not entirely clear which of these claims Kripke means to assert, LaPorte (1997: 99) and Okasha (2002: 205) have formulated their views concerning the necessity or contingency of an organism's membership of a particular taxon in terms of the essential properties of particular organisms. The thesis of essential membership is best understood as (3). For this reason, in this paper I focus mainly on claim (3), which is also, arguably, the most interesting one. I argue that it is true of a particular actual cat that it can exist in a possible world where it is not an animal.

My argument, however, works equally well against all three claims. In order to refute (1), I need to show that in at least one possible world, there is a cat which is not an animal. In order to refute (3), I need to show that a particular actual cat exists in a possible world where it is not an animal. Adding the further assumption that this particular cat is also a cat in this possible world, this will also suffice to refute claim (2). Therefore, if I can show that there is a possible world in which a particular actual cat exists and is a cat, but is not an animal, I will have succeeded in refuting all three possible readings of "cats are necessarily animals".³

3 Biological taxa and essentialist assumptions

The Kripke-Putnam thesis seems plausible in the cases of gold and water, although the case of water has been the target of criticism, mainly on the grounds that the structure of water is far more complex, varied, and unstable, than can be captured by the formula 'H₂O' (Needham 2002; Leslie 2013; Häggqvist & Wikforss, 2018). Nevertheless, other authors defend the claim, even while acknowledging this complexity, by highlighting the role of water's microstructure in explaining its macroscopic properties (Hendry, 2006; Hofer & Martí, 2019). Although a detailed assessment of this discussion is outside the scope of this paper, it seems plausible to maintain that 'water is H₂O' is a somewhat simplified version of the true theoretical identity. The statement 'cats are animals', however, differs from these sorts of statements regarding chemical substances and compounds in several ways.

To begin with, 'cats are animals' is clearly a more general statement than 'water is H₂O' or 'gold is the element with atomic number 79'. It is not, strictly speaking, an identity statement. The 'is' of 'cats are animals' expresses the 'is' of predication, not identity. In this way, 'cats are animals' is more akin to a statement such as 'gold is a metal'. While it is true that all cats are animals and all samples of gold are samples of metal, most animals are not cats, just like there are many metals besides gold. Nonetheless, 'gold is a metal' or, say, 'uranium is a radioactive substance' are, plausibly, just as much necessary a posteriori theoretical statements under Kripke's view, even if they are not identity statements. So this difference should not overly concern us.

³ I am grateful to an anonymous reviewer for encouraging me to increase the modal precision of the claims under dispute.

3.1 'Internal structure'

Putnam and Kripke assumed – as most people outside of philosophy of biology would have – that there must be some ‘hidden structure’ that makes an organism the kind of thing it is. Putnam suggests that it is the genetic code of a lemon that determines whether or not something is a lemon (1975: 158). Kripke’s view is more interesting, in that he talks not only about how we would not consider something a tiger if it had a very different ‘internal structure’, but also asks us to imagine those non-tigers as being ‘peculiar-looking reptiles’ (1980: 120). In this case biologists might concur, as something which was actually a reptile (i.e., more closely related to reptiles than to mammals) would certainly not be a tiger, no matter how much it might superficially resemble one. In both cases, though, biologists could still use both the genetic code and whatever ‘internal structure’ Kripke meant to refer to, but only as *evidence* of the real criterion of species membership, which is a relational property such as ‘being part of a particular chunk of the genealogical nexus’ (Okasha, 2002: 202).

While there is no universal agreement on whether species and higher taxa have any essential properties, there is widespread agreement that if they do, then they are certainly not intrinsic properties, but *relational ones*. This does clash with the Kripke-Putnam thesis insofar as the intrinsic ‘hidden’ microstructure of natural kinds is supposed to not only provide the true reference of the term, but also *causally explain* why the thing in question has the properties that it does. In biological taxa, however, these two roles come apart: what makes it the case that an organism belongs to a certain species and to certain higher taxa are not the same features that cause it to have the macroscopic properties it has – for the latter, we should look to its genetic composition, developmental history, and interactions with its environment (Okasha, 2002: 203–4).

The fact that theoretical statements concerning chemical substances are supposed to identify the microstructure of something, and those concerning biological taxa do not, is often seen as problematic. Häggqvist & Wikforss (2018: 918), for instance, worry that even if there is a microstructural criterion for chemical substances, it works *only* for chemical substances, and ‘will not generally work for other items on Putnam’s and Kripke’s list of natural kinds’. This is a curious point. On the face of it, it is somewhat puzzling that so many philosophers want to adopt (or reject) a microstructural view of *natural kinds* in general, when different natural kinds seem to have very little in common, other than playing certain roles in scientific theories and being the target of philosophical theorizing about natural kinds. On the contrary, it should be obvious that natural kinds in different scientific domains cannot all be based on the same kind of essential property, be it microstructure or something else. For example, while microstructure might be adequate for chemical elements and compounds, it does not seem to apply to elementary particles such as electrons which, according to our best current physical science, have no internal structure whatsoever.

In the case of biological taxa, it is even clearer that they cannot be based on microstructure. We could, if we so wished, provide the cat’s chemical composition, but that would not be very informative. We could also provide the genetic code of a cat, but that would vary from individual to individual (except for twins); much as people are inclined to think otherwise, there is simply “no such thing as the ‘species’ genotype”

(Leslie, 2013: 124). Furthermore, a cat's genotype would not amount to its microstructure, but only one aspect of it.⁴ For the complete microstructure, we'd have to provide a detailed map of all the cat's cells, plus their subcellular components, how the cells are connected to each other, etc. In any case, this would be valid for a single cat only, and for a single moment in time, since much of this structure is continuously changing throughout the life of an organism.

The failure of microessentialism concerning biological taxa has been generally accepted.⁵ But the less known question of essential membership is the one which is particularly relevant to assess the necessity of claims such as 'cats are animals'.

3.2 Essential membership

The second essentialist assumption generally made concerning organisms is that they belong essentially to the species and higher taxa they belong to.⁶ LaPorte (1997) characterized the thesis of *essential membership* as follows:

If, in any possible world, an organism belongs (or does not belong) to a particular biological taxon, then there is no possible world in which the organism ever fails to belong (or not to belong) to that taxon (LaPorte, 1997: 99).

LaPorte initially formulates this thesis in terms of *natural kinds* (1997: 98), but suggests this alternative phrasing in terms of *biological taxa* to incorporate the possibility that biological taxa are not natural kinds. The view that species and higher taxa are not kinds, but historical individuals, has been defended by a number of philosophers of biology, as well as biologists, on the grounds that they are not classes of things characterized by intrinsic properties, but spatio-temporally restricted historical entities, with a beginning, a certain spatio-temporal trajectory, and an end (Ghiselin, 1974; Hull 1976; Wiley & Lieberman, 2011). Since there does not seem to be a consensus on this point, I prefer to consider the phrasing above as the relevant thesis under consideration, because it is compatible with either view on the species individuality debate.

The thesis that particular organisms are such that they could not have belonged to a different species and higher taxa is an entirely separate claim from the fact that organisms belong to the species and higher taxa they in fact belong to in virtue of relational, and not intrinsic, properties. As Okasha (2002: 205) points out, the latter does not immediately refute the former; in fact, some *de re* essentialist claims, such

⁴This becomes evident when we consider the fact that the cat's genotype is also the genotype of its cells; yet the whole cat has a comparatively much more complex structure than one of its cells.

⁵With few exceptions, notably Devitt (2010).

⁶This question must be sharply distinguished from the related question of whether *type specimens* belong essentially to their species. Levine (2001) argues that *type specimens* raise a paradox because they seem to belong to their species necessarily *qua* type specimens, but contingently *qua* organisms. For discussion, see LaPorte (2003), Haber (2012), and especially Bokulich (2020). In this paper, I am concerned with the thesis of essential membership in species and higher taxa of organisms in general, and do not address the question of type specimens specifically.

as the necessity of origin, i.e. the claim that an individual organism has its biological antecedents essentially, are also relational.

In fact, LaPorte argues, even if biological species had internal essences, it would still not follow that individual members of those species would belong to them essentially (1997: 97), unless it was impossible for a particular organism to exist in a possible world and yet lack that property. But here the possibility that something might exist while lacking the internal (generally presumed to be microstructural) properties that make it the kind of thing it is runs against deep-seated intuitions. However, since species are *not* defined by intrinsic properties of any kind, whether or not it is possible for a particular organism to have existed while having different intrinsic properties is entirely beside the point (Okasha, 2002: 207). What matters is whether it could have lacked the extrinsic properties which actually make it part of a particular biological taxon. And it could indeed have lacked those.

In what follows, I argue that true a posteriori theoretical statements concerning biological taxa, such as ‘cats are animals’, are in fact not necessary. Before moving on to main argument, however, it is necessary to take a small detour through the details of phylogenetic systematics.

4 Phylogenetic systematics

Although historically there have been multiple classification systems in biology, ever since Darwin, – to be fair, even before, though not explicitly – the main classification system in biology is genealogical. Today, this means phylogenetic systematics, also known as cladistics. In the twentieth century, three distinct classification systems were proposed – cladistics, phenetics, and evolutionary taxonomy.

Evolutionary taxonomy aimed to be mainly a genealogical classification, but which also incorporated evolutionary change or divergence. According to this classification system, higher taxa should only include descendant species of a certain ancestral species, but they need not include *all* of those descendants; i.e., *paraphyly* was accepted. For instance, birds and mammals were given a rank comparable to that of reptiles because they were considered to have diverged quite considerably from them. So although classification had an evolutionary basis, there was plenty of subjectivity involved in deciding which groups were sufficiently different from which other groups (Richards, 2016: 107–12). In evolutionary taxonomy, the ranking of higher taxa was supposed to reflect the degree of divergence, diversification, and also evolutionary age of the different groups; however, when these conflicted, rankings would be a matter of judgement on the part of the taxonomist. Questions such as how many species should be included in a genus, for instance, were also to some degree a matter of preference, and genera containing very many species could be split for convenience.

Phenetics (or ‘numerical systematics’) rejected the evolutionary basis of taxonomy, mainly on the grounds that evolutionary relationships were poorly known, and attempted to eliminate subjectivity by classifying organisms purely by degree of similarity. Characters were identified and measured, and then statistical methods would be applied to yield a phenetic classification, ranked by degree of similarity. Unfortu-

nately, this approach turned out to introduce high levels of subjectivity back into the classification: first, in deciding what counts as a character; then, in deciding how to code the characters; then, in choosing a coefficient of similarity, with each one generating a different classification, and so on. But another important problem was that, in rejecting phylogeny, this classification was simply irrelevant to most of biology.

In contrast, phylogenetic systematics, which is used today, is a purely genealogical classification. It aims to be as objective as possible, by eschewing all judgements of similarity. It simply aims to represent the actual phylogenetic history of organisms. The groups that compose it do not depend on scientists' subjective opinions of which organisms look more similar, or what constitutes an important evolutionary innovation. Instead, phylogenetics works exactly like a family 'tree' that represents, as accurately as possible given what is known, someone's ancestors and the genealogical relationships between them. So, for instance, while in evolutionary taxonomy, sarcopterygians (fleshy-finned fishes that gave rise to the tetrapods) were classified together with actinopterygians (ray-finned fishes), because of their fish-like features; in modern phylogenetic classification, they are classified together with all of the terrestrial vertebrates, to which they are more closely related. If this sounds surprising, we should bear in mind that the purpose of phylogenetic classification is not to group together organisms which are more similar, but to capture their genealogical history.

In phylogenetic systematics, only monophyletic clades are accepted. A monophyletic clade (Fig. 1) is a group that includes a stem species plus all, and only, its descendants (Hennig, 1966; Wiley & Lieberman, 2011). The stem species thus defines the clade, which is composed of that particular species and all its descendants.⁷ New clades are generated (a process known as cladogenesis) whenever there is a speciation event, i.e. whenever a species divides into distinct species. When this happens, the original species which existed prior to the speciation event becomes the stem species of the new clade; it is the ancestor species of all the species within that clade. Later, when some of its descendant species themselves speciate, more clades are formed. Importantly, though, all of those clades are still sub-clades of the original clade. If a species belongs to a certain clade, neither it nor any of its descendants can ever 'move out' of it (Okasha, 2003). This is so regardless of whatever traits they might lose, or acquire.

5 On the contingency of species membership

It is natural to think that organisms belong essentially to the species they actually belong to. Again, this question should not be confused with the question of whether or not species themselves have essences. Species might have essences – possibly relational ones, as suggested by Okasha (2002) – or they might not. Either way, the question is the following: given a particular organism, does it belong essentially to the species it actually belongs to? In other words, could numerically the same organ-

⁷Throughout the paper, I assume stem-based definitions, which I take to better reflect the concept of monophyly as defined by Hennig (1966: 73), but see Sect. 8 for discussion of alternative ways to define the names of clades.

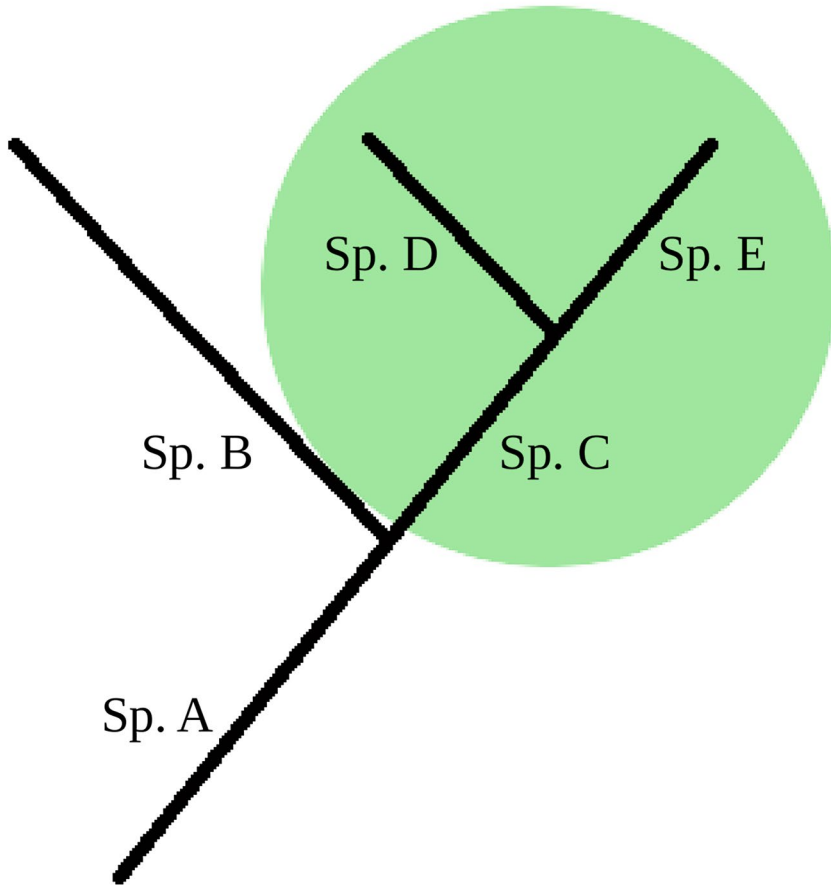


Fig. 1 Example of a phylogenetic tree. The clade composed of species C, D and E is monophyletic, since it includes species C (the stem species of this clade) and all of its descendants.

ism have existed without belonging to this particular species? It is intuitive to think that organisms belong essentially to their species, but there are several arguments against it.

For instance, Hull (1978), applying the biological species concept (based on capacity to interbreed), argues that an organism with a different origin – even, hypothetically, an artificial origin – that somehow turned out to be reproductively compatible with an existing species might, if it proceeded to mate with members of that species, *become* part of that species. This means that an organism might change species, even ‘while remaining numerically the same individual’ (Hull, 1978: 350). However, this falls short of claiming that the organism could have existed in the first place without belonging to the species it originally belonged to.

The existence of ring-species, such as the *Ensatina* salamander species complex, also speaks against the necessity of species membership. In these cases, organisms belonging to a population A can interbreed with organisms from population B, B

with C, and C with D, but populations A and D can no longer interbreed. In these examples of incomplete speciation, or speciation-in-progress, it might be indeterminate to which species a particular individual in an in-between population belongs to, since the species are not entirely separate yet.

The contingency of species membership applies not only to the biological species concept, but also to evolutionary and phylogenetic species concepts. As LaPorte (1997) argues, an organism which belongs to a given species in the actual world might exist in a possible world in which that species had undergone speciation at an earlier time, and that individual organism might have found itself on either side of the divide. Although this analysis assumes that species go out of existence when they split, which might be debatable, LaPorte suggests that the contingency of species membership might apply to any historically-defined species concept (1997: 106).

In fact, the contingency of species membership is true of phylogenetic and evolutionary species concepts, whether or not they follow Hennig's rule that a species goes out of existence upon speciation. The reason is that evolutionary and phylogenetic species concepts, which apply to species over time, are dependent on non-historical species concepts (e.g. the biological species concept) for the delimitation of speciation events (Okasha, 2002). The delimitation of speciation events is crucial for phylogenetics because it is the formation of new species that generates new clades. Since under all accepted non-historical species concepts, the properties that determine whether or not an organism belongs to a given species are not intrinsic to the organisms themselves, it is possible that, if a speciation event had occurred sometime earlier, an organism might find itself on one or the other of the reproductively isolated branches; thus organisms do not essentially belong to their biological species (Okasha, 2002: 206).

There are good reasons, then, to accept that organisms do not belong essentially to their species. However, it might not immediately seem to follow that they do not belong essentially to their higher taxa – after all, the process of speciation takes place at the species level, not at the level of higher taxa. However, as we have seen in Sect. 4, the process of cladogenesis is intimately associated with the process of speciation – which has consequences for the necessity of higher taxa membership, as we will see in Sects. 6 and 7.

6 LaPorte on higher taxa membership

As seen above, LaPorte has put forward some convincing arguments for the contingency of species membership. However, regarding the membership of organisms in higher taxa, he has defended two opposing positions: contingency (1997) and necessity (2004). These two views are assessed in Sect. 6.1 and 6.2, respectively. Unfortunately, both of his arguments are flawed.

6.1 LaPorte's argument for the contingency of higher taxa membership

In his 1997 paper, LaPorte argues not only against the notion that organisms belong essentially to their species, but also against their essential membership in higher taxa

(i.e. all taxa above the species level). For example, are individual mammals such that they are mammals in all possible worlds? (1997: 106). LaPorte replies in the negative. However, although his conclusion is correct, his particular argument in this paper is flawed. In the following discussion, for reasons already mentioned in Sect. 4, I focus exclusively on phylogenetic systematics.

LaPorte's example featuring the clade *Aves* (birds) is as follows (1997: 109–10). Suppose that a certain species of *Archaeopteryx*, let's call it *Archaeopteryx* sp. A, is the stem species of clade *Aves* in the actual world. It could have happened that *Archaeopteryx* sp. A could have budded forth 'a non-bird taxon' at a time before the branching of the actual first bird branch. Suppose, furthermore, that this branch led to a taxon 'having the same number of organisms, variation, and rank as the *Aves*', but composed of salamander-like creatures. In that case, those organisms that exist prior to the non-bird offshoot (which I am assuming are still members of the species *Archaeopteryx* sp. A, since the speciation event happens later) would fail to count as birds. So, LaPorte concludes, 'it is a contingent matter that any individual member of the relevant *Archaeopteryx* species is a bird'.

Although it is indeed a contingent fact whether or not any individual member of the relevant *Archaeopteryx* species is a bird (I assume that by 'bird' we mean a member of the clade '*Aves*'), the analysis is incorrect. Two things are misleading in the description: first, whether the additional branch is a 'non-bird taxon' remains to be seen, and must not be assumed; and second, we cannot suppose the additional branch to have 'the same rank as the *Aves*', since a sub-clade of a larger clade cannot, ipso facto, have the same rank as the higher clade it belongs to.

Let us continue to assume that *Archaeopteryx* sp. A designates the stem species of *Aves* in the actual world. Remember that in phylogenetics a clade is defined as a stem species plus all of its descendants. So, *Aves*=*Archaeopteryx* sp. A+all of its descendants. In the possible world suggested in LaPorte's example, the descendants of *Archaeopteryx* sp. A include not only all the species that comprise *Aves* in the actual world, but also an additional clade composed of salamander-like species (Fig. 2). Be that as it may, *Archaeopteryx* sp. A is still the stem-species of the clade, so the clade is numerically the same clade, although it includes many more species. It does not matter whether those additional species are bird-like or salamander-like. Since they are all descendants of the stem species of the clade, in this possible world we are considering, they all belong to the clade *Aves*.

Phylogenetic systematics might seem counterintuitive for this reason: it does not attempt to group organisms that are most similar; the point is simply to capture genealogy. So, for example, the clade *Aves* is included in the clade *Dinosauria*, because the clade *Dinosauria*, like all other monophyletic clades, is defined as the stem species plus all of its descendants – and some of those descendants include the birds. Birds are a sub-clade of the dinosaurs. For this reason, biologists often refer to 'non-avian dinosaurs' when they mean to refer to dinosaurs excluding birds.

Another example discussed by LaPorte is the case of fish. LaPorte argues that 'individual salmon, lungfishes, coelacanths, etc. fail to belong to a common, exclusive taxon', because the taxon '*Pisces*' is nonexistent (1997: 110). He is quite correct that there is no exclusive taxon '*Pisces*' to which only fishes, and no other organisms, belong. But he argues that this is an accident, due to the coming into existence of

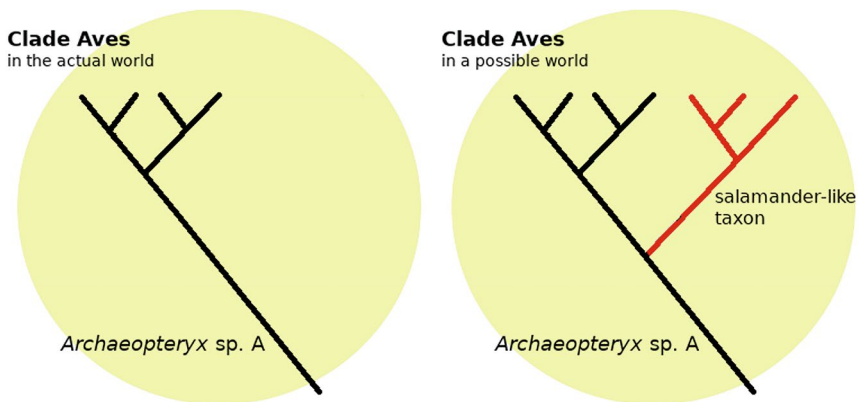


Fig. 2 Simplified phylogenetic tree representing the clade Aves in the actual world and in the possible world described by LaPorte (1997). *Archaeopteryx* sp. A is here assumed to be the stem species of the clade Aves for illustrative purposes.

non-fish descendants of fish, namely the tetrapods, and concludes that fish do not belong to ‘a fish taxon’, but they could have; so their membership of a higher taxon is contingent. However, as should be clear by now, this argument suffers from a similar problem to the one regarding birds. There *is* in fact a taxon that all fish belong to. It just so happens that this taxon *also includes* all the tetrapods (it is the clade Vertebrata). And this clade is, furthermore, *the same clade* that all the fish would belong to in a possible world in which the tetrapods never evolved. The reason for this is, again, that what defines the clade is not how many remarkably different groups of organisms have evolved within it, but simply that it is composed of a certain stem species plus all of its descendants.

In conclusion, LaPorte’s (1997) arguments are incorrect and cannot be used to support the thesis of the contingency of taxon membership. Perhaps for this reason, in 2004 LaPorte argued for the opposite thesis, i.e. the necessity of higher taxa membership under a phylogenetic framework, whilst maintaining his original thesis about the contingency of species membership.

6.2 LaPorte’s argument for the necessity of higher taxa membership

In 2004, although maintaining his earlier view that organisms are not essentially members of their species, LaPorte now argues that they are nevertheless essentially members of the higher taxa they belong to. In part, this move certainly seems to reflect a more accurate understanding of phylogenetics. LaPorte now argues that, according to phylogenetics, a higher taxon such as Mammalia designates ‘the clade whose members in any possible world are members of the ancestral group *G* or descendants thereof’ (2004: 51).

The reason he concludes this is because the theoretical statement that ‘Mammalia=the clade that stems from the ancestral group *G*’ is necessarily true. LaPorte argues that there is no possible world in which an organism belonging to a mammal species, such as *Panthera tigris*, descends from Mammalia’s stem group *G* and yet fails to be a mammal. He claims that the only way a member of *P. tigris* could fail to

be a mammal is if it did not descend from G , but since the members of *P. tigris* did descend from G in the actual world, there is no possible world in which a member of this species does not descend from G (2004: 51).

There is, however, one other possibility: individual members of a mammal species, such as *Panthera tigris*, could have failed to be mammals if they were to exist in a possible world where the clade Mammalia does not exist at all. In the next section, I argue that this is indeed possible; in fact, it follows from the contingency of species membership.

7 A new argument for the contingency of clade membership

Let us return to LaPorte's example from Sect. 6.2. Although LaPorte talks about "group G ", the standard understanding in biology is that clades are composed of a particular *stem species* and all of its descendants, and it is the speciation process itself that gives rise to new clades (see for instance Wiley & Lieberman 2011). In fact, LaPorte names his "group G " by comparison with Hennig's example of a certain *Archaeopteryx* species as the stem of Aves. But if individual organisms do not belong essentially to their species, then this no doubt applies to all organisms, including those that belong to the stem species of the clade under consideration. So it is possible that the individual organisms that were actually the ancestors of the clade Mammalia might have belonged to a different species.

Consider a particular cat, called Josephine, that exists in the actual world. In the actual world, Josephine is a cat, a mammal, and an animal. Now suppose that in the actual world, the stem species of Mammalia is 'therapsid X'. This species originated in a speciation event in which a previously existing species, 'therapsid A' (for 'ancestral therapsid'), speciated into two species: 'therapsid X' and 'therapsid Y'. Each of these later gave rise to other species, and thereby became the stem species of new clades. 'Therapsid X' became the stem species of Mammalia, and 'therapsid Y' the stem species of some other clade. Now imagine that in a possible world, 'therapsid A' did not speciate; in that world, the species 'therapsid X' and 'therapsid Y' never came to be. Nevertheless, 'therapsid A' continued to evolve, and the set of all its members came to include (some of) the very same organisms that in the actual world belong to the species 'therapsid X'. The descendants of 'therapsid A' eventually evolve into all the animals we know as mammals.

Since clades are understood in phylogenetics as being composed of a particular stem species and all of its descendants, it is reasonable to assume that if a certain clade x has stem species y , then in a possible world in which y does not exist, clade x does not exist either. Therefore, it is not the case that, in the possible world we are considering, the stem species of Mammalia is 'therapsid A' instead of 'therapsid X'. Rather, since in this possible world 'therapsid X' does not exist, neither does the clade Mammalia. The clade immediately above it, which has as its stem species 'therapsid A' exists in both worlds, but the clade Mammalia does not exist in the possible world we are considering.

Yet this does not entail that particular organisms which in the actual world belong to the clade Mammalia would not exist in that possible world. In order to maintain

that numerically the same organism, Josephine, exists in this possible world, I will assume the truth of Kripke's thesis of the necessity of origin.⁸ If the existence of an organism's actual ancestors is necessary for its existence, then all possible worlds where the organism exists also necessarily contain its ancestors. This might lead us to think that an organism's place in a lineage is essential to it (LaPorte, 1997: 103). Evidently, if an organism has its origin in its immediate ancestors necessarily, then that is equally true of its ancestors, which makes the entire lineage, all the way since the beginning of life, necessary for a particular organism's existence.

But if organisms do not belong essentially to their species, the existence of an organism's actual ancestors does not require their membership in particular species, or even the existence of those species; rather, what is necessary is the existence of its actual individual ancestor organisms. If organisms are not essentially members of their species, then, for any of an organism's individual ancestor organisms, it is possible that they might have existed and yet belonged to different species. Indeed, in the possible world we are considering, all the actual organisms that are Josephine's ancestors exist; the only difference is that some of them belong to different species than in the actual world. Some organisms which in the actual world belong to species 'therapsid X', in this possible world belong to species 'therapsid A' instead, while being numerically the same organisms. And this is indeed possible if species membership is contingent. Therefore, Josephine can exist in a possible world where she is not a mammal, because the clade Mammalia does not exist in that possible world.

If it is possible for an organism which belongs to the clade Mammalia to exist in a possible world in which the clade itself does not exist, then the membership of individual organisms in higher clades is also contingent. Its non-necessity stems from the non-necessity of species membership. LaPorte's (2004: 50) middle-ground position, that one can simultaneously defend the contingency of species membership but the necessity of higher taxa membership, turns out to be inconsistent.

If the above argument is correct, then it follows that, although it is a true theoretical statement that cats are mammals, it is not a necessary statement. Cats are not necessarily mammals. They are not necessarily animals either, since the Kingdom Animalia is another clade, composed of a particular stem species and all of its descendants, so exactly the same argument can be applied to it. And the same can be said of all other organisms and the higher taxa they belong to.

Yet Putnam and Kripke were not entirely wrong in their assertions. There are no possible worlds in which cats are demons, or tigers are robots. But we can express this modal intuition by claiming that cats and tigers are essentially organisms. Unlike 'Mammalia' or 'Animalia', which are the names of clades, 'organism' does not correspond to a biological taxon. 'Organism' is understood in biology as referring to any living entity, regardless of taxonomy. If life exists elsewhere in the universe, as is generally assumed in astrobiology, then 'organism' can apply to any material object that exists anywhere in the universe, provided it satisfies the condition 'being alive'.

⁸Note that the existence of an organism's ancestors in a possible world does not guarantee the organism's existence in that possible world; rather, the existence of its ancestors makes its existence possible. In other words: assuming the truth of the necessity of origin, the set of possible worlds where the organism in question exists is a subset of all possible worlds where its ancestors exist.

As such, it functions in the same way as other natural kind terms such as ‘water’ and ‘gold’, which are defined by intrinsic properties. In fact, if we replace ‘animal’ in Putnam’s and Kripke’s statements with ‘organism’, the problem disappears. Both ‘all cats are organisms’ and ‘all tigers are organisms’ are indeed necessary statements; there is no possible world in which cats or tigers exist but are not organisms.

8 Some objections

In this section I would like to briefly consider four possible objections to the argument made in this paper. The first one is that someone might say that ‘animal’ is being used in an excessively technical sense. Perhaps when we say that ‘cats are animals’ we do not mean by animal ‘a member of the Animal Kingdom’; instead, we intend to use some pre-theoretical notion of ‘animal’ (e.g. ‘a living thing that moves and is sensitive’). But if someone raises this objection, then they cannot at the same time claim that ‘cats are animals’ is a true theoretical statement, comparable to ‘water is H₂O’ or ‘gold is the element with atomic number 79’. Rather, it just means ‘cats are the sort of thing people usually call “animal”’. But that is not what the theoretical statement aims to achieve. It is also not how most philosophers who use statements like these in relevant contexts understand them. For instance, when defending animalism, Eric Olson explicitly states that, when he says that we are animals, by ‘animal’ he means ‘an organism of the animal kingdom’ (2015: 21).

A second objection is that, by accepting that an individual mammal organism might have existed without being a mammal, which is equivalent to saying that the same organism exists in a possible world where it is not a mammal, it might seem that we lose our purchase on the transworld identity of the organism. How can we know that we are identifying numerically the same individual organism in a possible world in which it is not a mammal? Unless we accept the possibility of ‘bare identities’ or haecceities, there must be *some* properties which ground the transworld identity of individual entities (Mackie & Jago, 2017). It is appealing to think of ‘animal’, ‘mammal’, or even the species an organism belongs to as its substance sortal, which would provide a candidate essential property on which to ground its identity across possible worlds. But it would certainly be question-begging to do so when the question of whether or not organisms belong essentially to their species and higher taxa is exactly what is under dispute. On the assumption that we are following a scientific understanding of what phylogenetic groups are, it cannot simply be assumed that they are substance sortals.

Furthermore, it is not clear that sortals are a good way to ground the identity of particular entities across possible worlds, since, even if belonging to a particular sortal were an essential property of the entity, that property would not, by itself, distinguish the individual entity from all other entities which belong to the same sortal; rather, what is needed is some *exclusive* essential property. More precisely, belonging to a sortal is never sufficient to ground the identity of a particular entity across possible worlds. It may be *necessary* for particular entities to belong to certain substance sortals – this is the view known as sortal essentialism. But even if sortal essentialism is true, biological taxa cannot be assumed to be good candidate sortals, precisely

because membership in them is, arguably, contingent. In the previous section, I suggested that individual organisms are essentially organisms. It is possible that the identity of individual organisms across possible worlds is grounded on their belonging to the substance sortal ‘organism’ together with details about their origin. What sortals cannot do is ground the transworld identity of individual entities in the absence of further, exclusive properties (whether these are qualitative properties or haecceities).

Two other objections come from phylogenetic systematics itself, and both involve a rejection of the requirement that clades be defined by their stem species. The first is the suggestion that, instead of clades being defined by their stem species, they could be defined by the actual organisms that existed at the time of the speciation event which initiated cladogenesis. However, this will not work, for two reasons: one is that, except in highly unusual circumstances (e.g. formation of new plant species by hybridization, which can happen in a single reproductive event), speciation is a very long process that goes on for generations, so it is hard to pinpoint which would be the relevant organisms. On the other hand, requiring the existence of all the actual organisms that existed between two speciation events seems overly demanding, especially since it is conceivable that a certain clade might have come into existence slightly earlier or slightly later, if the relevant speciation event had been completed slightly earlier or later than was actually the case. So, for instance, although the clade Mammalia necessarily had to originate from its actual stem species, this species might have included numerically different organisms. All this would mean is that numerically different individual mammals would exist today.

The second, and more significant, objection from phylogenetics is that there are alternative ways of naming clades – what phylogeneticists often call ‘defining the names of clades’ – which are not based on the stem species of the clade. Although all phylogeneticists agree that clades are composed of an ancestral species and all, and only, its descendants,⁹ in phylogenetic nomenclature there are two alternative ways of defining the names of clades, in addition to stem-based definitions: *node-based* definitions, and *apomorphy-based* definitions. The former defines the name of a clade stemming from the most recent common ancestor of two (usually extant) specified organisms, species, or clades, and the latter defines the name of a clade stemming from the first ancestor species to evolve a specified character (de Queiroz & Gauthier, 1994: 29).

Consider node-based definitions. For example, consider an alternative, node-based definition of Mammalia as “the clade originating in the most recent common ancestor of *Ornithorhynchus anatinus* (the duck-billed platypus) and *Elephas maximus* (the Asian elephant)”. There are two possible ways of reading this definition: (1) on a *de re* reading, the definition simply fixes the reference on a particular stem species. Because we are not directly acquainted with the stem species, we refer to it indirectly as ‘the (actual) species which was the most recent common ancestor of the platypus and the elephant’. The reference to the ancestral species is fixed; the clade

⁹ Both traditional phylogeneticists who follow the Linnaean system and proponents of the alternative system of phylogenetic nomenclature seem to agree on this point. For example, de Queiroz clearly states that clades designated by either of the definitions accepted in the PhyloCode are “defined as parts of phylogeny each of which is composed of an ancestor and all of its descendants” (de Queiroz, 2007: 957).

is still defined as a particular ancestral species plus all, and only, its descendants. If we interpret the definition in this way, we can maintain that, had the actual ancestral species not existed, the clade would not have existed either.

Alternatively, we can interpret the definition as *de dicto*. In this case, the reference is to the most recent common ancestor of the platypus and the elephant, *whichever it is*. On this reading, the identity of the stem species of the clade is not considered essential to the existence of the clade itself. In this case, the clade is *defined* by reference to the two extant species (the *specifiers*), rather than the stem species of the clade. So on this interpretation, it would be possible for the same clade to exist while having a different stem species, and the example of Sect. 7 fails.

But if a clade were to be defined in this way, then all we had to do was postulate a possible world in which at least one of the specifiers did not exist; that would be a possible world in which the clade did not exist either. In fact, this would be even less problematic than postulating hypothetical changes to the stem species, because these possible worlds need not involve any changes whatsoever in the entire lineage leading up to the organism in question. Even in the particular case where the individual organism happens to belong to one of the specifiers of the clade, there are possible worlds where it exists but the *other* specifier of the clade does not, and therefore the clade does not exist either. So, on this interpretation, too, there are possible worlds where a particular cat exists but is not an animal, because the clade Animalia does not exist in that possible world.

Apomorphy-based definitions are less preferred in phylogenetic taxonomy,¹⁰ but can be dealt with in a similar way. Either they simply fix the reference of the stem species, and the argument in Sect. 7 goes through unscathed; or they refer *de dicto* to whichever species first evolved a particular apomorphy, in which case we can postulate a possible world in which a different species first evolved the character in question.

9 Conclusions

I have argued that true a posteriori theoretical statements concerning biological taxa are not necessary; i.e., they are not true in all possible worlds. Organisms do not belong essentially to their species, and from this fact it follows that they also do not belong essentially to any of the higher taxa they actually belong to.

The reason philosophers have often been misled in their pronouncements concerning biological taxa stems from an excessive reliance on a priori intuitions: it just seems intuitively obvious that organisms could not have existed without belonging to the species or higher taxa they belong to, because it also seems intuitively obvious that what makes an organism the kind of thing it is must be some intrinsic essence which it could not have lacked. Yet we should remember that it once must also have seemed intuitively obvious that species were immutable. In fact, biology has disabused us of each of these notions.

¹⁰ Especially for crown clades. See article 9.9 of the PhyloCode (Cantino & de Queiroz, 2020).

While Kripke and Putnam were right in arguing that theoretical terms are not synonymous with descriptions, but refer to real kinds or groups of things in the world which are discovered through empirical investigation, expecting all natural kinds to be grounded in some ‘internal structure’ is yet another a priori assumption which, at least in the biological case, is untenable. But we would not stray too far from the spirit of Kripke’s account if we were to suggest that, just as the kinds themselves are discovered by science, so are the properties which ground them.

We should not expect to apply Kripke’s device for deriving necessary a posteriori theoretical claims from scientific discoveries with the help of some background essentialist assumptions, without verifying whether or not the essentialist assumptions required are warranted in the particular case at hand. In the biological case, if individual organisms do not belong to species and higher taxa in virtue of internal structural properties which they could not have lacked, then they might have existed without belonging to the species and higher taxa they belong to. It is possible, indeed, to derive modal knowledge from scientific claims, but only if we do not let our a priori intuitions get in the way.

Acknowledgements I am grateful to Samir Okasha, Tuomas Tahko, Francesca Bellazzi, Milenko Lasnibat, and three anonymous reviewers for helpful comments on previous versions of this manuscript. This work was supported by the British Society for the Philosophy of Science through a doctoral scholarship.

Funding details This work was supported by the British Society for the Philosophy of Science through a doctoral scholarship.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article’s Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article’s Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

References

- Bokulich, A. (2020). Understanding scientific types: holotypes, stratotypes, and measurement prototypes. *Biology & Philosophy*, 35(5), 1–28
- Cantino, P. D., & de Queiroz, K. (Eds.). (2020). *PhyloCode: A Phylogenetic Code of Biological Nomenclature*. Boca Raton, FL: CRC Press.)
- Dennett, D. C. (2017). Darwin and the Overdue Demise of Essentialism. In D. L. Smith (Ed.), *How Biology Shapes Philosophy: New Foundations for Naturalism* (pp. 9–22). Cambridge: Cambridge University Press.)
- de Queiroz, K., & Gauthier, J. (1994). Toward a phylogenetic system of biological nomenclature. *Trends in Ecology & Evolution*, 9(1), 27–31
- de Queiroz, K. (2007). Toward an integrated system of clade names. *Systematic Biology*, 56(6), 956–974
- Devitt, M. (2010). Species have (partly) intrinsic essences. *Philosophy of Science*, 77(5), 648–661
- Donnellan, K. S. (1962). Necessity and criteria. *The Journal of Philosophy*, 59(22), 647–658
- Fine, K. (1994). Essence and modality. *Philosophical Perspectives*, 8, 1–16

- Ghiselin, M. T. (1974). A radical solution to the species problem. *Systematic Biology*, 23(4), 536–544
- Haber, M. H. (2012). How to misidentify a type specimen. *Biology & Philosophy*, 27(6), 767–784
- Hägqvist, S., & Wikfors, Å. (2018). Natural kinds and natural kind terms: Myth and reality. *The British Journal for the Philosophy of Science*, 69(4), 911–933
- Hendry, R. F. (2006). Elements, compounds, and other chemical kinds. *Philosophy of Science*, 73(5), 864–875
- Hennig, W. (1966). *Phylogenetic Systematics*. Urbana and Chicago: University of Illinois Press.)
- Hofer, C., & Marti, G. (2019). Water has a microstructural essence after all. *European Journal for Philosophy of Science*, 9(1), 1–15
- Hughes, C. (2004). *Kripke: Names, Necessity, and Identity*. Oxford: Clarendon Press.)
- Hull, D. L. (1976). Are species really individuals? *Systematic Zoology*, 25(2), 174–191
- Hull, D. L. (1978). A matter of individuality. *Philosophy of Science*, 45(3), 335–360
- Kripke, S. A. (1980). *Naming and Necessity*. Oxford: Blackwell.)
- LaPorte, J. (1997). Essential Membership. *Philosophy of Science*, 64(1), 96–112
- LaPorte, J. (2003). Does a type specimen necessarily or contingently belong to its species? *Biology and Philosophy*, 18(4), 583–588
- LaPorte, J. (2004). *Natural Kinds and Conceptual Change*. Cambridge: Cambridge University Press.)
- Leslie, S. J. (2013). Essence and natural kinds: When science meets preschooler intuition. *Oxford Studies in Epistemology*, 4, 108–165
- Levine, A. (2001). Individualism, type specimens, and the scrutability of species membership. *Biology and Philosophy*, 16(3), 325–338
- Mackie, P., & Jago, M. (2017). Transworld Identity. The Stanford Encyclopedia of Philosophy (Winter 2017 Edition), Edward N. Zalta (ed.), <https://plato.stanford.edu/archives/win2017/entries/identity-transworld/>
- Okasha, S. (2002). Darwinian metaphysics: species and the question of essentialism. *Synthese*, 131, 191–213
- Okasha, S. (2003). Does the concept of “clade selection” make sense? *Philosophy of Science*, 70(4), 739–751
- Olson, E. T. (2015). Animalism and the remnant-person problem. In J. Fonseca, & J. Gonçalves (Eds.), *Philosophical Perspectives on the Self* (pp. 21–40). Bern: Peter Lang AG.)
- Putnam, H. (1962). It ain't necessarily so. *The Journal of Philosophy*, 59(22), 658–671
- Putnam, H. (1975). The meaning of ‘meaning’. In *his Philosophical Papers, volume 2: Mind, Language and Reality* (pp. 131–193). Cambridge: Cambridge University Press
- Richards, R. A. (2016). *Biological Classification*. Cambridge: Cambridge University Press
- Wiley, E. O., & Lieberman, B. S. (2011). *Phylogenetics: Theory and Practice of Phylogenetic Systematics, second edition*. (Hoboken, New Jersey: Wiley-Blackwell)
- Hacking, I. (2007). Putnam's theory of natural kinds and their names is not the same as Kripke's. *Principia: an International Journal of Epistemology*, 11(1), 1–24.
- Needham, P. (2002). The discovery that water is H₂O. *International Studies in the Philosophy of Science*, 16(3), 205–226.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.