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A Critique of Modern Biological Essentialism

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A Critique of Modern Biological Essentialism

by

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Abstract

According to a traditional view about the ontology of biological taxa, taxa are natural kinds with kind-specific essences. This view has been challenged by different types of arguments by both biologists and philosophers. However, in opposition to these arguments, philosophers have recently argued that biological taxa do contain essences if we further refine the traditional notion of biological essence. These new versions of essentialism are distinguished by how this refinement is carried out. According to Okasha's (2002) essentialism, essences are relational rather than intrinsic properties. For LaPorte (2004) and Griffiths (1999), essences are certain ancestor-descendant relationships. Sober (1980) suggests that Kripke's argument for origin essentialism might be extended to biological species. Devitt (2008) and Boyd (1999a,b) allow essences to be clusters of properties—rather than single properties. The arguments for these new forms of essentialism are based on assumptions informed by current biological systematics. For instance, whereas Okasha's argument is based on species concepts, LaPorte's and Griffiths' essentialisms rely on cladistics. The goal of my dissertation is to identify these assumptions and examine whether they can be used to substantiate biological essentialism. I argue that they cannot: theories in biological systematics do not support the view that biological taxa contain essences. However, by simply rejecting essentialism we are left with unanswered questions that essentialism was designed to solve, such as explaining the presence of a certain trait among conspecific organisms. For this reason, in the final chapter, I consider some possible directions as to how we can address the problems essentialist theories were designed to solve without assuming that biological taxa contain essential features. Moreover, since arguments for biological essentialism are typically inferences to the best explanation, in considering non-essentialist alternatives I cast doubt on whether essentialism provides the best answers to some questions about biological taxa.

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Introduction

This dissertation deals with some controversies concerning biological classification. This remark might seem surprising at first. For one might think that biological classification is a purely descriptive enterprise. As long as an organism's characters are agreed upon, how could there be any major disagreement concerning its classification? Biological classification is controversial because taxonomists disagree over the *sort* of features used to define biological taxa. As an example, consider these two ways of classifying the higher primates discussed in Prothero (2003).

Primates have traditionally been subdivided into two families, Hominidae (which only includes humans) and Pongidae (which includes all non-human apes). These groups are represented in figure 1. One might think that this classification is reasonable given how much we diverged in relation to non-human apes, as attested by human traits such as bipedalism, larger brains, and naked skin. However, according to an approach to classification called *cladistics*, biological taxa should contain all the descendants of a common ancestor, irrespective of their morphological dissimilarities. So, because humans and the rest of apes share a common ancestor (fig. 1), cladists do not think that Pongidae is a legitimate taxon. We should either expand Pongidae to include humans or include the non-human apes within

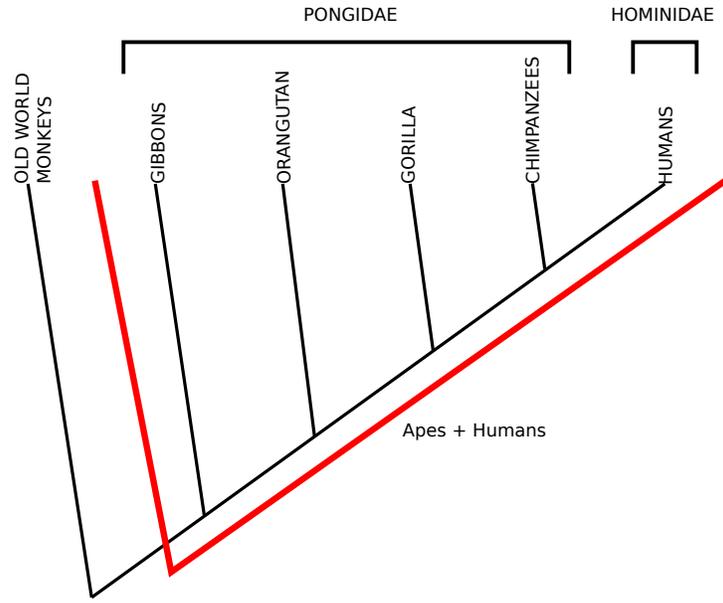


Figure 1: A tree depicting the genealogical relationships between higher apes and the taxa ‘Pongidae’ and ‘Hominidae’ as traditionally defined. From Prothero (2003, p. 54).

Hominidae. From a cladist standpoint, the Pongidae group is a “wastebasket” for non-human apes, possibly motivated by our anthropocentric bias (*ibid.*, p. 54). Note that the disagreement here is not a matter of semantics. The point that cladists are making is that morphological similarity is too ambiguous to serve as a criterion to define biological taxa. In contrast, a cladist would add, because there is a single tree of life, defining taxa in terms of common ancestry is not ambiguous: organisms do or do not share ancestors. My goal with this example is not to defend cladistics but to illustrate how biological classification can be a controversial subject. Organisms can be grouped together according to different features such as common ancestry and morphological similarity. Yet, the use of different features can produce conflicting classifications as the example with higher primates illustrates. Accordingly, theories about biological classification are characterized by the type of features they use to define taxa, such as common ancestry in the case of cladistics (Ereshefsky, 2001; Ridley, 1986).

This dissertation focuses on a particular approach to classification called *biological essentialism*. According to biological essentialism, the features used to define biological taxa should be *essences*. Biological essentialism has been widely discussed in both biology and philosophy. I will first introduce some views about essentialism from philosophy.

Philosophers of science frequently write that scientific theories group things together into special groups called *natural kinds*. The notion of ‘essences’ is often used to articulate what is unique about natural kinds. Putnam (1975) proposes this view when considering two natural kinds, ‘lemons’ and ‘acids’:

If I describe something as a *lemon*, or as an *acid*, I indicate that it is likely to have certain characteristics (yellow peel, or sour taste in dilute water solution, as the case may be); but I also indicate that the presence of those characteristics, if they are present, is likely to be accounted for by some “essential nature” which the thing shares with other members of the natural kind (*ibid.*, p. 104).

This quote illustrates two views typically associated with natural kind essentialism. Members of the same natural kind tend to share certain characteristics, such as yellow peel and sour taste. Further, this happens because members of the same kind share the same essential feature such as “being a proton-donor, in the case of acids” (*ibid.*, p. 104). Chemical elements such as ‘gold’ are another common example of natural kinds, with atomic numbers being their essences (Kripke, 1980). Atomic numbers are thought to be essential to chemical elements for two reasons: all and only members of gold share the same atomic number, and this atomic number accounts for nondefining features of gold such as color and mass. Unlike natural kinds, artificial kinds are only expected to share their defining features. Accordingly,

if biological taxa are natural kinds in Putnam's sense, then the essences of a taxon, say, *Homo sapiens*, should account for other shared traits among humans. Thus, the motivation for adopting a system of classification based on natural kinds is that it allows us to focus on a small set of features, a taxon's essence, but still infer many other features within this taxon.

We saw that within philosophy the notion of 'natural kinds' is used to characterize groupings in which both defining and non-defining characteristics are correlated to each other. This notion of natural groups also figures in discussions within biological systematics. One of the reasons is that natural groups seem to yield a more *stable* system of classification than artificial groups (Ridley, 1986, p. 8ff.). In other words, natural taxa seem to be less likely to be revised as new characters are described than artificial taxa. In a nutshell, the connection between taxonomic stability and natural classification goes like this. In natural classification the use of different characters will tend to produce the same taxa. By contrast, because non-natural taxa only tend to share a small set of features and no other, they seem to be more likely to be revised as new characters are taken into consideration. Accordingly, natural classifications seem to be better buffered against the influx of new information. While artificial groups are based on a selected set of features, natural groups are confirmed by independent lines of evidence. Summarizing so far, there are two major motivations for treating biological taxa as natural kinds: stability and predictive power. However, until now nothing has been said about whether living organisms actually cluster together into natural kinds. I consider this issue in the next paragraph.

Recall that for biological essentialists variation is confined to accidental features, leaving essential features invariant during a taxon's lifetime. The evolutionary biologist Ernst

Mayr, one of the key critics of biological essentialism, argued that the view that variation within a taxon has fixed limits is incompatible with Darwin's theory of evolution. For Mayr, there is no privileged feature within a taxon that is not susceptible to variation (Mayr, 1976, 1982, 1991). Following Mayr, philosophers of biology such as David Hull (1965) and Elliott Sober (1980) also argued that biological essentialism is ill-founded. Their criticisms were so influential that the rejection of biological essentialism has become the received view within philosophy of biology (see e.g., Ereshefsky, 2001; Sterelny and Griffiths, 1999). The incompatibility between biological essentialism and current biology then seemed to be an indisputable matter.

In a series of recent publications however, philosophers have claimed that biological essentialism is not only consistent with but justified by current biological systematics (e.g., Boyd, 1999a; Devitt, 2008; Griffiths, 1999; LaPorte, 2004; Okasha, 2002). To show that, the modern essentialists have proposed different ways of refining the notion of biological essence. Despite variations in their views, the modern essentialists all agree that the traditional anti-essentialist arguments do not show that biological essentialism is mistaken, but only that a particular conception of biological essence is incorrect. Also, the modern essentialists claim that their views vindicate some (or all) of the desirable features of the traditional forms of essentialism such as explanatory power. This dissertation takes a close look at this new essentialist wave within philosophy. In particular, it raises questions like the following. What novel insights are these modern versions of essentialism supposed to deliver? And how do they relate to current views in biological systematics? A considerable portion of this dissertation attempts to answer these questions by looking at different versions of modern essentialism. Here is a chapter-by-chapter preview.

After introducing the standard objections to biological essentialism in the next chapter, I dedicate two chapters to discuss history-based versions of biological essentialism (chapters 2 and 3). According to this version of essentialism, biological essences are ancestor-descendant relationships. For historical essentialists, even though there might not be a limit on how much phenetic variation a taxon might undergo, the ‘historical origin’ of a taxon is essential to it. An argument for historical essentialism must unpack what is meant by ‘historical origin’ and give a reason for why a taxon’s historical origin is not an accidental feature. There are two major arguments for this version of essentialism in the literature. According to one argument, biological essentialism is justified by an influential school in biological taxonomy, the cladistic school (Griffiths, 1999; LaPorte, 2004). I look at this argument in chapter 2. The other type of argument for historical essentialism does not rely on current systematics but on an argument from philosophy, Kripke’s (1980) argument for *origin essentialism*. This argument was originally suggested by Sober (1980) but he did not develop this suggestion any further. I examine Sober’s suggestion in chapter 3.

Next I move to versions of modern essentialism in which biological essences are not necessarily historical. These versions of essentialism are: Okasha’s (2002) relational essentialism, and two variants of the view that biological essences are clusters of properties, Devitt’s (2008) hybrid essentialism and Boyd’s (1999) homeostatic property cluster theory. According to Okasha, current species definitions, also known as *species concepts*, fix the extension of species taxa via ‘relational’ properties such as ‘being able to interbreed with one group of organisms and not another’. For Okasha these relational properties are species’ essences. While Okasha thinks that species’ essences do not contain ‘intrinsic’ properties such as having a certain genotype, Devitt’s and Boyd’s versions of essentialism allow intrinsic properties

to be part of a taxon's essence. Another common feature of Boyd's and Devitt's essentialisms is that essences are clusters of properties. All three versions of this essentialism are discussed in chapter 4.

The modern essentialists typically argue that their respective versions of essentialism are supported by current biological systematics. For instance, whereas Okasha argues that his relational essentialism is warranted by species concepts, LaPorte and Griffiths claim that historical essentialism is justified by cladistics. A recurrent theme in this dissertation is that the modern essentialists are mistaken in this respect: current systematics does not support biological essentialism. In order to show that, much of this dissertation focuses on the relation between biological essentialism and some biological theories such as cladistics (chapter 2), speciation theories (chapter 3), and species concepts (chapter 4). Despite the difficulties faced by biological essentialism, to simply state that essentialism is false seems to leave us in an unsettling position. For by rejecting essentialism we are left with unanswered questions that essentialism was designed to solve, such as explaining the presence of a certain trait among conspecific organisms. Possibly, the difficulties with essentialism indicate how we can improve our essentialist theories rather than showing that we have to reject essentialism altogether. I reject this suggestion. In the final chapter, I consider some ways to address the problems essentialist theories were designed to solve without assuming that biological taxa contain essential features. In other words, I show that essentialism should not be the default position, as many philosophers assume.

In sum, here is the overall shape of this dissertation. According to the modern essentialists, philosophers of biology and biologists are wrong to think that essentialism is uncongenial to current biology. Against the modern essentialists, I argue that there is a substantial gulf

between biological systematics and biological essentialism. In my view, seeing current systematics as justifying biological essentialism misrepresents how biological taxa are defined. Moreover, the fact that there are non-essentialist ways of accounting for problems that essentialist theories were designed to solve, I show that biological essentialism is not as compelling as the modern essentialists have argued.

Chapter 1

Biological essentialism, gradualism, and explanation

Contents

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Essentialism about biological taxa is the view that all and only the members of a taxon must contain a certain property, that taxon's essence. Biological essentialism has been challenged by both biologists and philosophers (e.g., Ghiselin, 1974; Hull, 1965; Mayr, 1976). According to these criticisms, biological essentialism is incompatible with current evolutionary theory. Because of these criticisms, the view that biological taxa do not contain essences

has become the received view among philosophers of biology (see e.g., Ereshefsky, 2001; Sterelny and Griffiths, 1999). However, in a series of recent papers, some philosophers have argued that this received view is incorrect (e.g., Devitt, 2008; LaPorte, 2004; Okasha, 2002). According to them, not only do these arguments fail to show that biological taxa do not contain essences, but that there are reasons in favor of the existence of biological essences. Despite variations in the new essentialists' arguments, we can identify a common pattern in their criticism of the received view.

The new essentialists typically invoke the distinction between *intrinsic* and *relational* properties. Briefly put, intrinsic properties are features that something has regardless of what is happening outside of itself. A paradigmatic example of intrinsic property is an object's mass. In contrast, some of the properties an object has depend on the relation between this object and something else. For example, different from an object's mass, an object's weight varies depending on whether it is on the Earth's or on the Moon's surface. In the case of biology, having a certain genotype (or phenotype) is an example of an intrinsic property whereas the property of being an ancestral taxon is a relational property. As I shall discuss in later chapters, the new essentialists believe that the received view's objections to essentialism are effective only if we think of biological essences as only containing *intrinsic*—as opposed to *relational*—properties.¹ In other words, for the new essentialists the classical arguments against essentialism (such as Mayr's) only apply to *intrinsic* essentialism. For them, the problem is not essentialism but intrinsic essentialism.

¹ As I discuss in later chapters, some essentialists like Devitt (2008) think that essences should be at least partly intrinsic. However, according to some new essentialists such as Okasha (2002), essences are exclusively relational.

Within mainstream analytic philosophy, examples of biological essences given by natural kind essentialists, such as Kripke and Putnam, are intrinsic properties. For instance, Kripke (1980, pp. 20–21) says that tigers are defined by their “internal structure”; Putnam (1975, p. 104) talks of lemons as being defined by their “chromosome structure”. According to the new essentialists, even though Putnam and Kripke were right that biological taxa contain essences, Putnam and Kripke misidentify what the essential properties of biological taxa are. In order to vindicate a notion of essences that is better substantiated by current biology, the new essentialists rely on current approaches to systematics such as cladistics (LaPorte, 2004) and species concepts (Okasha, 2002). So, another common theme among the new essentialists is that, different from what the promoters of the received view have argued, essentialism is not only compatible with current biology, but is justified by it.

The goal of this chapter is to introduce some of the key arguments that shaped the received view, proposed by Hull (1965), Mayr (1976), and Sober (1980). According to the new essentialists, these arguments only apply to intrinsic essentialism. The bulk of this dissertation discusses the new essentialists’ reasons for thinking so. But in this chapter, I will not consider the new essentialists’ criticisms of the received view. The role of this chapter is to simply introduce the necessary background for discussing the new essentialisms in the following chapters.

The first objection against essentialism I will discuss relates to arguments put forward by Hull (1965). According to Hull, biological essentialism is incompatible with the fact that speciation is most often a gradual process (section 1.3). Hull’s point is that speciation events can yield populations that are evolutionary intermediaries between subspecies and species, and that the existence of these intermediary stages is incompatible with biological

essentialism. In that section I also introduce Sober's (1980) suggestion against Hull that we can formulate essentialism in a more flexible way so that it is compatible with the gradual evolution of species. That is, for Sober, essentialism is *in principle* consistent with the gradual evolution of species.

A typical rationale for essentialism is that essences are required to explain similarities among members of the same taxon. In section 1.4 I introduce an argument proposed by Sober (1980) against the idea that essentialism can satisfy this rationale. According to Sober's argument, essentialist explanations are incompatible with current evolutionary explanations. Sober's position is rooted in Mayr's (1976) distinction between typology and population thinking. Sober and Mayr's view is that Darwin's evolutionary explanations replaced essentialist explanations.² In order to articulate this point, Sober introduces what he calls the *Natural State Model*. This model is supposed to be a description of the explanation model used by essentialist theories such as Aristotle's. The Natural State Model as used by essentialist theories contrasts with population thinking. A key difference between essentialism and population thinking is the level at which these explanations are supposed to take place. For essentialism, variation in a taxon is explained in terms of properties of *individual* organisms; for population thinking, such variation is explained by taking into consideration properties of *populations*. Sober's argument against essentialism is discussed in section 1.4.

But before I discuss these two objections against essentialism, section 1.1 introduces the

² As Sober puts it: “[n]atural selection is not just a novel explanation of evolution, it is a novel *kind* of explanation. Darwin did not simply expropriate the phenomena that earlier biologists wished to account for and supply them with a new explanation; he reformulated the very propositions that required explanation” (Sober, 1984, p. 135).

view that classifications in science require natural kinds with essential features. The underlying intuition of this view is that we can only reliably infer the features of the unobserved members from the observed members of a kind if each member of this kind shares some feature (e.g., have the same atomic composition). Otherwise we have no guarantee that the unobserved members of a kind will resemble the observed ones. Kind essentialism is the view that the kind's shared feature required for inductive inferences is an essence. I end this chapter with a section summarizing some of the points introduced in this chapter.

1.1 Natural kinds and essentialism

Enumerative induction is a type of argument used to justify the truth of generalizations of the form 'all F s are G ' such as 'all ravens are black.' In enumerative induction we observe that many ravens are black and we then extrapolate that the non-observed ravens are also black. However, as Hempel's (1945) and Goodman's (1983) puzzles show, enumerative inductions can be unreliable depending on which predicates F and G we pick. In what follows, I consider Goodman's (1983) riddle of induction.

In order to formulate his riddle, Goodman (1983) introduces the predicate *grue*. Suppose that all emeralds observed before the time t are green. The predicate *grue* is defined as applying "to all things examined before t just in case they are green but to other things just in case they are blue" (*ibid.*, p. 74). The predicate "grue" is then defined in such a way that the fact that all emeralds observed before t are green provides equal support to the prediction that all emeralds are green and to the prediction that all emeralds are grue. But these two predictions are incompatible with each other: if an emerald is grue after t ,

then this emerald is not blue. The puzzle posed by the grue example is not simply that (enumerative) induction is fallible. That’s uncontroversial. The problem is that by using grue-like predicates, the same set of observations can be used to confirm an indefinite number of conflicting predictions. But that seems absurd.

As Goodman formulates the problem, the predicate “green” is *projectible*, whereas the predicate “grue” is not. So, in order to provide a solution to this riddle, there must be a constraint that the predicate (or kind) “green” satisfies but that the kind “grue” does not. A possible approach is to say that there is a naturalness constraint that only the kind “green” satisfies (Quine, 1969). According to this approach, the predicate “green” is a *natural* kind in the sense that their members share a certain natural similarity that warrants our extrapolation from observed to unobserved emeralds.³ Nonetheless, such an approach faces the challenge of accounting for how such naturalness constraint can justify induction. Godfrey-Smith (2011) provides such an account. I discuss his view in the next paragraphs.

If we are interested in investigating how many teenagers smoke, an expected procedure would be to collect a random sample of teenagers. However, as one might correctly point out, attaining a random sample of teenagers may not be straightforward. The teenagers may not tell the truth when asked, for instance. But the important feature of this example is that the warrant of our inference has nothing to do with whether the kind ‘teenagers’ is projectable but to the way we collect our sample. In this example, randomness and the sample size are what justify our extrapolation from observed to unobserved cases. Accordingly, the

³ Solutions to Goodman’s puzzle not based on this naturalness constraint have also been proposed. See e.g. Jackson (1975).

naturalness constraint does not have to be used to justify this type of inductive inference.⁴

However, Godfrey-Smith adds that for many induction-like inferences we cannot obtain random samples; yet, we can acquire knowledge of generalizations from nonrandom samples. For this type of induction, Godfrey-Smith claims that the naturalness constraint plays a central role. Because of the natural structure of kinds, this type of induction is such that “one instance of an F would be enough, in principle, if you picked the right case and analyzed it well” (*ibid.*, p. 39). An example Godfrey-Smith provides is one of Chargaff’s rules on DNA’s composition. Before Watson and Crick discovered the double helix structure of DNA, Chargaff proposed the rule that the composition of DNA is such that the amount of cytosine equals the amount of guanine, and that the amount of thymine equals the amount of adenine. Because this rule was based on the study of nine kinds of organisms, Chargaff was cautious when asserting his results. However, given Watson and Crick’s discovery it becomes clear that Chargaff’s rule is justified because DNA molecules share a certain structure. According to this example, the naturalness constraint (i.e., sharing the double helix structure) is the bridge between Chargaff’s observations and the non-observed cases (i.e., Chargaff’s rule generalized for *every* doubled stranded DNA molecule).⁵ So, even though the naturalness

⁴ Godfrey-Smith’s suggestion is that, even though the sample of teenagers may not be perfectly random (i.e., not every teenager has exactly the same chance of being in the sample), we should think of the smoking surveys as “a useable approximation to random sampling.”

⁵ Another example Godfrey-Smith provides is Millikan’s discovery of electron’s charge. The sample used by Millikan was not random; Millikan’s argument that charge varies discretely (rather than continually) was not based on a very large sample but on 58 oil drops. As Godfrey-Smith (2011, p. 45) describes Millikan’s study, “[h]is aim was to get a few well-

constraint may not play a role for every type of induction, it seems that this constraint shows why certain inductions, such as Chargaff's, are reliable.

Biological essentialism is a specific account of what this naturalness constraint is with respect to biological taxa. Biological essentialism typically holds that all and only members of a biological taxon contain essential features that causally explain why they share certain features.⁶ For instance, in a defense of biological essentialism with respect to species taxa, Kitts and Kitts (1979) argue that species taxa must have essences in order to explain why species are reproductively isolated from each other. Their view is that two species are reproductively isolated because their members share distinct essential features. In short, essentialists explain differences among taxa by ascribing uniquely shared features to each taxon.

Essential properties are contrasted with *accidental* properties. A kind's essential property is a property that the kind's members must have, whereas accidental properties are properties that members of a kind could have or lack.⁷ As an example, one might think that even

behaved cases that would show the phenomenon clearly and permit a measurement.”

⁶ An exception here is Okasha's (2002) version of biological essentialism according to which essences do not have an explanatory role. For him, instead of explaining shared traits among the members of the same taxon, essences have the role of fixing the extension of species taxa. Okasha's essentialism is discussed in chapter 4.

⁷ Note that the view that biological taxa contain properties that all and only its members *must* share is not controversial. For instance, it is necessary that all and only the members of a taxon say, *t*, is a member of *t* (Sober, 1980, p. 354). The challenge faced by the essentialist is to find a *nontrivial* property that all and only the members of a taxon must share.

though something could only be gold if it has atomic number 79, we can have gold objects with different masses. Nonetheless, what we consider as being possible (and necessary) can vary depending on the kind of possibility we are interested in. For instance, even though the existence of superman is *logically* possible (i.e., we can describe superman without contradiction), he is not *physically* possible—since superman is supposed to fly faster than the speed of light (Dennett, 1995, pp. 104–105).⁸ So the interpretation of the claim that biological taxa contain essential features depends on the range of possible circumstances we consider relevant.⁹ A central motivation for essentialists to use modality is due to the explanatory role that essences are supposed to fulfill. Essences are not designed to explain only the features of existing organisms, but also past and future members of a taxon. For this reason, essences have to be properties of any *possible* member of a taxon.¹⁰

⁸ For further discussion about the different grades of possibility, see Dennett (1995, chap. 5) and Fine (2002).

⁹ For Kripke’s (1980) version of essentialism, the relevant notion of possibility is *metaphysical*. Fine (1994) characterizes metaphysical necessities as based on “the identity of objects.” See Soames (2011) for a discussion of Kripke’s notion of metaphysical possibility and how that contrasts with Kripke’s epistemological notion of possibility. In the case of de Queiroz’ biological essentialism, the (possible) circumstances he seems to be interested in are different phylogenetic hypothesis (de Queiroz, 1992). I discuss de Queiroz’ view in later chapters.

¹⁰ Even though essentialism might be false, the introduction of modal considerations when providing explanations seems inevitable. For instance, when one explains why an allele became fixed in a population, one does that by showing why this allele has fixed in contrast to another allele. An event is explained by showing why it occurred rather than a *contrasting alternative* (Sober, 1984, 1986). Since such contrasting alternatives are ways

Thus far I highlighted some of the features of essentialism. Essentialist theories typically attempt to account for the distinction between projectible and non-projectible kinds by providing a natural constraint. The underlying intuition is that projectible kinds satisfy this natural constraint whereas non-projectible kinds do not. Essentialists formulate this natural constraint as an essential property that all and only the members of a kind share. Essences contrast with accidental properties. That is, a kind's essential property is a feature that the kind's members *cannot* lack. Given these preliminary considerations, I now move to some of the classical arguments against biological essentialism. I begin with the argument that there are evolutionary mechanisms that make it unlikely that species contain essences.

1.2 Essentialism and species variation

An argument for essentialism should show why variation within and among species are compatible with uniquely shared essences. However, it is unlikely that such an argument could be provided (Ereshefsky, 2010b). On one hand, there are evolutionary mechanisms that cause variation among conspecific organisms such as mutation, sexual selection, and recombination. Sexual selection for example produces 'sexual dimorphisms', variations between males and females of the same species regarding a range of traits, such as the ornamented tails in

things *could* have been, the use of modal contexts in explanations seems inescapable. As Dennett summarizes this point, "if we are to explain the way things *are*, it must be against a background of how things *might* have been, or *must* be, or *couldn't* be" (Dennett, 1995, p. 118). So if essentialism is false, that's not simply because it introduces modal considerations.

male peacocks and the long tail in male widowbirds (Pryke and S. Andersson, 2005). On the other hand, there are evolutionary mechanisms that cause distinct species to share the same features, such as phyletic constraints and convergent evolution. In cases of convergent evolution, distantly related taxa evolve the same phenotype and, sometimes, through the same genetic pathway (Arendt and Reznick, 2007). So, convergent evolution occurs not only at the phenotypic level but also at the genetic level. An example illustrating that is the convergent evolution in threespine stickleback (*Gasterosteus aculeatus*) and ninespine stickleback (*Pungitius pungitius*). In both species, a reduction in pelvic structure is a convergent phenotype affected by the same gene, the *Pitx1* gene (ibid., pp. 29–30).

Details aside, the anti-essentialist argument outlined in this section is this. According to biological essentialism, the evolution of species is confined to the ‘accidental’ features of a species, leaving the essence of a species intact during its lifetime. However, there is no biological justification for thinking that the causes of variability within a species, such as mutation, must leave a core of essential features intact. Similarly, there is no evidence for thinking that convergent evolution respects the essentialist view that different species must have distinct essences. In sum, the problem with species essentialism is that it postulates limits to species variability that are not validated by the mechanisms that cause the evolution of species.

1.3 Essentialism and species evolution

Hull (1965) argues against the view that species definitions are descriptions of the essential feature of a species. He summarizes his argument in the quote:

The only basis for a natural classification is evolutionary theory, but according to evolutionary theory, species developed gradually, changing one into another. If species evolved so gradually, they cannot be delimited by means of a single property or a set of properties ([ibid.](#), p. 320).

Hull's argument is that speciation yields populations that can be at intermediary stages between being a subspecies and being a species. However, essentialism does not allow populations to be at an intermediary species status—a population must either be a species or a subspecies. Therefore, Hull concludes, essentialism is false. Because of our limited lifespan we cannot directly observe gradual speciation to assess Hull's argument. But we can indirectly observe how gradual speciation occurs by taking into account a special type of species called *ring species* (D. Irwin, J. Irwin, and Price, [2001](#); Mayr, [1942](#), [1963](#)).

A well-studied example of a ring species is the salamander *Ensatina eschscholtzii* (Wake and Schneider, [1998](#); Wake, Yanev, and Brown, [1986](#)).¹¹ As [figure 1.1](#) shows, the geographic distribution of this species forms a ring around the Central Valley of California. *E. eschscholtzii* expanded from its ancestral range in northern California southward down the coast and inland, encircling the Central Valley and meeting in the south. Even though adjacent populations in the ring can interbreed, the terminal populations in the south rarely hybridize. Ring species are key to understanding how gradual speciation occurs. That is because ring species show how individual variation along the ring can accumulate and result in reproductive isolation between the terminal populations of the ring. In other words, it

¹¹ The following discussion about ring species assumes that species are defined as groups of interbreeding populations.

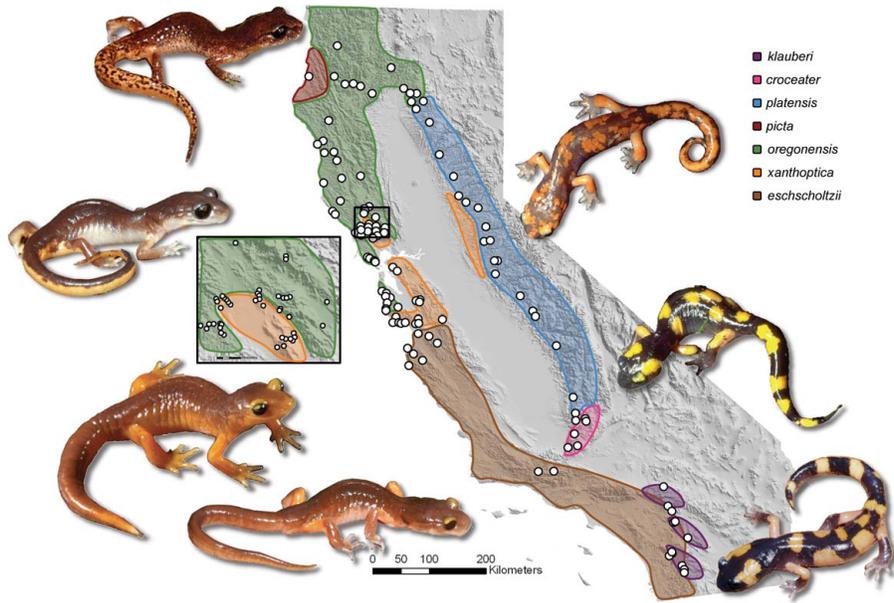


Figure 1.1: Geographic distribution of the ring species *Ensatina eschscholtzii*. From Pereira and Wake (2009, p. 2290).

is as if the subspecies in a ring species were different snapshots of a speciation process (D. Irwin, Bensch, and Price, 2001; D. Irwin and J. Irwin, 2002; Wake, 1997). In the *Ensatina* complex for instance, moving southward is like going forward in time towards increasingly reproductively isolated populations. Thus, a remarkable feature of ring species is that they allow us to indirectly observe how speciation might occur.

According to Hull, essentialism is incompatible with gradual speciation. Because ring species illustrate gradual speciation, they are a suitable test case for Hull's argument. Ring species do not seem to be in agreement with biological essentialism. For as we move southward in the *E. eschscholtzii* ring for instance, we find a chain of intergrading populations. There is no cutoff point that separates the two reproductively isolated populations in southern California from other populations in the ring. Features like genetic distance and color variation gradually build up along the ring (Jackman and Wake, 1994). So the challenge ring

species pose to biological essentialists is to show how gradual divergence, as illustrated by the *Ensatina* complex, is compatible with species-specific essences. Hull's argument implies that essentialists cannot meet this challenge. For him, the evolution of a new species is not marked by the acquisition of a new essence, but by a gradual accumulation of genetic and morphological differences.¹²

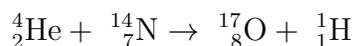
Different from Hull (1965), Sober (1980) thinks that essentialism is compatible with the gradual evolution of species. Sober's argument begins with the observation that the elements in the periodic table can be understood as containing essences, if we take the atomic number of each chemical element as its essence. Sober's reason for thinking that chemical elements

¹² We can distinguish two meanings of the word "gradualism" in the context of evolutionary theory (Ridley, 2004). One of them is that view that complex adaptations (e.g., human eye) evolve by piecemeal steps. The other sense of "gradualism" is *phyletic gradualism*. This type of gradualism contrasts with Eldredge and Gould's punctuated equilibrium theory (Eldredge and Gould, 1972; Gould, 2002). Both phyletic gradualism and the punctuated equilibrium are theories about the evolutionary rates at and between speciation events. For phyletic gradualism the rate of evolution during and after speciation events is much like the same. For the punctuated equilibrium theory, evolutionary change between speciation events is low, whereas speciation events are marked by rapid change. The thesis that adaptations evolve gradually is required for Darwin's theory to be true; phyletic gradualism is not required. Hull's argument is not committed to phyletic gradualism. What is required for his argument to run is the uncontroversial assumption that in evolution the species status is not always clear-cut; i.e., there are populations that are intermediaries between the subspecies and species status. For this reason, the validity of Hull's argument does not depend on the fact of whether punctuated equilibrium is true or not. See Ereshefsky (2001, pp. 96–97) for further discussion.

have essences is described in the quote:

Not only is it the case that all actual samples of nitrogen happen to have atomic number 14; it is necessarily the case that a thing is made of nitrogen if and only if it is made of stuff having atomic number 14. Moreover, this characteristic atomic number plays a central role in explaining other chemical properties of nitrogen (*ibid.*, p. 355).

In short, there are two reasons why Sober thinks that the atomic numbers of chemical elements are essences. First of all, it is not possible to have the same chemical element with different atomic numbers, and different chemical elements must have distinct atomic numbers. Furthermore, the property of ‘having atomic number 14’ explains some of the chemical properties of nitrogen. Sober further argues that chemical elements have essences even if we suppose that the boundaries between chemical elements are not always clear-cut. To motivate this idea, Sober considers the case in which nitrogen transmutes into oxygen, represented by the formula:



Based on this example, Sober raises the question of whether we can identify a point in which the nitrogen nucleus becomes an oxygen nucleus. In response to this question, Sober says:

There *may* be a precise and principled answer to this question which is given by the relevant physical theory. But then again there may not. I would suggest

that which of these outcomes prevails really does not matter to the question of whether essentialism is a correct doctrine concerning the chemical kinds. It may well be that having a particular atomic number is a vague concept (*ibid.*, pp. 357–358).

The point of Sober’s argument is that although nitrogen and oxygen have different essences (i.e., different atomic numbers), we may not be able to draw a sharp line showing when nitrogen transformed into oxygen. By analogy, Sober concludes, the gradual evolution of species is not sufficient to show that species’ essentialism is false.

In response to Sober (1980), Ereshefsky (2001) claims that Sober’s reasoning is not sufficient to show that essentialism is compatible with the gradual evolution of species:

if an entity lacks a specific essence, then essentialists have nothing to appeal to in explaining its nature. If Sober is right that no scientific concept is absolutely precise and consequently some entities have indeterminate essences, then instead of shoring up essentialism he has furthered the case against it (*ibid.*, pp. 97–98).

Sober’s (1980) point against Hull (1965) is that the essentialist can accommodate the gradual evolution of species by allowing cases in which it is indeterminate whether a population contains a certain essence or not. According to Ereshefsky’s (2001) reply to Sober, if the essentialist grants that, then the main rationale for adopting essentialism, explanatory power, is compromised. In allowing a more flexible notion of essences which makes room for cases in which it might be indeterminate whether a taxon has an essence or not, the

essentialist runs the risk of not being able to justify why we need essences after all.¹³

Briefly, Hull (1965) raised the point that essentialism is not compatible with the gradual evolution of species. In response to Hull, by using the transmutation of chemical elements as an example, Sober (1980) argues that biological essentialism is compatible with species gradualism. One potential concern raised by Ereshefsky (2001) is that by allowing cases in which it is indeterminate whether a taxon contains an essence, essentialism might be cut off from its main rationale; viz., to explain shared similarities within a taxon. I will leave this discussion at this point. I return to it in later chapters. My goal in this section is to motivate the idea that the gradual evolution of species puts some strain on the view that biological taxa contain essences. A satisfactory argument for biological essentialism should then be able to address this issue. In the next section, I introduce Sober's (1980) treatment of Mayr's distinction between typological and population thinking and the anti-essentialist argument that stems from this distinction.

¹³ A potential challenge when assessing whether essentialism is compatible with species' vagueness is that the degree of resolution in the application of the notion of species seems to vary depending on the context (cf. Sober (1980) fn. 4, p. 358). As an example, Mayr was interested in studying ring species because he wanted to investigate how species originate (Mayr, 1963). In such a scenario, a notion of species that brings to the fore the different stages in the evolution of a species would be desirable. However, if one is interested in assigning a species name to the *Ensatina* complex, overlooking such intermediary stages in the evolution of species might be desirable.

1.4 Essentialism and population thinking

According to Aristotle, heavy objects in the sublunar sphere tend to be at their ‘natural state’—i.e., at the center of Earth—unless they are subject to ‘interfering forces.’ Sublunar objects are found at different locations because of deviations from their natural state. If there were no interfering forces, all objects would be at the center of the Earth. Aristotle uses a similar type of explanation in his theory of sexual reproduction. According to him, if reproduction occurs without interference, then the offspring will resemble the male parent. These two explanations are instances of the following schema: the kind’s members tend to be in their natural state unless some interfering force is at play. Sober (1980) calls this model of explanation, the *Natural State Model*. Sober describes this model as follows:

If an object is not in its natural state, we know that the object must have been acted on by a force, and we set about finding it. We do this by consulting our catalog of known forces. If none of these is present, we might augment our catalog, or perhaps revise our conception of what the natural state of the system is (*ibid.*, p. 361).

Although the word ‘natural’ has been dropped, Sober (1980) observes that the Natural State Model is a respectable mode of explanation in contemporary science. A modern example is Newton’s law of inertia. According to this law, in an inertial system if there is no force acting upon a particle the value of the particle’s momentum remains constant. In the general theory of relativity, objects move along paths called ‘geodesics’ unless some force acts upon them. In population genetics, according to Hardy-Weinberg principle, the genotype frequencies of a population remain constant unless some disturbing forces occur, such as

non-random mating, selection, mutations, migration, and genetic drift (*ibid.*, pp. 360–361).¹⁴

Sober employs the Natural State Model to spell out what Mayr earlier called *typological thinking* (or essentialism). For Mayr, typological thinking is the view that variation within a species is due to imperfect realizations of a type (Mayr, 1976). Sober’s suggestion is that Mayr’s notion of ‘typological thinking’ is an instance of the Natural State Model. However the Natural State Model (or Mayr’s notion of deviation from a type) does not seem sufficient to characterize what essentialism is. As discussed above, the Hardy-Weinberg principle obeys the Natural State Model, yet this principle is not committed to essentialism. In addition to the Natural State Model, essentialist theories are characterized by the level of organization at which essentialist explanations take place. As I shall discuss below, essentialism explains variation within a group by assigning properties to each *individual* organism rather than populations.

As Mayr puts it, typological thinking contrasts with *population thinking*. Rather than postulating types, population thinking describes evolution in such a way that “[a]ll organisms and organic phenomena are composed of unique features and can be described collectively only in statistical terms” (*ibid.*, p. 28). Mayr illustrates the difference between typological and population thinking by applying them in two contexts. Mayr first looks at how ty-

¹⁴ The Natural State Model also plays a role in some currently held conceptions of health and disease: “[n]otice that our ‘modern’ conceptions of health and disease and our notion of normality as something other than statistical average enshrine Aristotle’s model. We therefore are tempted to make only a conservative criticism of Aristotle’s biology: we preserve the form of model he propounded, but criticize the applications he made of it” (Sober, 1980, p. 363).

ological and population thinking could be used to vindicate the existence of races. The typologist would explain the gaps between races by assigning different essences to each individual member of a race. For the populationist however, the difference between races would be a consequence of the fact that the average phenetic difference between different populations is large enough (Mayr, 1976, 2002). A second example focuses on how the typologist and the populationist would describe selection processes. Under typological thinking, selection would be understood as selection of superior types. In contrast, for a populationist like Darwin, “[e]very individual has thousands or tens of thousands of traits in which it may be under a given set of conditions selectively superior or inferior in comparison with the mean of the population” (Mayr, 1976, p. 29). In sum, typology and population thinking account for variation in different ways. Whereas typologists explain variation by singling out invariant features of individual organisms, the populationist attempts to explain variation in terms of how features are distributed in a population.

A further example illustrating the difference between typological and population thinking is provided by Sober (1980). In this example Sober describes some of the history that led to the population thinking employed by Darwin in the *Origin of Species*. In this example, Sober highlights different interpretations of the law of errors (*ibid.*, p. 365ff.).

The first interpretation of the law of errors discussed by Sober is due to Bernoulli, Laplace, and Laplace. According to them, a discordant set of observations should be interpreted as having one single true value; the inconsistent readings are thought as consequence of interfering forces. This interpretation of the law of errors is an instance of the Natural State Model: in nature there is only one value, but the interfering forces cause the observation to deviate from the right value. The observation is thus thought as the combination of

two factors: what determines the real value plus the interfering forces.¹⁵

Sober thinks that Galton’s work on heredity provided an alternative to the Natural State Model.¹⁶ Galton proposed a theory of inheritance according to which the contribution of an ancestor would be halved in every generation. A person receives one half of its hereditary endowment from his father (the other half from his mother), one fourth from each of his grandparents, and so on (see Mayr, 1982, pp. 784–785). According to Sober, Galton’s work is a “nascent form” of the population thinking used by current evolutionary biologists.¹⁷ In Galton’s work, variation was not understood as a deviation from a type. Instead:

For Galton, variability is *not* to be explained away as the result of interference with a single prototype. Rather, variability within one generation is explained by appeal to variability in the previous generation and to facts about the transmission of variability (Sober, 1980, p. 368).

Galton’s view on heredity is a further example of population thinking. He explained the variation in terms of previous variation in populations—instead of appealing to invariant

¹⁵ Under this interpretation, the theory of errors aims to account for variation in our observations rather than in nature. According to Sober, this situation changed in 1930s with Quetelet’s work. For Quetelet, the inconsistent observations are not due to human mistake, but produced by nature itself. But Quetelet was still committed to the Natural State Model since he held the view that without interfering forces there would be no variation.

¹⁶ Even though Sober thinks that Galton’s work provided an alternative to the Natural State Model, Sober remarks that Galton was sympathetic to the notion of type. See Sober (1980, p. 367ff.).

¹⁷ Like Sober, Mayr also thinks that Galton was relevant for introducing population thinking into biology. See Mayr (1982, p. 47).

features of individual organisms. Whereas the essentialist sees variation as something that has to be explained away, Galton explained diversity in terms of earlier diversity.

So far I have described how Mayr and Sober articulate the distinction between essentialism (or typological thinking) and population thinking. They are two ways of explaining variation. Current evolutionary theory is a case of population thinking rather than essentialism. For Sober, this is sufficient to show that essences do not exist. This conclusion is based on what Sober (1981) calls the *atheistic* principle of parsimony: “*we should hypothesize that an entity does not exist, if its postulation is to no explanatory point*” (ibid., p. 145).¹⁸ In sum, because evolutionary theory discredits the Natural State Model as a model of explanation for organismal variation, Sober concludes that biological essences do not exist.

¹⁸ This principle contrasts with the *agnostic* principle of parsimony according to which an entity should not be postulated if it is not needed to explain anything. If we apply this agnostic principle to Sober’s point that essentialism is not needed in current biology, then we could only be agnostics about the existence of essences (rather than denying its existence). Nonetheless, Sober thinks that we have good reasons to endorse the atheistic principle of parsimony. His argument is based on well-known episodes in history of science: “[o]ne of the advantages which special relativity is supposed to have over Lorentz’s theory is its parsimoniousness with respect to the aether. But this parsimoniousness does not consist in the fact that special relativity is silent on the question of the aether’s existence; rather, the theory implies that there is no such thing. . . . A recent controversy in evolutionary theory exemplifies the same pattern of thinking. We would have a reason to think that group selection does not exist, if every adaptation could be accounted for by way of individual selection alone” (Sober, 1981, p. 145).

Biological essentialism is a particular view about what the explanation of the gaps between species should look like.¹⁹ The gaps between species is explained by the fact that conspecific members share an essence that is not shared by members of other species. Sober's and Mayr's objection is that evolutionary biology can provide an explanation of the variation between species without using the essentialist model of explanation. Thus, if essences are explanatory, then the essentialists have to show why postulating essences is needed. As we shall see in the next chapters, that's exactly what many new essentialists will try to do.

1.5 Summary

In this chapter I motivated the view that kind essentialism is relevant for scientific theorizing. As discussed, kind essentialism seems to be required to infer the properties of unobserved members of a kind from the observed members. For instance, because (double stranded) DNA molecules have the same structure, we can justify Chargaff's rule about the composition of DNA. Biological essentialism applies the same set of intuitions to biological taxa. Nevertheless, some maintain that biological essentialism is incompatible with evolutionary theory. For Hull (1965), essentialism is incompatible with the gradual evolution of species. According to Sober (1980), biological essentialism is untenable because current evolutionary theory does not postulate essences.

Next chapter: My goal with this chapter was to highlight some of the pressing challenges for biological essentialism. These are the challenges that the modern versions of essentialism

¹⁹ Except for Okasha's (2002) essentialism in which essences are not explanatory.

aim to overcome. In the next chapter I introduce a modern version of essentialism according to which the anti-essentialist arguments presented in this section are neutralized if biological essences are defined as ancestor-descendant relationships.

Chapter 2

Historical Essentialism¹

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¹ Much of the content of this chapter was previously published by Pedroso (2012).

The goal of this chapter is to examine a modern version of essentialism articulated by Paul Griffiths (1999) and Joseph LaPorte (2004). According to their view, biological taxa are natural kinds whose essences are ancestor-descendant relations. They thus propose a form of *historical essentialism*. This brand of essentialism contrasts with Hull (1978) and Ghiselin's (1974) view that biological taxa should be thought as *individuals*. Both historical essentialists and the promoters of the individuality thesis agree that the membership conditions for species are fixed by historical relations. Whereas Hull and Ghiselin take that as an argument against the view that biological species are natural kinds with essential features, LaPorte and Griffiths maintain that species' historicity is a reason for thinking that biological taxa are natural kinds with historical essences. So even though they agree that species taxa are historical entities, they hold opposing views about the ontology of species taxa. Griffiths' and LaPorte's reasons for rejecting the individuality thesis are discussed in section 2.1.

The main argument used by LaPorte and Griffiths in favor of historical essentialism is that the dominant school of classification, cladism, defines biological taxa in terms of ancestor-descendant relations. Section 2.2 outlines this argument for historical essentialism; in sections 2.3 and 2.4 I argue that cladism does not support historical essentialism. The main motivation for thinking that cladism justifies historical essentialism is the assumption that cladists define biological taxa in terms of genealogical relations. However, in section 2.3 I point out that an influential group of cladists, *pattern cladists*, do not define biological taxa in terms of genealogical relations but in terms of characters of individual organisms. I use this fact to make the point that citing cladism alone is not sufficient to warrant the

existence of historical essences; historical essentialists must also provide a further argument showing why we should favor *process cladistics*, a version of cladistics that defines biological taxa in terms of genealogical relations. Nevertheless, this is not the only problem historical essentialists face. Historical essentialism has been defined by LaPorte and Griffiths as the view that sharing a certain ancestor is an essential attribute of biological taxa (section 2.2). As I argue in section 2.4, the use of genealogical relations by process cladists does not warrant historical essentialism. As we shall see, process cladism sorts taxa into groups but does not identify which taxon is the most recent common ancestor of a group. For these reasons, historical essentialism is not justified by cladistics, be it pattern or process cladistics.

2.1 Natural kinds and history

One of the objections to the position that biological taxa are natural kinds is that membership in species and higher taxa depends on *history*, and natural kinds cannot be historically delimited (Ghiselin, 1974; Hull, 1978). As Hull and Ghiselin articulate this objection, natural kinds are not historically delimited because their members are not spatiotemporally restricted. For instance, an atom is an instance of the kind gold if it has atomic number 79, independent of its time and location in the universe. However, if we follow Darwin's lead in thinking that classifications of organisms should be genealogical, then the members of a taxon are spatiotemporally restricted: "in the typical case, to *be* a horse one must be *born* of horse" (Hull, 1978, p. 349). As an alternative to the view that biological taxa are natural kinds, Hull and Ghiselin claim that biological taxa should be thought as *individuals*. In short, their insight is that organisms are conspecific not because they necessarily share

a certain property, the taxon's essence, but because they are (spatiotemporally restricted) parts of the same species.²

LaPorte (2004) and Griffiths (1999) find this objection unconvincing. They think that natural kinds are not historical only if we subscribe to the view that kind-essences are intrinsic properties. According to them, natural kinds can be historically delimited and, for this reason, biological taxa can be understood as natural kinds. LaPorte and Griffiths propose a version of essentialism called *historical essentialism*, according to which certain ancestor-descendant relationships are essential features of biological taxa. In their view biological taxa can be natural kinds and, yet, historically delimited.

Nevertheless, showing that natural kinds can be historical is not the only reason LaPorte and Griffiths present in favor of historical essentialism. Most importantly, they think that historical essences address an important issue about biological taxa. They claim that essences explain why organisms belonging to the same taxon tend to share certain features. As an example, consider LaPorte's comment on polar bears:

A lot is explained by an object's being a polar bear. That it is a polar bear explains why it raises cubs as it does, or why it has extremely dense fur, or why it swims long distances through icy water in search of ice floes. . . . The polar bear kind is a useful one for providing significant explanations. It is a natural kind. (LaPorte, 2004, p. 19).

In a similar fashion, Griffiths justifies his appeal to essences on the grounds that generalizations involving taxon names have "counterfactual force":

² See Ereshefsky (2001, 2010b) for further details.

A hierarchical taxonomy based on strict phylogenetic principles will collect more of the correlations between characters, from molecular to behavioral, than any other taxonomy we know how to construct. Such a taxonomy will group organisms into natural kinds because it will predict with considerable force many properties of individuals (Griffiths, 1999, p. 222).

LaPorte and Griffiths assume that it is not a matter of coincidence that members of the same taxon tend to share certain similarities. Instead, they claim that all members of a taxon—past, present, or future—tend to be alike in some respect (e.g., in respect to how they raise their cubs). That’s why modal considerations are relevant to historical essentialists. If historical essences were defined as properties of existing organisms only, then historical essences couldn’t explain why future (and past) members of a taxon tend to be alike. But since historical essences are supposed to be explanatory, they must be construed as properties of any *possible* member of a taxon.

In this chapter, my focus is not whether historical essences have explanatory import. Rather, my goal is to reject the argument LaPorte and Griffiths put forward for the existence of historical essences. Their argument for historical essentialism is introduced in the next section.

2.2 Biological Taxa and Historical Essences

Suppose that in the actual world the same group of organisms is picked out by membership conditions formulated in terms of genealogy (e.g., descent from a common ancestral species) and in terms of certain morphological features. Even though both conditions demarcate the

same group in the actual world, they may yield different groups in nonactual circumstances. In the debate about biological essentialism, the focus is on how membership conditions operate in both actual and nonactual circumstances. For essentialism is a view about what is the defining property of a taxon in *every* circumstance. A central reason nonactual circumstances are relevant for LaPorte and Griffiths is that essential features are supposed to explain why members of the same taxon, be they actual members or not, tend to share certain features. For instance, when LaPorte states that “A lot is explained by an object’s being a polar bear” (LaPorte, 2004, p. 19), he is not referring to existing polar bears only, but to any polar bear that *might* exist. The goal of this section is to introduce LaPorte’s and Griffiths’ views of biological essentialism. I start with LaPorte’s view.

2.2.1 LaPorte’s historical essentialism

A *clade* is a group of organisms containing a single common ancestor and all and only the descendants of that ancestor. For example, the zoologist Kevin de Queiroz defines “Mammalia” as “the clade stemming from the most recent common ancestor of horses and echidnas” (de Queiroz, 1995, p. 224). For de Queiroz, this definition assigns an essential property to the taxon Mammalia:

Just as it is logically necessary for a person to be married (and male) to be a husband, it is logically necessary for an organism to be part of the clade stemming from the most recent common ancestor of horses and echidnas to be a mammal (ibid., p. 224)

De Queiroz uses two taxa, horses and echidnas, to serve as “reference points” in his definition of “Mammalia”. Call these reference points *specifiers*.³ So, given a taxon x and its specifiers, de Queiroz’s notion of historical essence can be stated as follows:

(QU) It’s necessary that, for all y , y is a member of the taxon x if and only if y descends from the most recent common ancestor of the specifiers of x .⁴

In a paper criticizing de Queiroz’s (1992) view on taxon definitions, Ghiselin (1995) makes the following remark:

As to counter-to-fact conditionals, it should be evident that the clade being named was the same clade that exists now, before the parts that are enumerated came into existence, and that it would be the same clade even if history had been somewhat different (*ibid.*, p. 221).

When applied to the taxon Mammalia, Ghiselin’s remark implies that it is contingent, not necessary, that Mammalia ever gave rise to horses and echidnas. Thus, if Ghiselin is correct, then biological taxa do not contain historical essences as defined by de Queiroz (i.e., (QU)).

LaPorte (2004) proposes a version of historical essentialism that takes into consideration Ghiselin’s aforementioned remark. LaPorte’s argument comprises two premises: (1) biological taxa are clades; and (2) clades have historical essences. In favor of (1), LaPorte

³ See Sereno (2005) for a discussion about specifiers.

⁴ This definition depends on the identity of the specifiers (i.e., horses and echidnas). For this reason, one might object that this definition is satisfactory only if the identity conditions of the specifiers are specified. De Queiroz’ definition has been criticized for not providing such identity conditions. See Nixon and Carpenter (2000, pp. 299–300) for an example.

claims that “[c]ladists, who belong to the increasingly dominant cladistic school of systematics, identify higher taxa, like Mammalia (the mammals), Aves (the birds), or Serpentes (the snakes), with clades” (*ibid.*, p. 11). In brief, LaPorte’s argument for (1) is that practicing systematists endorse (1). Now I turn to LaPorte’s justification for (2).⁵

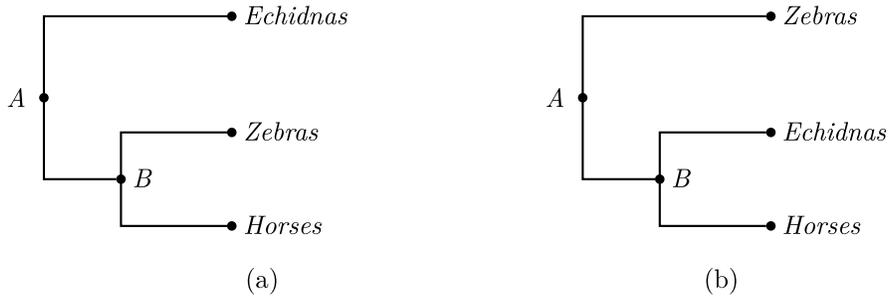
LaPorte’s (2004) formulation of the notion of historical essence is similar to de Queiroz’s (1992; 1995). However, in order to deal with Ghiselin’s remark, LaPorte adopts the following maneuver:

To make the essentialist lesson clear, I propose to *name* that group that happens, as a matter of contingent fact, to be the most recent ancestor common to both the horse and echidna. I give it the name ‘*G*.’ A cataclysm could have wiped out *G* before it ever gave rise to the horse or the echidna. But although it is contingent, not necessary, that *G* gave rise to the horse and the echidna, it is *necessary* that any organism belonging to the clade Mammalia be descendent from *G*, and that any organism belonging to the clade Mammalia be descended from *G* (LaPorte, 2004, p. 12).

LaPorte’s idea is that the specifiers of Mammalia (i.e. horses and echidnas) do not have to be necessarily the same. Rather, the invariant feature of Mammalia is the property of having *G* as the most recent ancestor. For LaPorte the specifiers are only necessary to fix the most recent ancestor of Mammalia in the actual world. Thus, LaPorte agrees with Ghiselin that it

⁵ My goal of this section is to only present LaPorte’s argument for historical essentialism without assessing it. The discussion about the validity of his argument is postponed until sections 2.3 and 2.4.

Figure 2.1: Trees depicting different phylogenetic relations for the same taxa.



is a contingent matter that Mammalia gave rise to horse and echidnas. However, as opposed to Ghiselin, LaPorte insists that Mammalia contains an essential feature. In this way, given a clade x where G is the most recent common ancestor of the specifiers of x in the actual world, LaPorte’s notion of historical essence can be described as follows:

(LP) It’s necessary that, for all y , y is a member of x if and only if y descends from G .

In order to illustrate the difference between de Queiroz and LaPorte’s notion of historical essence, consider two counterfactual situations represented by the trees in Figure 2.1. Suppose that the ancestral taxa A and B are distinct. Using de Queiroz’s definition of the taxon Mammalia, Mammalia represents the clade “ $A + B + Echidnas + Zebras + Horses$ ” on the tree (a), but the clade “ $B + Echidnas + Horses$ ” on the tree (b). However, according to LaPorte’s definition, these two groups identified by de Queiroz’s definition cannot be the same taxon Mammalia, because they have different most recent common ancestors in these two trees: A on the tree (a) and B on the tree (b). For de Queiroz we pick whatever the most recent common ancestor of the specifiers is in a particular possible world: A on the tree (a), B on the tree (b). In contrast, for LaPorte, we pick the most recent common ancestor of Mammalia in the actual world and then use this ancestry as an essential feature

of Mammalia in nonactual circumstances.

2.2.2 Griffiths' historical essentialism

According to Griffiths (1999), biological taxa contain historical essences because they are defined by relations of common ancestry. He illustrates his view with the following example:

Nothing that does not share *the historical origin* of the kind can be a member of the kind. Although Lilith might not have been a domestic cat, as a domestic cat she is necessarily a member of the genealogical nexus between the speciation event in which that taxon originated and the speciation event at which it will cease to exist. It is not possible to be a domestic cat without being in that genealogical nexus (*ibid.*, 219, emphasis added).

From the above quote, we can extract the view that biological taxa contain historical essences in the sense that all the members of a taxon must share the same “historical origin”. The above quote thus suggests that sharing the same “historical origin” is an essential feature of biological taxa.

Griffiths' formulation of historical essence appeals to the notion of “historical origin”. Griffiths thinks that “historical origin” should be understood according to cladism: “[i]t is not possible to be a domestic cat without being in that genealogical nexus. Furthermore, *cladistic taxa and parts and processes defined by evolutionary homology have no other essential properties*” (Griffiths, 1999, 219, emphasis added). In another quote, Griffiths says:

The fundamental kinds of the physical sciences . . . have their properties because of their internal microstructure. But biological taxa, the other classic example

of natural kinds, have their causal homeostasis guaranteed quite differently. The most successful attempt to date to sort organisms into kinds which represent rich clusters of properties that can be relied upon to hold up in unobserved instances *is phylogenetic systematics . . . A cladistic classification of an organism or part allows reliable inferences about its structure, development, and behavior* (Griffiths, 1996, p. S5, emphasis added).

Thus, for Griffiths, sharing the same “historical origin” is an essential attribute of biological taxa.⁶ Moreover, by using cladistics, Griffiths thinks that we can define “historical origin” in terms of common ancestry. In the following section I compare Griffiths’ view with LaPorte’s view of historical essences.

2.2.3 Griffiths and LaPorte on historical essences

Both LaPorte and Griffiths claim that common ancestry (as understood by cladists) is an essential feature of biological taxa.⁷ Moreover, they use the same line of argument for his-

⁶ One might point out that even though Griffiths occasionally makes claims containing modal locutions (as in the quoted passages), the whole modal business may well be less important to him than it is for LaPorte. Nonetheless, as discussed in the Introduction, Griffiths uses his theory about natural kinds to explain why certain generalizations about biological taxa have “counterfactual force”. For this reason, in addition to the passages I quoted, there is further evidence that Griffiths is concerned with nonactual circumstances.

⁷ With respect to species taxa, LaPorte and Griffiths agree that sharing the same “historical origin” is at least part of the essence of species taxa. In particular, Griffiths states that, unlike higher taxa, species essences contain properties other than “belonging to a certain genealogical nexus”: “Taxa at the species level have rather more complex essences, because

torical essentialism; namely that historical essentialism is true because of how the dominant school of classification, the cladistic school, defines biological taxa.⁸ This argument for historical essentialism can be formulated as a *modus ponens*: **(1)** if cladistically defined taxa satisfy (LP), then historical essentialism is true; **(2)** cladistically defined taxa satisfy (LP); therefore, **(3)** historical essentialism is true. A potential argument against historical essentialism can question the premise (1)—one might deny that scientific theories can count as evidence for essentialism for instance (see e.g. Mellor, 1977). This is *not* the type of argument I develop in this chapter. Instead of rejecting (1), my goal is to show that the premise (2) is false; in my view, cladistics does not support the claim that sharing a *particular* most recent common ancestor is a defining feature of biological taxa.

in their case these genealogical forces are supplemented by factors such as gene flow, selection, and developmental canalization” (Griffiths, 1996, p. S5). LaPorte thinks that a reasoning similar to the one applied to higher taxa can be applied to species taxa as well: “Mammalia and Aves are higher-level groups that contain many species. Similar reasoning reveals that *species* have essential properties on standard historical conceptions. Species, such as the horse species *Equus caballus* or the ostrich species *Struthio camellus*, necessarily stem from their ancestral groups just as clades do, though a species differs from a clade in that its descendants do not all have to belong to it” (LaPorte, 2004, p. 12).

⁸ Using scientific theories to back up essentialist theories is a commonplace in contemporary philosophy. Kripke (1980) and Putnam (1975) proposed this sort of argument to defend essentialism about natural kinds. In addition to LaPorte and Griffiths, other philosophers of biology such as Okasha (2002) and Wilson, Barker, and Brigandt (2007) appeal to current biology to defend different versions of essentialism about biological taxa.

2.3 Argument 1: process and pattern cladistics

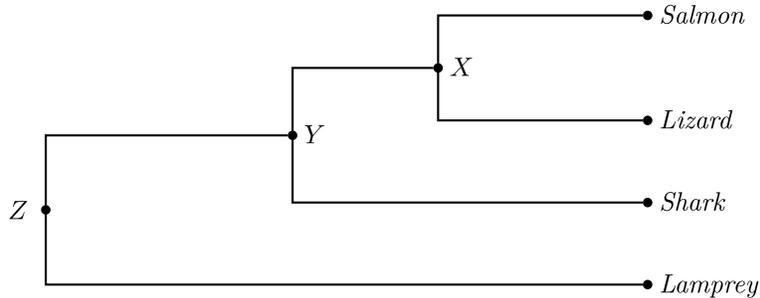
In this section I distinguish two schools within cladistics: process cladism (subsection 2.3.1) and pattern cladism (subsection 2.3.2). Griffiths (1999) and LaPorte (2004) appeal to cladistics in order to justify their claim that biological taxa have historical essences. However, I will argue in this section (subsection 2.3.3) that pattern cladistics does not support historical essentialism. Hence, citing cladism alone does not justify historical essentialism. Cladism supports historical essentialism only if an additional premise is provided, namely that we have sufficient reason to accept process cladism and reject pattern cladism. However, as I argue in the next section (section 2.4), even if such an additional premise is provided, cladistics still does not support historical essentialism. But first we must give some background information concerning cladism.

2.3.1 Hennig's System

In order to describe his system of classification, Hennig (1966) distinguishes the following groups, based on their ancestry and descent (these examples are illustrated in Figure 2.2):

- A *monophyletic group* contains the common ancestor and all of its descendants. Examples: Vertebrata (Z + Y + X + lamprey + shark + salmon + lizard); Gnathostomata (Y + X + shark + salmon + lizard); and Osteichthyes (X + salmon + lizard).
- A *paraphyletic group* contains the common ancestor and some—but not all—of its descendants. Example: Pisces or “fishes” (Y + shark + salmon).
- A *polyphyletic group* contains some of the descendants of a common ancestor but not

Figure 2.2: A tree depicting the ancestral-descendant relations between different taxa. The letters “X”, “Y”, and “Z” represent hypothetical ancestors of the terminal taxa. Adapted from Kitching et al. (1998, p. 11).



the common ancestor itself. Example: lamprey + salmon.

According to Hennig (1966), every higher taxon must be monophyletic. This supposition is a distinguishing feature of Hennig’s system in relation to other schools of taxonomy. Different from pheneticists such as Sokal and Sneath (1963), Hennig does not accept overall similarity as a criterion for delimiting biological taxa. And in contrast to evolutionary taxonomists such as Mayr (1969), Hennig does not allow paraphyletic groups—e.g. fishes in Fig. 2.2 (Y + shark + salmon).⁹

Monophyletic groups are discovered via analysis of characters. The characters used in cladistic analysis should be translated into discrete characters (e.g. “DNA sequences”)—as opposed to characters that vary continuously (e.g. “leaf length”).¹⁰ Each character in

⁹ For further details about the different schools of taxonomy, see Ereshefsky (2001, ch. 2), Hull (2001), and Schuh (2000, ch. 1).

¹⁰ The statement that “cladistics only use character with discrete variation” is a simplification. Discrete characters can be expressed in terms of characters that vary continuously. For example, the discrete state “leaves ovoid” can be described in the terms of a character varying continuously, the distance from the base to the widest point on the leaf (see

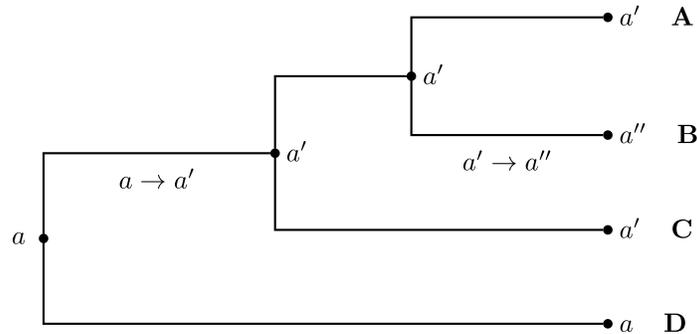
cladistic analysis has exclusive “states”. For instance, the character “mode of reproduction” has the states “viviparity” and “oviparity”.¹¹ However, not every character provides reliable evidence for inferring phylogenetic relations. For instance, if we consider a group containing a limpet, a barnacle, and a crab, even though barnacles and limpets look alike, the barnacle shares a more recent common ancestor with the crab than it does with limpets (Ridley, 1986, p. 4).

We should distinguish two types of character states: *plesiomorphies* are character states that are present in the common ancestor of the group of species under study; *apomorphies* are character states that evolved after the common ancestor, within the group of species under study. Apomorphies can be *autapomorphic* (unique to one group) or *synapomorphic* (shared between two or more groups). Consider the tree depicted in Fig. 2.3. For this tree, even though a' is a character state shared by the taxa A and C, this state does not imply that A and C share a more recent ancestor not shared by B. The situation is different when we consider the terminal taxa A, C, and D. In this case, because the character a' is an apomorphic (or derived) state present in A and C whereas D contains the plesiomorphic (or ancestral) state a , there is evidence that A and C share a more recent ancestor not shared by D.

Stevens, 1991; Thiele, 1993). For further details about character analysis in cladistics, see Kitching et al. (1998, ch. 2) and Schuh (2000, ch. 5).

¹¹ Hennig (1966) did not draw the distinction between character and states. This distinction only appeared with the rise of numerical approaches to taxonomy, in the middle of the 20th century (Freudenstein, 2005).

Figure 2.3: A tree representing the phylogenetic relations between the terminal taxa A, B, C, and D. The lower case letters a , a' and a'' represent character states. The expression “ $x \rightarrow y$ ” represents a change in the character states among the members of the lineage from x to y .



It should be noted that the distinction between plesiomorphies and apomorphies is meaningless if we don't specify the group of biological taxa under study. In a group of two taxa, the distinction between ancestral (or plesiomorphic) and derived (or apomorphic) character states does not occur. The distinction between derived and ancestral character states requires at least three taxa. Furthermore, a character state can be derived or ancestral depending on the taxa considered. For instance, in Fig. 2.3, the character state a' is ancestral if we are studying the phylogeny of A, B, and C, but derived if we are studying the terminal taxa A, C, and D.

2.3.2 Cladistics after Hennig

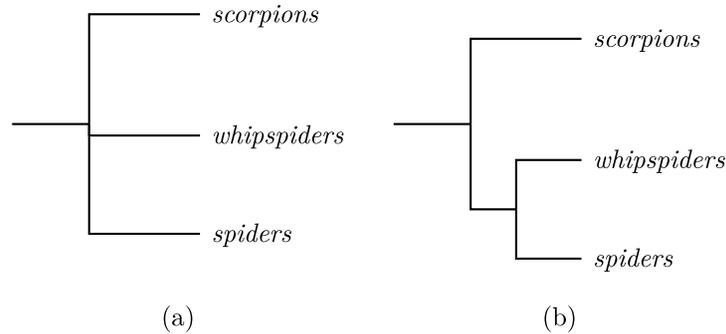
Some cladists after Hennig have argued that not only is the assumption of evolution unnecessary for justifying cladistic methods, but cladistics would be better off if formulated independently of evolutionary theory (Brower, 2000; Nelson and Platnick, 1981; Platnick, 1979, 1982, 1985). In this way of understanding cladistics, systematics is supposed to pro-

vide evidence for evolution—rather than the opposite. This version of cladistics is usually referred as “pattern cladistics”—as opposed to “process cladistics” which includes Hennig and others sharing the assumption that evolution is necessary to justify cladistics.

An important motivation for pattern cladistics is the idea that the evolutionary models used to justify cladistics involve contentious claims (cf. Beatty, 1982; Platnick, 1985, p. 90). For example, Hennig subscribed to the view that dichotomous trees (i.e., each node in a tree can only give rise to two line segments) should be favored, instead of trees with more than two branches. In some passages, Hennig seems to justify this methodology by appealing to a specific speciation model, according to which speciation events only happen via splitting of an ancestral species into two new species (Hennig, 1966, pp. 207–11).¹² For Platnick (1979), this speciation model has the following nontrivial consequences: (i) there is no speciation without splitting; and (ii) species become extinct at branching points. Both (i) and (ii) are contentious claims in evolutionary theory. (i) is inconsistent with theories of speciation in which speciation may occur: (a) via gradual change in a single lineage (or anagenesis); and (b) by hybridization. With respect to (ii), it excludes the possibility of an ancestral species surviving past a speciation event (Wiley, 1981, p. 105). According to pattern cladistics, if the methods of cladistics can be justified without appealing to a specific model of speciation, then cladistics becomes compatible with different theories about speciation. So, if pattern cladistics is adopted, then one cannot reject cladistic methods because it appeals to faulty

¹² Hennig himself is not entirely clear about his view on this issue. For Hennig also suggests that the use of dichotomous trees in cladistics is just a “methodological principle”—instead of being an empirical claim. For a discussion about Hennig’s view about the principle of dichotomy, see Rieppel (2010).

Figure 2.4: Examples of a trichotomous (a) and dichotomous (b) tree. From Platnick (1979, p. 540).



models of evolution.

Alternatively Platnick (1979) proposes a justification for Hennig's commitment to dichotomous trees without relying on any theory about speciation. For Platnick (1979, 1985) dichotomous trees should be favored not because of any assumption about evolution, but because dichotomous trees contain higher information content. In order to show this, Platnick (1979) considers an example of a dichotomous and a trichotomous tree for the same terminal taxa, drawn in Fig. 2.4. The trichotomous tree in Fig. 2.4a predicts that, if we take a sample of the terminal taxa, then we will find the presence of: 1. apomorphies shared by all three terminal taxa; and 2. characters unique to each terminal taxon (i.e., autapomorphies). In addition to 1. and 2., the dichotomous tree in Fig. 2.4b also predicts the presence of: 3. synapomorphies only shared by whipspiders and spiders.

Based on this difference between the trees in Fig. 2.4a and Fig. 2.4b, Platnick argues that dichotomous trees are preferable to trichotomous trees because they allow us to test an additional hypothesis (i.e., 3.).¹³ No specific theory of speciation is therefore necessary to

¹³ Following Popper (1968), Platnick (1979) assumes, conjectures with more empirical con-

justify the preference for dichotomous trees.

2.3.3 Pattern cladistics and historical essences

Promoters of pattern cladistics have proposed non-evolutionary explanations for other methodological assumptions adopted by Hennig (1966), such as the *principle of parsimony* as used in cladistics. The principle of parsimony is a method of phylogenetic inference according to which, given a set of phylogenetic hypotheses about a group of taxa, we should favor the hypothesis that requires the fewest changes in character state. Brower claims that parsimony is justified not because of evolutionary reasons, but simply because the use of this principle provides “the simplest theoretical framework necessary and sufficient to account for the data” (Brower, 2000, p. 144). Brower’s view is that the principle of parsimony is a general principle in science and, accordingly, it does not require an evolutionary explanation.

As opposed to pattern cladists, process cladists follow Hennig and justify cladistic methods using evolutionary history. For instance, Ridley (1986) thinks that parsimony is justified because evolutionary change is relatively improbable.¹⁴ Wiley (1979, 1981) argues

tent (or, more falsifiable) are preferable to conjectures with less empirical content. This assumption is crucial in Platnick’s argument: if less falsifiable conjectures can be more preferable, then Platnick’s conclusion (i.e. dichotomous trees are preferable to trichotomous trees) would not follow from his argument. For a general discussion of the different uses of Popper’s views in evolutionary theory and cladistics, see Hull (1999) and Sober (1988).

¹⁴ In more detail, Ridley’s point is that:

It is unlikely enough that all the mutations should arise and be selected for in

that cladistic analysis should contain evolutionary information but, different from Hennig (1966), he grants that the trees obtained from cladistic analysis may exhibit trichotomous branching—e.g. the case in which a lineage is dichotomized but the ancestral species survives the speciation event (Wiley, 1981, p. 105). The question of whether evolution should rely on evolutionary theory is still an ongoing debate (e.g. Brower, 2000; Kluge, 1997, 2001; Scotland, 2000). My intention in highlighting this dispute is not to provide an answer to this question but to make the point that not every cladist appeals to genealogy when defining biological taxa.

As discussed in section 2.3.1, Hennig’s definition of monophyly is *genealogical*: a monophyletic group contains the common ancestor and all of its descendants. However, as discussed above, pattern cladists do not think that the branching diagrams obtained from cladistic analysis, cladograms, are depictions of evolutionary history. Instead, cladograms are simply summaries of character distribution, devoid of any genealogical information. As an alternative to a genealogical definition of monophyly, pattern cladists hold that biological taxa should be defined in terms of characters (Baum and Donoghue, 1995). An example of

one species, but that similar events should take place independently in another is even more improbable. Shared characters are therefore more likely to be due to common ancestry than to convergence. The eye shared by humans and chimps is less likely to be convergent than described from a common ancestor (Ridley, 1986, p. 82).

However, the view that parsimony is justified because homoplasies (shared characteristics due to independent evolution) are rare has been strongly criticized. See Sober (1988, 2004) for further details.

a character-based definition of monophyly is provided by Farris (1974): a group is monophyletic if its group membership character appears uniquely derived and unreversed.¹⁵ Thus, although both process and pattern cladistics use apomorphies to diagnose monophyletic groups, *only process cladistics defines biological taxa in terms of genealogical relations*. This contrast between process and pattern cladistics brings to the fore an important limitation of the aforementioned argument for historical essentialism; i.e., that historical essentialism is justified given how cladists define biological taxa.

Arguments that appeal to consensus of a group—like the cladistic school—are convincing only if there is evidence of such a consensus. As discussed above, an important group of cladists, the pattern cladists, define taxa in terms of characters instead of genealogy. Thus to argue for historical essentialism based on cladistics falsely assumes that cladists for the most part define biological taxa in terms of evolutionary history. Hence, if cladistics supports historical essentialism, then additional premises must be provided: that process cladism is right and that pattern cladism is wrong.¹⁶

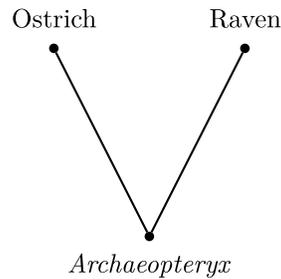
¹⁵ Given a character with states 0 (ancestral) and 1 (derived), a group membership character is reversed when it transformed from state 1 to 0. For further details, see Platnick (1977).

¹⁶ One potential concern with my argument of this section is that, even though historical essentialism is a view of nonactual circumstances, my argument is not premised on modal considerations. That might raise the suspicion that my argument is not properly addressing historical essentialism. However, despite the fact that the conclusion of LaPorte and Griffiths' argument is a modal claim (i.e., biological taxa contain historical essences), not every premise in their argument is a statement about nonactual circumstances. As discussed earlier, one of the premises in their argument is an assumption about how cladists define biological taxa and that's the premise I'm targeting at in this section.

However, one may object, pattern cladists can define biological taxa without relying on genealogical relations, but still believe that common ancestry is an essential attribute of biological taxa. I agree that this might be the case; pattern cladists could be historical essentialists. But I think this objection misses the point of my argument. My point is not about whether pattern cladistics is *consistent* with historical essentialism; rather, my thesis is that an important form of cladism, pattern cladism, does not *justify* historical essentialism. Hence, if cladistics justifies historical essentialism, then only process cladism can perform such a role.

One might also object that LaPorte and Griffiths have process cladism in mind when they appeal to cladism to justify historical essentialism. For this reason, the objection continues, my point that pattern cladistics doesn't justify historical essentialism is irrelevant to the discussion about historical essences. I find this objection unsatisfactory because, even if LaPorte and Griffiths refer to process cladism in their argument (or any other version of cladism), this does not exempt them from showing why the chosen version of cladism is better off than pattern cladism when defining biological taxa—mainly when we take into consideration that pattern cladistics is a prominent view in current systematics. For their defense of historical essentialism is not presented as being conditioned upon process cladistics being correct. Nevertheless, even if historical essentialists can justify why they favor process cladistics, in the next section I argue that cladistics (be it pattern or process cladistics) provides an inadequate justification for historical essentialism.

Figure 2.5: A tree representing the ancestor-descendant relations between *Archaeopteryx*, ostrich, and raven. From Kitching et al. (1998, p. 12).



2.4 Argument 2: monophyly and historical essences

Suppose there is a clade, the clade Aves, containing the taxa *Archaeopteryx*, ostrich and raven, as drawn in Fig. 2.5. So, in the actual world, *Archaeopteryx* is the most recent ancestor of the clade Aves. According to historical essentialism, *Archaeopteryx* should be the most recent ancestor of Aves in *nonactual* worlds as well. As LaPorte states it, if *A* is the (actual) stem of Aves (i.e., a species of *Archaeopteryx*), then “The relevant clade [Aves] includes, in any possible world, all and only the organisms in and descended from species *A*” (LaPorte, 2004, p. 12). Thus, what is controversial about historical essentialism is not that *Archaeopteryx* is the most recent ancestor of Aves in the actual world (that’s taken for granted in our Aves example). Rather, the controversial bit is the claim that *Archaeopteryx* is also the most recent ancestor in nonactual worlds. The goal of this section is to assess this controversial claim.

For historical essentialists Aves has *Archaeopteryx* as its most recent ancestor in nonactual worlds because of how cladists define Aves. As discussed, cladists define biological taxa as monophyletic groups. Thereby, the argument for historical essences in Aves comprises two premises: that in the actual world, *Archaeopteryx* is the most recent ancestor of Aves; and

that in every possible world that Aves exists, Aves is a monophyletic group. I shall argue that this line of reasoning is not valid. Both premises can be true and, yet, *Archaeopteryx* may not be the most recent ancestor of Aves in a nonactual world. To define Aves as a monophyletic group is not sufficient to guarantee that Aves has the same most recent ancestor in nonactual worlds as it does in the actual world.

The argument for historical essences depends on how we define “monophyly”. Like Hennig, one might define what a monophyletic group is genealogically: monophyletic groups contain a common ancestor and all of its descendants. According to this way of defining monophyletic groups, apomorphies are used as *evidence* rather than a *definition* of monophyletic groups. Alternatively, like Farris (1974), one might define monophyletic groups in terms of apomorphies (cf. Baum and Donoghue, 1995). Accordingly, there are two ways one can interpret the argument for historical essentialism depending on the definition of monophyletic groups one chooses. In what follows, I show that the argument for historical essences fails in both ways of defining monophyletic groups.¹⁷ I begin considering the definition of

¹⁷ Earlier I argued that the argument for historical essences can only take off if process cladistics is right and pattern cladistics is wrong. Based on that, one might object that once we embrace process cladistics then there is no motivation for defining monophyletic groups in terms of characters. For this reason, the objection continues, the only way historical essentialists can define monophyletic groups is in terms of genealogy—which makes the definition of monophyly in terms of characters irrelevant to my argument. However, considering both ways of defining monophyletic groups is relevant because that makes my two arguments against historical essentialism independent from each other. That leaves room for someone to find my first argument unconvincing but, still, accept the argument from this section.

monophyletic groups in terms of apomorphies.

According to the argument for historical essentialism, because Aves is a monophyletic group, the most recent common ancestor of Aves in nonactual worlds is also *Archaeopteryx*. In fact, to know that ostrich, raven and *Archaeopteryx* form a monophyletic group in a nonactual world gives us the information that they all share *a* more recent common ancestor in that world. However, I shall argue, because apomorphies are not sufficient to single out the most recent common ancestor, we do not know what is *the* most recent common ancestor. Accordingly, apomorphies alone cannot guarantee that Aves has *Archaeopteryx* as its most recent common ancestor in nonactual worlds. The fact that Aves shares certain apomorphies is compatible with ostrich being the most recent common ancestor, for instance. Here is my reason why apomorphies do not single out *Archaeopteryx* as an ancestral taxon in nonactual worlds. In order to determine whether *Archaeopteryx* is the common ancestor of the clade by using characters, *Archaeopteryx* must have a feature not shared by the other two taxa (i.e. ostrich and raven).¹⁸ Thus there are two ways a historical essentialist might try to argue that *Archaeopteryx* is the common ancestor of the clade Aves by utilizing apomorphies: (I) there is a synapomorphy shared by ostrich + raven but absent from *Archaeopteryx*; and (II) *Archaeopteryx* contains an autapomorphy, a character not shared by the group ostrich + raven. However, neither (I) nor (II) provide evidence for the claim that *Archaeopteryx* is the common ancestor of the clade.

Concerning (I), ostrich + raven contain the synapomorphy of having a pygostyle (the bone

¹⁸ The following discussion is based on Kitching et al. (1998, pp. 12–14) comments about the clade depicted in Fig. 2.5.

where the tail feathers attach) not shared by *Archaeopteryx*. Nevertheless, there are many animals that do not have a pygostyle such as humans. The property of not having a pygostyle then fails to show that *Archaeopteryx* is the common ancestor of the clade. Regarding (II), even if *Archaeopteryx* possesses an autapomorphy, this does not imply that *Archaeopteryx* is the ancestral group of the clade. For there is no connection between possessing an autapomorphy and appearing earlier in time. For instance, the autapomorphies unique to *Homo sapiens* do not make humans the ancestral species of other taxa in the Hominidae. Therefore, even though apomorphies provide membership conditions for a monophyletic group, they do not distinguish which taxon is the most recent ancestor of the clade.¹⁹

Now consider the definition of monophyletic groups in terms of genealogy (i.e., monophyletic groups contain a common ancestor and all of its descendants). Once again, the historical essentialist faces the same problem: the assumption that Aves is a clade in every possible world it exists tells us that the members of Aves all descend from *a* common ancestor without specifying which taxon is *the* most recent common ancestor. Aves can be a clade and, yet, *Archaeopteryx* in particular may not be most recent ancestor of Aves. In order to show why that's the case, consider the distinction between *cladograms* and *phylogenetic trees*.

Cladograms are used to represent hypotheses about monophyletic groups; and cladograms display taxa at their tips only. Phylogenetic trees are representations of ancestor-descendant relationships and their internal nodes stand for biological taxa. For instance, the cladogram

¹⁹ For further references about the impossibility of using apomorphies to identify ancestral taxa see: Engelmann and Wiley (1977), Wiley (1981, pp. 105–107), Kitching et al. (1998, pp. 13–14), and Schuh (2000, pp. 84–86).

Figure 2.6: A cladogram expressing the relation among the taxa A, B, and C.

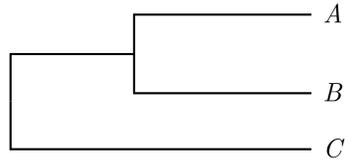
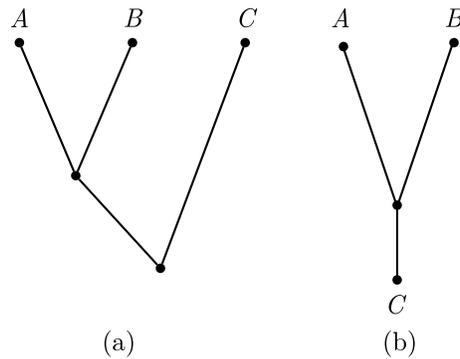


Figure 2.7: Phylogenetic trees expressing different ancestor-descendant relationships among the taxa A, B, and C. From Sober (1988, p. 23).



in Fig. 2.6 tells us that the taxa A and B belong to a clade that does not contain C. However, different ancestor-descendant relationships are consistent with the cladogram in Fig 2.6. Some of these ancestor-descendant relationships are depicted by the phylogenetic trees in Fig. 2.7. According to Fig. 2.7a, the common ancestor of A and B is not an ancestor of C; in Fig. 2.7b, C is an ancestor for both A and B. Even though these two phylogenetic trees represent different ancestor-descendant relationships, they are both compatible with the cladogram in Fig 2.6.²⁰

A way of describing the difference in information content between cladograms and phylogenetic trees is via the contrast between *sister-group* and *ancestor-descendant* relations. To

²⁰ For further details about the relation between cladograms and phylogenetic trees, see Sober (1988), 21–25.

establish that *Archaeopteryx* belongs to a clade containing ostrich + raven only shows that *Archaeopteryx* shares a more recent ancestor with the group ostrich + raven than to a third group.²¹ Otherwise stated, *Archaeopteryx* and ostrich + raven are sister-groups. Nothing is said about whether *Archaeopteryx* is the common ancestor of the remaining taxa of the clade. The idea here is that the sister-group relation is collateral, not ancestral-descendant (Hull, 2001, pp. 223–24). Thus, instead of specifying ancestral-descendant relations, cladograms only supply sister-group relations.

The difference between cladograms and phylogenetic trees is important for us because hypotheses about monophyletic groups give us cladograms, not phylogenetic trees. But, as discussed above, cladograms don't specify which taxon *in particular* is the most recent ancestor of Aves. From a cladogram representing the clade Aves, we cannot extract the information that *Archaeopteryx* is the most recent ancestor of Aves. In contrast, historical essences specify what is *the* most recent common ancestor of Aves. Hence, to understand monophyly in genealogical terms does not vindicate the existence of historical essences. Moreover, as I argued previously, we get an analogous result if we consider the set of apomorphies that the members of Aves share. Apomorphies alone do not contain any information about which taxon is the common ancestor of Aves. So, no matter if monophyletic groups are defined in terms of characters or in term of genealogy, Aves can be monophyletic groups in every possible world without possessing historical essences.

²¹ As observed by Sober, “Judgments of monophyly are *contrastive*: two items belong to a monophyletic group only in contrast to a third one that does not” (*ibid.*, p. 19).

2.5 Summary

In Griffiths (1999) and LaPorte (2004) we find the claim that cladism supports historical essentialism. Given that cladistics is the dominant school in taxonomy, this seems to be a powerful argument for historical essentialism. In this chapter, however, I presented two reasons showing why cladistics does not justify historical essentialism: (1) arguments that appeal to a consensus of experts are convincing only if such a consensus in fact exists. I argued that the consensus necessary to warrant historical essentialism among cladists is absent (sec. 2.3); (2) cladistic definitions do not specify which taxon is the most recent ancestor of a clade. So cladism does not identify the historical essence of a taxon. Consequently cladism does not offer a justification for historical essences (sec. 2.4). If sound, these two arguments show that historical essentialism, as proposed by Griffiths (1999) and LaPorte (2004), is unjustified.

Next chapter: LaPorte and Griffith's historical essentialism was supposed to be a replacement for intrinsic essentialism. But now this form of essentialism is cast into doubt. In the next chapter I examine another type of argument for historical essences. This argument was suggested by Sober (1980). According to him, Kripke's argument for origin essentialism could be extended to biological species. The goal of the next chapter is to examine whether Sober is correct in thinking that such an extension is plausible.

Chapter 3

Origin essentialism

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Kripke’s (1980) origin essentialism is the view that an individual could not have had a different origin from the one it actually had. The connection between Kripke’s origin essentialism and philosophy of biology is largely due to Hull and Ghiselin’s species-as-individuals

thesis (Ghiselin, 1974; Hull, 1978). According to Hull and Ghiselin, species such as humans and Indian rhinos are *individuals* rather than natural kinds. But if species are individuals, then we might apply Kripke's (1980) argument for origin essentialism to biological species. This suggestion was made in Sober (1980). However, Sober does not pursue this suggestion any further. The goal of this chapter is to challenge Sober's suggestion that species have Kripkean origin essences.¹

Origin essentialism is a debated topic in contemporary metaphysics (see e.g., Forbes, 1985; Hawthorne and Gendler, 2000; Robertson, 1998; Salmon, 2005). However, an examination of whether origin essentialism applies to species taxa has not received much attention in the literature. Yet if Kripke's argument for origin essentialism applies to species taxa, key issues in philosophy of biology could be advanced. Such issues include whether biological species contain essential features, the membership conditions for species, and the historical nature of species. Nonetheless, it is not obvious that Kripke's argument applies to species taxa. Arguments for origin essentialism typically concentrate on individual organisms and artifacts (e.g., chairs and tables) rather than biological species. Hence, if origin essentialism is true about species, then an additional argument must be provided. More precisely, it should be shown that premises true about individual organisms and artifacts are also true about biological species.

The first challenge with extending Kripke's argument to biological species is that Kripke's original argument fails to derive origin essentialism (section 3.2). Nathan Salmon (2005) pro-

¹ More recently, Neil Williams (2011) has also suggested that we might be able to apply Kripke's argument for origin essentialism to species (if thought as individuals) but, like Sober, he does not follow up on it.

poses an influential reformulation of Kripke's argument. My discussion of origin essentialism will be mostly based on Salmon's reformulation of Kripke's argument. Arguments for origin essentialism hinge on assumptions on how artifacts (e.g., tables) or individual organisms come into existence from their origins (e.g., from a hunk of wood in the case of tables; from sperm and egg in the case of individual organisms). Regarding biological species, our views about how species originate are molded by speciation models. Accordingly, I discuss some speciation models in section 3.3. Based on this discussion, I advance some arguments against the view that Salmon's argument can be extended to biological species (section 3.4). According to those arguments, two notions used in Salmon's argument, the notion of an individual's 'origin' and the notion of 'plan' do not have counterparts that are applicable to biological species. Consequently, even if we assume that Salmon's reformulation of Kripke's argument is satisfactory, we have compelling reasons to think that this argument cannot be extended to biological species. I describe Kripke's and Salmon's argument more thoroughly in an appendix to this chapter for further reference. Reading this appendix is not required to follow this chapter.

3.1 The importance of origin essentialism to philosophy of biology

Within mainstream analytic philosophy, biological species have been commonly treated as natural kinds with essences. For instance, Kripke talks of tigers as being natural kinds defined by their "internal structure" (Kripke, 1980, pp. 20–21); Putnam suggests that lemons form a

natural kind with “chromosome structure” as their essence (Putnam, 1975, p. 104). Rather than being natural kinds, Hull and Ghiselin argue that species taxa are *individuals* since species are spatiotemporally restricted—i.e., species’ members cannot occur anywhere in time and space.² Conspecific members must be linked by ancestor-descendant relationships. In contrast, Hull and Ghiselin claim that membership in a natural kind is spatiotemporally *unrestricted*. For instance, any atom with atomic number 79 belongs to the natural kind gold, regardless of the atom’s time and location. Moreover, whereas kind essentialists claim that conspecific members must share an essence, promoters of the species-as-individuals thesis insist that species’ members can change indefinitely (see e.g., Hull, 1978, p. 347). In short, we can distinguish two main approaches to species ontology: natural kinds with essences (e.g., Kripke and Putnam), and individuals with no essential feature (e.g., Hull and Ghiselin).

For Hull and Ghiselin, kind essentialism is not compatible with the role of genealogy in species’ individuation. As discussed in the previous chapter, Griffiths (1999) and LaPorte (2004) disagree. According to them, species can be thought as historical entities while still being natural kinds with essences. For Griffiths and LaPorte, essences are certain genealogical relations. In other words, species for them contain *historical essences*. The challenge in arguing for the existence of historical essences is to find a genealogical relation that conspecific members *must* have. That’s not obvious since the genealogical relations connecting

² In addition to being spatiotemporally restricted, Hull and others have claimed that individuals should also be *cohesive*. Nevertheless, there is some disagreement on how we should understand the notion of ‘cohesion’ in this context. See Ereshefsky (2001, p. 112ff.) for further discussion.

conspecific members can be *accidental* rather than essential features of a species (Ghiselin, 1995). However, the fact that ancestor-descendant relations are relevant to determine the boundary of, say, *Canis lupus* does not imply that these relations are essential to this species. For instance, Chihuahuas are domestic dogs (*C. lupus familiaris*) in part because they are genealogically connected to other members of *C. lupus*. Yet, *C. lupus* would be the same species even if Chihuahuas had not evolved. Ancestor-descendant relations can matter for species individuation without being species' essences. Historical essentialists then need to provide an additional argument showing why certain ancestor-descendant relations are essential to species.

Sober suggests the following argument:

Kripke (1980) has suggested that each individual human being has the essential property of being born of precisely the sperm and the egg of which he or she was born. If such individuals as organisms have essential properties, then it will presumably also be possible for individuals like *Drosophila melanogaster* to have essential properties as well (Sober, 1980, p. 359).

Instead of appealing to cladistics (like LaPorte and Griffiths), Sober's suggested argument relies on Kripke's (1980) argument for origin essentialism. If applicable to species, Kripke's argument implies that species have origin essences. Sober's suggestion thus paves the way for an alternative type of argument for historical essences.

Summing up so far. Some like Ghiselin (1995) insist that genealogical relations are relevant for species individuation without being species' essences. But if Kripke's argument applies to species as Sober (1980) suggests, then we could move forward in this debate about

the role of genealogy to species' individuation. In particular, we would have the result that the species-as-individuals thesis is consistent with species' essentialism after all.

In addition to the debate over species ontological status, origin essentialism is also relevant in discussions concerning taxonomic nomenclature. An pressing topic in contemporary systematics is whether the Linnaean system should be replaced by a new set of rules, the *phylogenetic nomenclature* (or PhyloCode), as articulated by de Queiroz and Gauthier (de Queiroz, 1992; de Queiroz and Gauthier, 1994). This debate is still a matter of controversy (see e.g. de Queiroz, 1995; Ghiselin, 1995; Nixon and Carpenter, 2000). One type of argument used against the PhyloCode is that this system of nomenclature is committed to essentialism about origins and that this brand of essentialism is problematic (Keller, Boyd, and Wheeler, 2003; Rieppel, 2006). As an example, Rieppel (2006) claims that even though some stability can be obtained in the PhyloCode (since it treats taxon names as rigid designators), the PhyloCode is unsatisfactory because it is committed to origin essentialism.

[A] phylogenetically defined taxon name “necessarily”, i.e., rigidly, refers to a monophyletic taxon, and it is by virtue of that necessity (rigidity) that a greater stability of the meaning of taxon names is supposed to obtain under the rules of PhyloCode. *But such stability of meaning comes at the cost of “origin essentialism”* (ibid., p. 191, emphasis added).

For Rieppel, because the PhyloCode is committed to origin essentialism, the PhyloCode is not applicable to biological taxa.³ An examination of whether origin essentialism applies to biological taxa will not settle the debate about whether we should adopt the PhyloCode.

³ See Ereshefsky (2007) for a criticism of Rieppel (2006).

But still, such an examination might assist us in evaluating some of the arguments used in debates about taxonomic nomenclature such as Rieppel's.

Rieppel's claim concerning the "the cost of 'origin essentialism'" suggests that we have a proper grasp of what counts as a taxon's origin according to Kripke's theory. Nonetheless, Kripke's examples do not give us enough resources to determine what counts as a species' origin (section 3.4.1). Therefore, Rieppel's claim about the costs of Kripke's origin essentialism (as applied to biological taxa) is questionable. For it is not clear what origin essentialism amounts to if true about biological taxa. A separate issue is that Rieppel insinuates that we must adopt origin essentialism if we accept that taxon names are rigid designators (see *ibid.*, p. 190ff.). But that is not correct either: from the fact that a name is a rigid designator, it does not follow that origin essentialism is true about the name's referent. As I will discuss, rigid designation is not sufficient to derive origin essentialism. We also need to add a premise describing how an individual is formed from its origin (section 3.4.2). For this reason, one might grant that origin essentialism is not suitable for biological taxa, but still think that taxon names are rigid designators.

In brief, an examination of whether Kripke's argument applies to species taxa could help us advance two philosophical issues within biological systematics: the ontological status of species and the justification of taxonomic codes. Let us begin with Kripke's argument and then see if it applies to biological taxa.

3.2 Sober's suggestion needs to be qualified

In order to illustrate what origin essentialism amounts to, Kripke considers a table and the block of wood that the table is made from. He then asks: “could *this table* have been made from a completely *different* block of wood?” (Kripke, 1980, p. 113). It is important to note that Kripke is not asking whether we can be wrong about the correct block of wood that this table was made of; rather, Kripke's question supposes that we know what is the correct block of wood that this table came from. Kripke's question has the following format: given that this table was made from this block of wood, could this table have been made from a different block of wood? Kripke's answer to this question is negative. For him, “if a material object has its origin from a certain hunk of matter, then it could not have had its origin in any other matter” (*ibid.*, p. 114). After granting that some qualifications may be needed since the notion of ‘hunk of matter’ is ambiguous, Kripke adds that “something like a proof” can be presented in favor of this principle.

Sober's suggestion assumes that Kripke's argument is successful. However, this assumption is false; Kripke's argument is not sufficient to derive origin essentialism (see appendix). Much of the discussion within metaphysics about origin essentialism is focused on whether we can amend Kripke's (1980) original argument (see e.g., Hawthorne and Gendler, 2000; Robertson, 1998; Salmon, 1979). But since Kripke's original argument does not imply origin essentialism, Sober (1980) was wrong to think that Kripke's version of origin essentialism could save essentialism in biology. Nonetheless, Salmon (2005) proposed an influential reformulation of Kripke's argument. In this way, one might rephrase Sober's remark as saying that Salmon's reconstruction of Kripke's argument could vindicate biological essentialism.

The rest of this chapter focuses on this modified version of Sober’s suggestion. That is, my subsequent discussion concerns whether Salmon’s reconstruction of Kripke’s argument applies to species.

The premises in Salmon’s argument are formulated in terms of Kripke’s table example. Salmon’s premises contain expressions such as ‘hunks of wood,’ ‘is constructed from’ and so forth. So, in order to test whether Salmon’s argument applies to species, we have to first translate these expressions into terms that apply to species. Evolutionary biologists have developed a wide range of speciation models for describing how species evolve. Such models constitute a reasonable starting point for thinking how these translations can be carried out. A quick overview of speciation models is provided in the next section. Based on that section, I move to Salmon’s argument and to the question of whether it applies to species in section 3.4.

3.3 Speciation Models

The biological species concept (BSC) is a commonly used species definition in speciation studies (Butlin, Bridle, and Schluter, 2009; Coyne and Orr, 2004; Gavrillets, 2003; Turelli, Barton, and Coyne, 2001). This is not to say that BSC is the only species concept that can be used to study speciation. For instance, Wiens (2004) argues for the use of a lineage-based species concept—as proposed by Mayden (1997) and de Queiroz (1998)—to study speciation. However, even those that propose to study speciation under an alternative species concept grant that “[s]peciation research based on the BSC has led to exciting advances in our understanding of the evolution of intrinsic reproductive isolation mechanisms” (Wiens, 2004,

p. 914). Discarding results about speciation based on BSC is not a viable position within current discussions of speciation. For there are important results about speciation that rely on Mayr's BSC that are backed up by substantial empirical work (see e.g., Coyne and Orr, 2004; Lessios, 1998; Rice and Hostert, 1993). And given that my goal in this section is to simply introduce some standard views on speciation—rather than providing a comprehensive discussion about speciation, my choice of focusing on BSC is reasonable.

According to the BSC, species are “groups of interbreeding natural populations that are reproductively isolated from other such groups” (Mayr, 2000, p. 17). Hence, according to the BSC, speciation occurs when isolating barriers evolve between populations. Therefore, under the BSC, the central goal of speciation models is to understand the conditions under which isolating barriers among populations evolve. Isolating barriers can be divided into two main groups: *postzygotic* and *prezygotic* barriers. Prezygotic isolation occurs when there are mechanisms that prevent interspecific crosses. An example of prezygotic isolation is when potential mates do not meet because of their different breeding seasons. In the case of postzygotic isolation, members of two species do interbreed, but their hybrid offspring has low viability or fertility. Mules constitute a case of postzygotic isolation since they are viable hybrids that are incapable of producing offspring.⁴

Depending on the type of isolation barrier that evolved, different speciation models may be used. For example, the Dobzhansky-Muller speciation model is used to explain postzygotic—instead of prezygotic—isolation (see Coyne and Orr, 2004, pp. 269–272). Another important feature when characterizing models of speciation is the geographical relation

⁴ For further details about reproductive barriers, see Mayr (1963, pp. 89–109).

between an ancestral population and a speciating population. When the new formed species is geographically apart from its ancestor, we have a case of *allopatric speciation*. Such a geographical isolation may be a consequence of physical (as opposed to biological) barriers such as the presence of a river or a mountain range. There are also *non-allopatric* models of speciation in which the new species is not geographically isolated from its ancestor—meaning that they can meet each other.⁵ In what follows, I introduce two empirical studies illustrating how allopatric speciation occurs. The first study I consider is Podos' (2001) paper on reproductive isolation in Darwin's finches.

Large and strong beaks in Darwin's finches are selectively advantageous in environments in which hard seeds are available. By contrast, smaller beaks are well adapted to probe for insects. So depending on the environment, Darwin's finches might evolve distinct beaks' morphologies. Podos (2001) makes two further observations about Darwin's finches: (i) the songs emitted by Darwin's finches are a function of beak morphology; and (ii) dissimilar mating signals can produce prezygotic isolation. Thus, if two populations of Darwin's finches live in geographically isolated islands with distinct food supplies, then they might evolve

⁵ Two types of non-allopatric speciation are usually distinguished in the literature. *Sympatric* speciation occurs when the ancestral and the speciating populations occupy a single geographical area. *Parapatric* speciation constitutes an intermediary case between allopatric and sympatric types of speciation in the sense that the ancestral and the speciating populations are spatially adjacent (i.e., they can only meet each other in a specific geographical range). Since the speciation examples I will consider are of populations evolving in allopatry, I will not discuss non-allopatric models of speciation any further. For a review, see Turelli, Barton, and Coyne (2001, p. 335ff.).

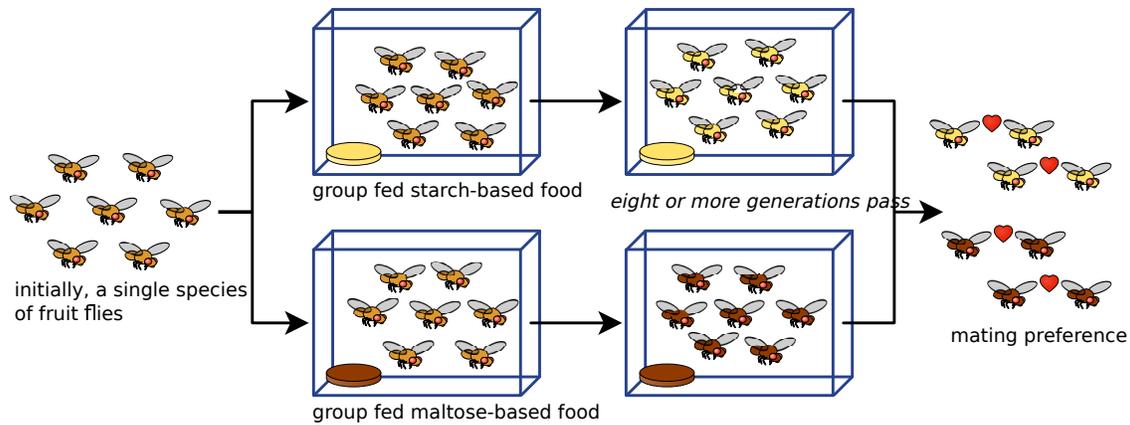


Figure 3.1: A laboratory experiment conducted by Dodd (1989) showing that divergent selection in isolated populations of *Drosophila pseudoobscura* can cause the evolution of reproductive isolation.

different beak shapes. Because of (i) and (ii), the evolution of different beak shapes may cause prezygotic isolation. In such a scenario, the adaptations (i.e., different beak shapes) are acquired due to a difference in food supply and the development of reproductive isolation is a byproduct.

My second example is a laboratory experiment described in Dodd (1989) with eight populations of *Drosophila pseudoobscura* (figure 3.1). Four of these populations were placed in a starch-based medium; and the remaining four were placed in a maltose-based medium. After a number of generations she observed that the flies evolved adaptations to their respective food supplies. Clipping the top of right wings for identification, Dodd placed these two groups together to test their mating choices. The result was that they showed significant isolation index: the flies reared in starch-based medium would tend to mate with other flies reared in the same environment, and the same was true about the flies reared in maltose-based medium. The fruitflies in Dodd's experiment evolved prezygotic isolation. Like Darwin's finches example, the reproductive isolation was incidental (from the point of

view of natural selection): “[r]eproductive isolation was not the target of selection, and there was no a priori reason to believe that adaptation to starch or maltose should have any effect on mating behavior, yet isolation developed” (*ibid.*, pp. 1309–1310).

The above two examples illustrate the process of allopatric speciation: we start with two populations evolving under different environmental conditions (e.g., presence or not of hard seeds) which, due to adaptation and/or drift, become reproductively incompatible with each other (e.g., use of different mating signals). In both examples, reproductive isolation evolved as a byproduct. This is in direct contrast to the reinforcement model of speciation in which the evolution of isolating barriers is directly favored by natural selection (i.e., the occurrence of hybrid progeny is selected against).⁶ These examples not only illustrate how geographical isolation may lead to speciation, but they also show that reproductive barriers need not be selectively advantageous in order to evolve.

In addition to Dodd’s (1989) and Podos’ (2001) studies, further empirical evidence has been presented in favor of the allopatric model of speciation (e.g., Coyne and Orr, 2004; Rice and Hostert, 1993), making it a well-established model of speciation. Given that it is a standard account of how species evolve, I will use the allopatric model to see how we can apply Salmon’s argument to biological species.

⁶ In the reinforcement model, natural selection ‘reinforces’ the reproductive isolation between two populations that already exhibit some degree of postzygotic isolation by favoring the evolution of prezygotic isolation. For a review about reinforcement, see Noor (1999).

3.4 Two problems with applying Salmon's argument to species

Like Kripke, Salmon thinks that if a table has its origin from a certain hunk of wood, then this table could not have had its origin in any other hunk of wood. Even though Kripke and Salmon focus on tables, the argument for origin essentialism is supposed to apply to any individual that has “a physical origin”:

Kripke's argument is perfectly general. . . . In fact, the argument seems to apply to virtually any sort of object that may be said to have a physical origin and composition. . . . In this way, if Kripke's argument is successful, variants of it may be used to establish several strong essentialist theses concerning the origin and composition of a variety of both animate and inanimate objects (Salmon, 2005, p. 199).

In order to apply Salmon's argument to species, we need to have an account of what counts as a species' origin. Additionally, such an account should render the premises in Salmon's argument true. Based on the discussion about speciation from the previous section, the goal of this section is to show that Salmon's argument fails to apply to species.

I will concentrate on two premises in Salmon's argument that are especially puzzling when applied to species. In Salmon's argument, an individual's origin has to satisfy specific constraints. Salmon formulates these constraints with reference to tables. For instance, one constraint is that every part of a hunk of wood must be used to construct a table to count as a table's origin. Otherwise origin essentialism would be false. I will return to this point

later. We will see how these constraints could be satisfied in the table example. But I will argue that these constraints do not apply to species. I discuss this issue in section 3.4.1. The second problem is with Salmon’s notion of “plan.” Salmon’s idea is that a table is always constructed from a hunk of wood according to a plan. A plan describes the assembly process used to construct a table. Salmon’s premise is that, given a table t constructed from a hunk of wood according to a certain plan, then any table constructed from the same hunk of wood according to the same plan must be the very table t and no other. Nonetheless, in section 3.4.2 I will argue that species do not evolve according to a plan.

3.4.1 Problem 1: what counts as a species’ origin?

In Kripke’s argument, for a hunk of wood to count as a table’s origin, it must satisfy the following principle (Salmon, 2005, pp. 199–200):

(Pr) A table t is (originally) constructed from hunk h just in case:

- (I) *every* (original) part of the table t comes from hunk h ; and
- (II) *every* part of h was used to construct the table t .

The principle (Pr) is indispensable in the argument for origin essentialism. To remove either (I) or (II) in (Pr) would allow the same table to have more than one origin at the same time—which would mean that origin essentialism is false (*ibid.*, p. 200). To see this, suppose we remove the condition (I) in (Pr). This allows a table to be constructed from h even though parts of this table do not come from h . In this situation, the *same* table can be constructed from distinct hunks of matter (e.g., the legs and the top of a table can come from different pieces of wood) and, consequently, from different origins (Figure 3.2).

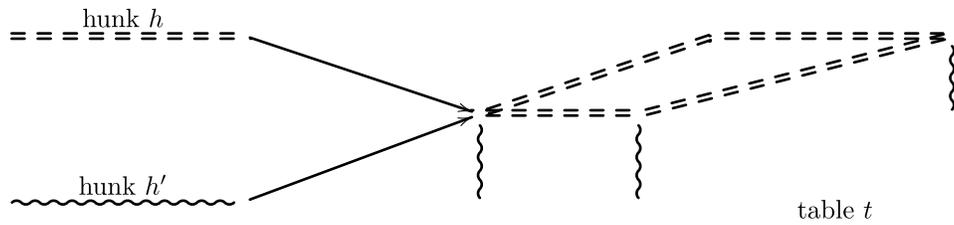


Figure 3.2: A table t in which the top is made of hunk h whereas the legs come from a distinct hunk h' . Without the clause (I), h and h' would be distinct origins for the table t .

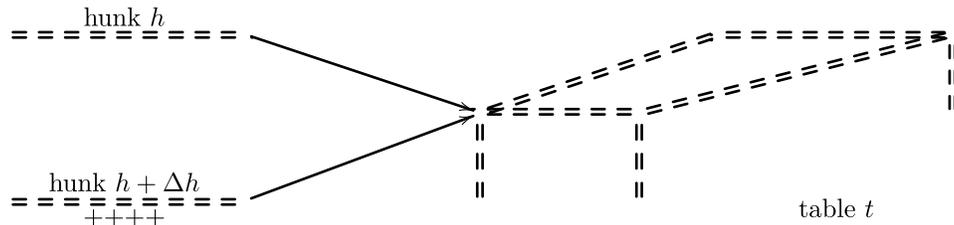


Figure 3.3: Without the clause (II) in (Pr), if the hunk h is sufficient to make the table t , then the same would be true if we add some hunk of matter to h —this additional hunk is represented by ‘++++.’

Thus the condition (I) cannot be excluded. Now suppose the clause (II) is removed. In this case, if t is constructed from h , then t can also be constructed from the hunk h plus an additional hunk of matter Δh —provided that Δh is not used to make t (Figure 3.3). So in this situation we would also have a case incompatible with origin essentialism since the table t would have two origins, h and $h + \Delta h$. Therefore, origin essentialism is true only if a table’s origin is understood in such a way that the situations represented by Figures 3.2 and 3.3 are ruled out. If a table’s origin does not satisfy the principle (Pr), then the cases depicted in the above two figures would count as counterexamples to origin essentialism—since in both drawings we have the same table with more than one origin.

According to (Pr), there is no original part of the table t that does not come from the hunk h , and h is entirely used in constructing t . In the case of tables, postulating (Pr) does

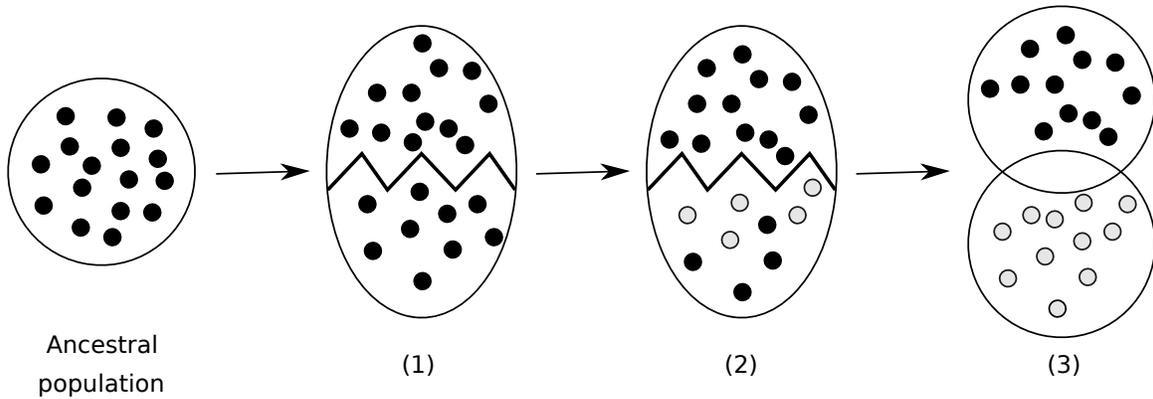


Figure 3.4: A schema of a speciation process following the allopatric model. Initially, an ancestral population splits off because of a geographical barrier such as a river (1). Significant divergence occurs after some generations (2), causing these two lineages to be reproductive isolated (3).

not seem problematic. The point I will make in this section is that there is no equivalent of (Pr) that applies to species. Consequently, it is doubtful that Salmon’s reformulation of Kripke’s argument can be extended to biological species.

In Salmon’s argument for origin essentialism we find the notions of ‘hunk of matter’, ‘parts of a hunk of matter’ and the relation ‘... is constructed from ...’. In order to re-write (Pr) for species we must find correlates of these notions in current theories of speciation. We earlier considered a standard model of speciation, the allopatric model. A schema depicting this speciation model is shown in Figure 3.4. The drawn speciation schema indicates how we can adapt Salmon’s argument for origin essentialism to biological species. More specifically, based on the schema from Figure 3.4, we could use the translation chart outlined in Table 3.1 to rewrite Salmon’s argument to species. Given this translation chart, origin essentialism about species amounts to the view that a species could not have had speciated from a population different from the one it actually descended from. The principle (Pr) thus becomes:

(Pr)_{sp} A species *S* speciated from an ancestral population *A* only if:

Original expressions	Translations
'table'	'species'
'hunk of matter'	'ancestral population'
'parts of a hunk of matter'	'members of a population'
'... is constructed from ...'	'... speciated from ...'
'... comes from ...'	'... descends from ...'
'... is used to construct ...'	'... is an ancestor of ...'

Table 3.1: A translation chart showing how Salmon’s argument could be applied to biological species.

(I)_{sp} *every* (original) member of S is a descendant from some member in A ; and

(II)_{sp} *every* member of A is an ancestor of some member in S .

A difficulty with $(Pr)_{sp}$ is that it is not evident which ancestral population ‘ A ’ is referring to. Thus, in order to evaluate $(Pr)_{sp}$, we first need to specify which type of ancestral population a species’ origin is. Kripke’s table example is not of much help here. In the case of tables, a table’s origin is “the very matter” that it was originally made of (*ibid.*, pp. 225–226). Yet, the same reasoning cannot be applied to species. For a species is not *made of* (or assembled from) an ancestral population. As an alternative, based on the allopatric model, one may assume that ‘ A ’ denotes a geographically isolated population that S evolved from. But before I examine this alternative, let us take a closer look at the principle $(Pr)_{sp}$.

The role of the original principle (Pr) is to exclude certain scenarios in which the same table has more than one origin (these scenarios are illustrated in figures 3.2 and 3.3). The principle $(Pr)_{sp}$ is supposed to fulfill an analogous role for species. As an example, this principle is designed to exclude the possibility that the same species S in figure 3.5 contains more than one origin. In order to fulfill this role, S ’s origin should be a very specific type of ancestral population. According to the principle $(Pr)_{sp}$, *every* single member of S and its

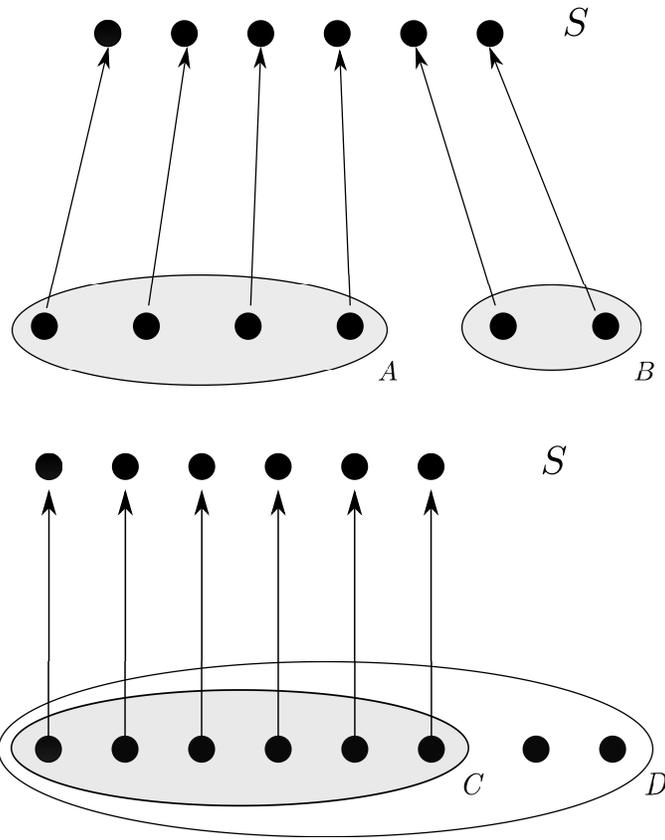


Figure 3.5: The arrows represent ancestor-descendant relationships. In these figures, A , B , C and D represent ancestral populations of the species S . However, since origin essentialism implies that S must have a single origin, at most one of these ancestral populations can be S 's origin.

origin must be linked by ancestor-descendant relations.⁷ From all the ancestral populations in figure 3.5, only the population C satisfies the principle $(Pr)_{sp}$. In this way, this principle rules out members in S 's origin that did not produce fertile offspring (or that died before reproducing), and immigration of organisms to S that do not descend from its origin.

My position is that $(Pr)_{sp}$ is unsatisfactory because it assumes that every member in a species' origin should have descendants in S (i.e., $(II)_{sp}$). In my view, this notion of species' origin is uncongenial to the allopatric model. For the sake of comparison, consider the parallel assumption for tables (i.e., (II)). This assumption is designed to block the following type of counterexample to origin essentialism. Intuitively, if a table t is constructed from y , then t could also be constructed from y plus Δy , where Δy is any extra portion of matter. But that is incompatible with origin essentialism because t would have two origins, y and $y + \Delta y$. The underlying intuition of Kripke and Salmon's argument, encapsulated in (II) , is that Δy is not a legitimate part of t 's origin. The reason is that Δy is redundant in the sense of not being used in t 's construction. However, the same line of reasoning is not applicable to species. The correspondent assumption for species, $(II)_{sp}$, says that every member of a species' origin must leave descendants in S . However, members in an ancestral population that failed to produce viable offspring are not less implicated in the evolution of S than organisms that produced viable offspring. Species that evolve by allopatry are (generally)

⁷ In more detail, recall that $(Pr)_{sp}$ contains two clauses, $(I)_{sp}$ and $(II)_{sp}$. While the clause $(I)_{sp}$ states that every member of S must descend from its single origin, for $(II)_{sp}$ every member of S 's origin has to be an ancestor of some member in S . Regarding the figure 3.5, A and B are incompatible with $(I)_{sp}$, and D is incompatible with $(II)_{sp}$. The ancestral population C satisfies both clauses.

due to selective pressures acting on geographically isolated populations, regardless of which particular members have left offspring. Thus, members of an ancestral population that do not leave descendants in S are still members of that ancestral population. For the allopatric model, a new species comes from an ancestral population but not every member of that ancestral population needs to have offspring in the new species. In other words, Kripke and Salmon's argument assumes that a table's origin is the 'smallest' portion of matter that is sufficient to construct it. But unlike the table example, the notion of the 'smallest beginning' of a species has no correspondent in the allopatric model.

This section centered around the discussion of what a species origin is. But in addition to a specific conception of an individual's origin, Salmon's argument also requires a premise concerning how an individual is assembled from its origin. The next section discusses this additional premise. As I shall argue, this premise is also at fault when applied to biological species.

3.4.2 Problem 2: the notion of 'plan' is not applicable to species

In his argument for origin essentialism, Kripke seems to implicitly assume that, "[i]f it is possible for a table x to be originally constructed from a hunk of matter y , then necessarily, any table originally constructed from hunk y is the very table x and no other" (*ibid.*, p. 206). However, as noted by Salmon, this assumption is implausible because one can use the same hunk of wood to construct different tables (at different times). Consequently, Salmon (2005) suggests a reformulation of Kripke's assumption that does not contain this implausible consequence.

In order to reformulate Kripke's premise, Salmon takes into consideration not just the hunk of wood that a table was made of, but also the way that this table was constructed—or, more simply, the *plan* used to construct the table. Here is how Salmon reformulates Kripke's original assumption. Suppose that a table t was constructed from a hunk of wood h . According to Salmon, there is a plan P which specifies how this table was assembled. Salmon's proposed assumption is this: if a table is constructed from the same material h and *according to the same plan* P , then we will obtain the same table t and no other. In this way, if we change the plan used to construct the table from a hunk of wood, the resulting table may be different.

The notion of 'plan' as used by Salmon is an empirical thesis; its justification relies on particular assumptions of how tables are made from hunks of wood. As Salmon puts it, his reformulation of Kripke's assumption "is a substantive metaphysical principle that is not entailed by the theory of direct reference. It is supported by a set of intuitions that are entirely separable from our intuitions concerning reference and intensionality" (*ibid.*, p. 211). Consequently, even if we accept Kripke's remarks on the semantics of proper names, Salmon's use of the notion of plan demands further justification. Salmon proposes this additional justification in the quote:

If two tables in two different possible worlds are constructed from the very same stuff in precisely the same way and, let us assume, with exactly the same structure atom for atom, how can they fail to be the very same table? What more could one ask? What more is there to being *this very table*? (*ibid.*, p. 211).

Salmon's insight is that if we fix a table's t origin and its plan, then a table constructed

under these conditions will be the same table t . Now that we have a preliminary understanding of Salmon's notion of 'plan' in hand, I turn to the question of whether Salmon's notion of 'plan' can be applied to species.

Salmon's thought experiment cannot be extrapolated to biological species without further modifications. For unlike the table example, a new species is not an atom for atom assemblage of its ancestral population—since the members of a new species belong to a generation different from the population they came from. If there is a notion of plan applicable to species, then that should be formulated in terms of how a lineage stemming from an ancestral population A *evolved* into the species S . One could simply say such a lineage followed the same plan if it 'evolved in the same way.' However, this characterization will not suffice since the resulting notion of plan is not informative enough. There is an indefinite range of mechanisms that shape evolution (e.g., genetic interactions, development, co-evolution, and so forth) and, without any further clarification, it's not apparent which evolutionary mechanisms must be operative in the evolution of a lineage for it to produce the same species.⁸ Thus, to make the notion of species' plan is biologically sound, we need to unpack what it means to say that a population 'evolved in the same way'.⁹

⁸ Moreover, a satisfactory notion of plan cannot also boil down to something like 'being able to produce a certain species and no other'; otherwise the resulting notion of plan would be vacuous.

⁹ One might simply insist that it's simply *intuitive* that if a lineage evolves in the same way as before (whatever that might be), then the same outcome should come about (e.g., the same species will evolve). I will return to this point at the end of this section. For now my focus is on whether we can find support for the notion of species' plan within evolutionary theory.

The goal of speciation models is to understand the evolutionary mechanisms that cause a lineage to speciate. In the case of the allopatric model, speciation is explained by the fact that populations evolving in allopatry can undergo genotypic and/or phenotypic divergence causing them to be reproductively isolated. For example, in Dodd's (1989) experiment, the populations evolving in allopatry undergo some genetic response due to a difference in the environment (maltose- and starch-based media). This genetic response affected the mating behavior causing the two *Drosophila* lineages to evolve some degree of reproductive isolation. In this way, one might think that the allopatric model can supply a notion of plan for species. In what follows however, I argue that this is not true.

Even though one might think that speciation models provide sufficient conditions for the evolution of *a* new species, such models do not specify the conditions for the evolution of *a particular* species, such as platypus. For instance, the allopatric model of speciation, and other BSC-based models, are in the business of explaining how reproductive isolation can evolve between geographically isolated populations. Yet, from the fact that two populations are reproductively isolated, we cannot infer anything about which particular species taxon will evolve. In contrast, Salmon's notion of plan as applied to species should indicate which conditions the evolution of a lineage has to satisfy in order to produce the exactly same species. Speciation models such as the allopatric model do not provide a plan for any particular species. But Salmon's notion of plan requires that.

As the allopatric model illustrates, speciation theory does not support the notion of plan. However, one might object, that does not imply that we cannot formulate a notion of plan for species based on evolutionary theory at large. According to this objection, there is still the possibility of interpreting the expression 'evolve in the same way' using resources from

evolutionary theory other than speciation models. However, the assumption that species evolution follows a plan is implausible given current evolutionary theory. In order to see that, suppose that a species S evolved from an ancestral population A . In order to validate a notion of plan to species, we should make sense of the idea that the evolution of the species S followed a set of conditions (or a plan) such that, if a lineage stemming from A were to evolve according to the same plan, then the same species S would have evolved and no other. A species' plan then posits a deterministic process: if certain conditions are obtained, then the same species has to evolve and no other. However, stochasticity plays a central role in evolutionary explanations (see e.g. Beatty, 2006; Desjardins, 2011; Gould, 1990; Travisano et al., 1995). Even though natural selection is not a stochastic process, evolution is shaped by different types of stochastic processes, such as mutation, genetic drift, and random changes in the environment (Lenormand, Roze, and Rousset, 2009). Hence, evolutionary theory is not the right *type* of theory for supplying a notion of plan to species. An example that makes that salient is Gould's (1990) observations on the extinct forms discovered in the Burgess Shale in British Columbia.

Gould (1990) refers to the Burgess Shale to make two related points. The first one is that the Burgess fauna shows that the history of life after the diversification of multicellular organisms in the Cambrian explosion was not just a process of increasing diversification but also of considerable elimination.¹⁰ As Gould (1990, p. 47) points out, "a 90 percent chance of death would be a good estimate for major Burgess lineages". Moreover, Gould also

¹⁰ The Cambrian explosion (570 Myr) marks the first appearance of multicellular animals with hard parts. The Burgess fauna appeared just after the Cambrian explosion, 530 Myr.

encourages the view that the extinction of many of Burgess lineages did not happen because they were outcompeted by other groups but because most lineages were eliminated by chance. Even though many of the eliminated lineages had about the same chance of survival as the ones that survived, they went extinct nonetheless (*ibid.*, pp. 47, 50, 239). The Burgess Shale case illustrates one type of stochastic factor relevant for the evolution of a species; viz., random elimination of competitors. In the case of allopatric speciation, other stochastic factors are relevant. For instance, the genetic divergence between two lineages evolving in allopatry depends on which mutations took place. And mutation is another stochastic process from the view of evolutionary theory. Thus, while evolutionary explanations relies on stochastic factors, a species' plan describes speciation as a deterministic process. Accordingly, evolutionary theory is not the right *type* of theory to warrant the thesis that species evolve according to a plan.

So far I looked at two strategies for substantiating the notion of plan for species. I started with a standard speciation model, the allopatric model. I have pointed out that the allopatric model is concerned with how new species evolve without taking into consideration which species taxa they belong to. For this reason, the allopatric model does not support the notion of plan for a particular species, which Salmon's notion of plan requires. Moreover, evolutionary theory is not the right type of theory for supplying a notion of plan. While the notion of plan depicts speciation as a deterministic process, an evolutionary account of species evolution is stochastic. Nevertheless, one might object that I have not yet provided reasons against Salmon's argument in favor of the notion of plan.

In regard to tables, Salmon (2005) does not spell out what a plan is. What he does is to provide a intuition pump for the view that, for every table, there must be a plan that

guarantees that the exactly same table could be assembled—provided that we start from the same hunk of wood. According to this thought experiment, a table’s plan would guarantee that we could have an atom for atom replica of this table and, consequently, the very same table (*ibid.*, p. 211). One might insist that in the same way that Salmon didn’t have to appeal to physics to justify his notion of plan, we do not have to take into consideration evolutionary theory to warrant a notion of plan for species. This objection assumes that the justification of a notion of plan for species is independent of our theories about how evolution works. In my view, however, this assumption is wrong-headed. Current evolutionary theory shows that the expression ‘evolve in the same way’ is overly cryptic. Evolution is not the product of a single mechanism. And if we cannot establish what ‘evolve in the same way’ means, then we have no means whatsoever to evaluate the notion of ‘plan’ as applied to species (besides, speciation is not a domain that humans are particularly skilled at having the right intuitions). Therefore, I am not convinced that intuition pumps are the right approach to settle issue of whether the notion of ‘plan’ applies to species. But even if the reader disagrees with me, Salmon’s intuition pump has the problem of not being compatible with the view that species are individuals. I will now move to this issue.

According to Salmon’s thought experiment, a physical replica of a table made from the same “stuff” cannot fail to be the same table. As Salmon says, if two tables (in different possible worlds) are the same atom for atom, “how can they fail to be the very same table? What more could one ask? What more is there to being *this very table*?” (*ibid.*, p. 211). Even though this line of reasoning can be applied to tables, it is problematic when applied to species. As discussed earlier, Hull and Ghiselin’s view that species are individuals is the main rationale for applying Kripke’s argument to species (for origin essentialism is a theory

about individuals, not natural kinds). However, one of the consequences of thinking that species are individuals is that two species can be qualitatively indistinguishable from each other and, yet, fail to be the same species (Hull, 1978). As an example, once a species goes extinct, no matter how similar a new species is to the extinct species, it can never be the same species as the extinct one. The reason is that “species are segments of the phylogenetic tree. Once a segment is terminated, it cannot reappear somewhere in the phylogenetic tree” (*ibid.*, p. 349). In a nutshell, Salmon’s thought experiment is based on the intuition that an atom for atom replica of a table from the same hunk of matter should be the same table and no other. This intuition is incorrect when applied to species though. For instance, species extinction is an irreversible process. Under the species-as-individuals thesis, two indistinguishable species may not be the same species. One might think that this consequence of the species-as-individuals thesis is misguided. However, that counts as a reason against applying Salmon’s argument to species, not for it. For origin essentialism is a thesis about individuals, not kinds. In sum, the assumption that species evolve according to a plan is not substantiated by current evolutionary theory, and it is incompatible with the view that species are individuals. Salmon’s notion of ‘plan’ is not applicable to species.

3.5 Summary

Origin essentialism has played an important role in discussions about species membership, mainly because of Ghiselin and Hull’s argument that species are individuals instead of natural kinds. In this chapter I pointed out that Kripke’s original argument is not sufficient to derive origin essentialism. However, Salmon (2005) proposes an influential reformulation of

Kripke's original argument. Based on Salmon's reformulation, I proposed two reasons against the possibility of applying Salmon's argument to species. The first one is that species do not have the type of origin that is required to run the argument for origin essentialism. The second reason is that there is not a notion of 'plan' that is suitable to species. Therefore, contrary to what some have suggested such as Sober (1980), Kripke's argument for origin essentialism—as well as Salmon's reformulation—cannot be extended to biological species.

Next chapter: thus far I discussed two versions of new essentialism in which essences are historical relations. In chapter 2, I looked at Griffiths (1999) and LaPorte's (2004) argument that cladistics supports their notion of historical essences. In this chapter I considered Sober's (1980) suggestion that Kripke's argument could be extended to biological species. In the next chapter I look at other versions of biological essentialism. Like the historical versions of essentialism discussed previously, the essentialist views discussed in the next chapter maintain that biological essences do not have to be exclusively intrinsic. But different from the history-based forms of essentialism, they do not maintain that essences need to be historical.

Appendix: Kripke and Salmon on origin

essentialism

The goal of this appendix is to introduce Kripke's argument for origin essentialism, its shortcomings, and Salmon's reformulation of Kripke's argument. Kripke's argument is based on the possible world semantics he formulates for predicate modal calculus (Kripke, 1963). This semantics can be used to capture the modal notions of 'it is necessary that' and 'it is possible that' if represented by the operators ' \Box ' and ' \Diamond ', respectively. There are two important features in Kripke's semantics that distinguishes it from the classical logic semantics. According to Kripke's semantics, the truth value assigned to a formula is relative to *possible worlds*: the truth value of the same formula may differ depending on the possible world we consider. These possible worlds are related by a specific relation, the *accessibility relation*. This relation serves to capture the informal idea that a state of affairs is only possible with respect to the 'point of view' of a certain world. For instance, for a sentence ' $\Diamond\phi$ ' to be true in our world, the *actual world*, it is not only necessary that there is a world, say ω , in which ' ϕ ' is true but also that ω is accessible from the actual world. In this way, depending on how the accessibility relation is defined, the evaluation of a formula containing a modal operator does not have to include all possible worlds but only the 'relevant' collection of worlds. Finally, Kripke's argument also makes use of the notion of *rigid designator*. For this present discussion, the definition used is that a term rigidly designates an individual just in case it refers to the same individual in every possible world that this individual exists and

never designates anything else.¹¹

1. Kripke's original argument

Kripke's argument for origin essentialism starts with the following statement:

Let '*B*' be a name (rigid designator) of a table, let '*A*' name the piece of wood from which it actually came. Let '*C*' name another piece of wood. Then suppose *B* were made from *A*, as in the actual world, but also another table *D* were simultaneously made from *C*. ... Now in this situation $B \neq D$. (Kripke, 1980, p. 114).

This gives the first two premises in Kripke's argument:

(K1) Given a wooden table *B*, a hunk of wood *A* that *B* is made of, and another hunk of wood *C* in the actual world, it is possible that *B* is still made of *A* while a different table *D* is made from *C*.

(K2) The names '*B*' and '*D*' are rigid designators.

Figure 3.6 provides a representation of the conjunction between (K1) and (K2): if the state of affairs depicted in the topmost picture is true in the actual world, then the state of affairs depicted in the bottom picture is possibly true.

Kripke wants to prove that $\Box(B \neq D)$. For sake of a reductio, assume that the negation of the desired conclusion holds; i.e., that $\Diamond(B = D)$ is true. Thus, there is a possible world

¹¹ For further details on Kripke's possible world semantics, see Kripke (1963). Regarding rigid designators, see Salmon (2005, 32ff.).

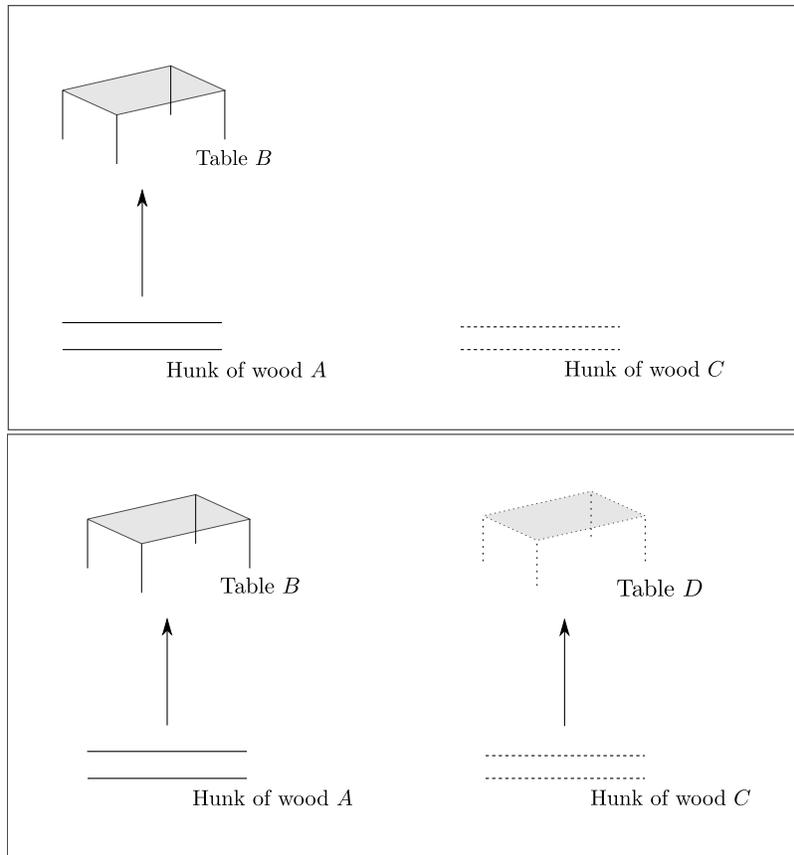


Figure 3.6: A representation of Kripke's premise '(K1)&(K2)'.

accessible from the actual world, say ω , in which $B = D$ is true. By hypothesis, ' B ' and ' D ' are rigid designators (premise (K2)). Moreover, as argued by Kripke (1980), the following thesis holds:

(K3) True identity statements containing rigid designators are necessarily true.

Hence, because of (K3), $\Box(B = D)$ is true in ω .

An additional premise in Kripke's argument is:

(K4) The accessibility relation between possible worlds is symmetric.¹²

¹² So according to (K4), if ω accessible from the actual world, then the actual world is accessible from ω .

Since $\Box(B = D)$ is true in ω , and ω is accessible from the actual world, with (K4) we get to the conclusion that $(B = D)$ is true in the actual world.¹³

Since $B = D$ is true in the actual world, from (K2) and (K3) it follows that $\Box(B = D)$. That is, if the names ‘ B ’ and ‘ D ’ refer to the same table in the actual world, then they refer to the same table in every possible world (accessible from the actual world) in which this table exists. However, it is reasonable to think that there is a possible world accessible from the actual world that $B \neq D$ holds (i.e., (K1)). See Fig 3.6). Thus assuming $\Diamond(B = D)$ leads us to a contradiction. Therefore, it is not possible that ‘ B ’ and ‘ D ’ are co-referential terms.

2. Kripke’s argument does not derive origin essentialism

Origin essentialism is typically understood as the view that an object could not have had an origin different from the one it actually had. Assuming that ‘ $\mathcal{M}(x, y)$ ’ stands for the relation ‘ x is entirely made from hunk y ’, given a table B entirely constructed from hunk A , origin essentialism can be described as:

$$(\text{OE}) \quad \Box \forall x (x = B \rightarrow \mathcal{M}(x, A))$$

Thus, according to origin essentialism, if a table is not made of hunk A , then this table cannot be B .

The converse of the above formula is not a necessary commitment for an origin essentialist.

¹³ In more detail, since ‘ $\Box(B = D)$ ’ is true in ω , the formula ‘ $B = D$ ’ is true in every possible world that is accessible from ω . Because of (K4), we know that the actual world is accessible from ω . Hence, ‘ $B = D$ ’ is true in the actual world.

According to the converse of (OE), the hunk A can only be transformed into the table B and no other. However, one might endorse (OE) and accept that, for worlds in which B does not exist, the hunk A is used to construct something different from B such as a chair. Accordingly, origin essentialism should be construed as (OE), not as its converse. However, Kripke’s conclusion that $\Box(B \neq D)$ does not imply (OE), however. In order to see that, suppose there is a possible world in which the table D does not exist, but in which the table B is made from C . In such a possible world, we do not have a counterexample to the sentence “ $\Box(B \neq D)$ ”—since D does not exist in this world. However we have a counterexample to origin essentialism. For according to origin essentialism, the table B cannot be made from the hunk C (for B is constructed from A in the actual world). For these reasons, Kripke’s argument alone is not sufficient to derive origin essentialism. Salmon (2005) proposes a reformulation of Kripke’s argument in which (OE) is derived. I discuss Salmon’s version in the next section.

3. Salmon’s reformulation

Kripke’s assumption (K1) is based on the premise that “if it is possible for table B to be constructed from hunk A , then it is also possible that table B be constructed from hunk A and in addition hunk C be made into a table, *some table or other*” (Salmon, 2005, p. 202, emphasis added).¹⁴ This premise states that two separate possible state of affairs (viz., ‘ $\Diamond\mathcal{M}(B, A)$ ’ and ‘ $\Diamond\mathcal{M}(D, C)$ ’) are jointly possible (viz., ‘ $\Diamond(\mathcal{M}(B, A) \wedge \mathcal{M}(D, C))$ ’). For

¹⁴ The expression ‘some table or other’ is crucial in the above quote. Although this quote specifies which table is made from hunk A (viz., the table B), note that it does not specify which table is constructed from hunk C .

this reason, Salmon (2005) calls this assumption the ‘compossibility premise’. A further assumption in the compossibility premise is that A and C are non-overlapping hunks of matter (i.e., A and C cannot have any matter in common). With this proviso, Salmon (2005) proposes the following formulation of the compossibility premise:

(**KCp**) For any possible table x and any possible hunks of matter y and y' , if

1. y' and y do not overlap;
2. it is possible for table x to be originally constructed from hunk y ;
3. it is possible for a table to be constructed from y' ;

then:

it is possible that: table x be originally constructed from hunk y ; and some table or other x' be originally constructed from hunk y' .

In addition to (KCp), Salmon’s reformulation of Kripke’s argument relies on a further premise. As Salmon remarks, Kripke seems to implicitly assume that, “If it is possible for a table x to be originally constructed from a hunk of matter y , then necessarily, any table originally constructed from hunk y is the very table x and no other” (ibid., p. 206). When applied to our original example, this gives us:

$$\Box \forall x [x \text{ is a table} \rightarrow (\mathcal{M}(x, A) \rightarrow x = B)] \tag{3.1}$$

However, the above thesis is implausible since one can use the same hunk of wood to construct different tables (at different times). Because of this reason, Salmon (2005) suggests a

reformulation of (3.1) that does not contain this implausible consequence.

In order to reformulate (3.1), Salmon takes into consideration not just the hunk of wood that a table was made of, but also the way that this table was constructed—or, more simply, the *plan* used to construct the table. Let $\mathcal{P}(x, y)$ be the predicate ‘ x is made of hunk y according to a certain plan P .’ Salmon proposes the following new thesis:

$$(K5) \quad \Box \forall x [x \text{ is a table} \rightarrow (\mathcal{P}(x, A) \rightarrow x = B)]$$

Unlike (3.1), (K5) does not state that A can only be used to construct the table B . Rather, according to (K5), the hunk A will give rise to the same table B , *provided that we use a certain plan and no other*. In this way, if we change the plan used to construct the table from hunk A , the resulting table may be different from B . Principle (K5) seems plausible: if a table is constructed from the same material and in the same way, then it seems reasonable to assume that we have the same table and no other.

With these premises in hand, we can turn to Salmon’s argument. Suppose a possible world ω in which a table B is made from the hunk A . For sake of a reductio, suppose the negation of (OE). This gives us:

$$\Diamond \exists x (x = B \wedge \neg \mathcal{M}(x, A)) \tag{3.2}$$

According to the above formula, there is a possible world, say ω^* , such that B is not made of A . So, in ω^* , B is made from something other than A , say J . Hence, because of (K5), it follows that B is made of J in every possible world, provided that we use a certain plan, say

P. Assuming that the accessibility relation is symmetric, ‘ $\Box(\mathcal{P}(B, J))$ ’ holds in ω .¹⁵

Since hunk *J* does not overlap with *A*, the compossibility premise (i.e. (KCp)) allows us to create a possible world ω^{**} from ω such that the following holds: (i) *B* is made of *A* (like in ω); and (ii) a table *K* is created from hunk *J*. Thus, in this possible world, $K \neq B$. Thus, there is a possible world in which, independently of the plan used to construct the table from hunk *J*, the resulting table is not *B*. However, this contradicts $\Box(\mathcal{P}(B, J))$ —derived in the previous paragraph. Therefore, (OE) is true.

¹⁵ Note that ‘*P*’ refers to a certain plan whereas ‘ \mathcal{P} ’ refers to the relation ‘... is made of ... according to the plan *P*’.

Chapter 4

Other versions of modern essentialism

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My goal in this chapter is to introduce three other versions of new essentialism: Okasha’s (2002) relational essentialism (section 4.2); Boyd’s (1999) HPC theory (section 4.3); and Devitt’s (2008) hybrid essentialism (section 4.4). Species concepts play a key role in the arguments for these versions of essentialism. For this reason, before I introduce these versions of essentialism, I review three prominent species concepts.

4.1 Species concepts

There are two meanings associated to the word ‘species.’ The word ‘species’ may refer to species taxa, such as *Homo sapiens* and *Canis lupus*. Alternatively, ‘species’ may refer to the species category (or the species rank) that contains all species taxa (Mayr, 1982, pp. 253–254). Defining a species taxon, such as *Homo sapiens*, consists of distinguishing *Homo sapiens* from other taxa. A definition of the species category, however, specifies what *Homo sapiens* and other species taxa have in common that distinguish them from taxa in other ranks, such as subspecies and genera. In short, species concepts are definitions of the species rank (Ereshefsky, 1992; Mayden, 1997). The goal of this section is to introduce three species concepts: the biological, the ecological, and the phylogenetic species concepts.

4.1.1 The Biological Species Concept (BSC)

According to the Biological Species Concept (BSC), biological species are “groups of interbreeding natural populations that are reproductively isolated from other such groups”

-
1. Mechanisms that prevent interspecific crosses (premating mechanisms)
 - (a) Potential mates do not meet (seasonal and habitat isolation)
 - (b) Potential mates meet but do not mate (ethological isolation)
 - (c) Copulation attempted but no transfer of sperm takes place (mechanical isolation)
 2. Mechanisms that reduce full success of interspecific crosses (postmating mechanisms)
 - (a) Sperm transfer takes place but egg is not fertilized (gametic mortality)
 - (b) Egg is fertilized but zygote dies (zygote mortality)
 - (c) Zygote produces an F_1 hybrid of reduced viability (hybrid inviability)
 - (d) F_1 hybrid zygote is fully viable but partially or completely sterile, or produces deficient F_2 (hybrid sterility)
-

Table 4.1: Classification of isolating mechanisms. From Mayr (1963, p. 92).

(Mayr, 2000, p. 17). In this species definition, the word “interbreeding” means “propensity for interbreeding”: members of two populations do not have to *actually* interbreed in order to be conspecific. For instance, two populations may be geographically isolated and, yet, belong to the same species.

The mechanisms that prevent interbreeding (and, accordingly, gene flow) between different species are called *isolating barriers* (or *isolating mechanisms*). Isolating barriers are not the same as ‘geographical barriers’ such as a river that prevent gene flow between organisms. Rather, isolating barriers are supposed to be the product of organismal attributes, such as different mating behavior. A classification of the different isolating barriers found in nature is described in Table 4.1.¹

BSC characterizes species as forming *gene pools*: gene flow occurs between conspecific organisms via reproduction but generally not between different species. The notion of repro-

¹ For further details about isolating mechanisms, see Mayr (1963, pp. 89–109).

ductive isolation is used to explain why these gene pools are stably formed: “[i]n sexually reproducing organisms, *the stable coexistence of genetically distinct groups in sympatry requires reproductive barriers between them. . . . Without reproductive barriers, the groups would fuse*” (Coyne and Orr, 2004, p. 31).² But how do these reproductive barriers evolve? Do they have to be selectively advantageous? Natural selection can be used to explain the evolution of isolation barriers without supposing that reproductive barriers are selectively advantageous. In other words, natural selection does not have to directly favor the acquisition of reproductive barriers. As discussed in the previous chapter, the evolution of isolating barriers can be a byproduct of evolutionary divergence.³ For instance, in the example of Darwin’s finches (Podos, 2001), there is selection pressure for distinct beak sizes (because of differences in food supply) but, as an incidental consequence, the two populations of Darwin’s finches evolved reproductive isolation (since the evolved differences in beak size influenced their mating behaviors).

² Sympatric groups are populations that occupy a single geographical area.

³ In some passages though, Mayr seems to suggest that the evolution of reproductive barriers is selectively advantageous:

[A]s soon as sex (out-crossing) had been invented there was a simultaneous premium for the possession of mechanisms that would prevent out-crossing with potential mates that were genetically too different. Any zygote lacking such devices (or having them only poorly developed) would most likely not leave any viable offspring, simply owing to individual selection. And this explains the maintenance of the so-called isolating mechanisms (Mayr, 1988, p. 432).

One important consequence of BSC is that it is not applicable to asexual organisms—for a group of asexual organisms cannot be “reproductively isolated.” According to Mayr, the delimitation between asexual species is arbitrary, based solely on phenotypic characters (Mayr, 2004, p. 190). Because the genotype of asexual organisms is preserved from generation to generation, Mayr claims that there is no demand for “any isolating mechanism to protect the integrity of their genotype” (Mayr, 2000, p. 25).

4.1.2 The Ecological Species Concept (ESC)

According to BSC, the stable existence of sympatric species requires the presence of isolating barriers. The Ecological Species Concept (ESC) tries to make precise the intuition that, for sympatric species to coexist, they should deploy distinct ecological resources. The study conducted by Levine and HilleRisLambers (2009) motivates this intuition. By assembling communities of annual plants on serpentine soils in California, Levine and HilleRisLambers (2009) provide evidence that: (i) “in absence of niche differences, the common species become more common and the rare species more rare”; and (ii) in the case in which there are niche differences, “the per capita population growth rates of the common species decreased as each became increasingly common.” Thus, at least in the case of this study, *stable* coexistence of species requires populations to occupy different niches; without niche differences, species diversity is not preserved.

In opposition to BSC, promoters of ESC argue that reproductive isolation is not necessary for explaining the stable coexistence of species. For example, consider the two oak species *Quercus robur* and *Q. petraea*. According to Muir, Fleming, and Schlötterer (2000), these

species hybridize extensively and, yet, their respective populations exhibit differences in leaf and fruiting structures.⁴ Also, even though these two species are sympatric, they occupy distinct niches. While *Q. robur* grows in wetter habitats, *Q. petraea* is more drought-resistant. This example suggests that differences in the niches of populations may be the cause of the divergence between these two species despite gene flow. But most importantly, this example encourages the view that reproductive isolation is not a necessary condition for the evolution of species. Species may evolve without being reproductively isolated.⁵

As discussed above, the motivating intuition for ESC is that different species use different ecological resources and this is responsible for the stable coexistence of (sympatric) species. A classical definition of ESC is given by Van Valen (1976):

A species is a lineage (or a closely related set of lineages) which occupies an adaptive zone minimally different from that of any other lineage in its range and which evolves separately from all lineages outside its range (Van Valen, 1976, p. 233).

⁴ Muir, Fleming, and Schlötterer (2000) used 20 microsatellite loci as evidence that *Q. robur* and *Q. petraea* form different species. A potential criticism of Muir et al study is that the fact that these two species differ at many loci indicates that gene flow between these two species is not very high, which makes them compatible with BSC (Coyne and Orr, 2004, p. 44).

⁵ Van Valen (1976) mentions another example of oaks species, *Quercus macrocarpa* and *Q. bicolor*, in which there is extensive exchange of genes despite being different species. See Coyne and Orr (2004, p. 43ff.) for a discussion of whether this example is problematic for BSC.

Van Valen’s ESC is based on the notions of “lineage” and “adaptive zone.” Van Valen’s (1976) elucidates what he means by “lineage” in the quote:

A lineage is a clone or an ancestral-descendant sequence of populations. A population is a group of individuals in which adjacent individuals at least occasionally exchange genes with each other reproductively, and in which adjacent individuals do so more frequently than with individuals outside the population (*ibid.*, pp. 233–34).

Finally, Van Valen (1976) characterizes “adaptive zone” as “some part of the resource space together with whatever predation and parasitism occurs on the group considered” (*ibid.*, p. 234).⁶ To sum up, according to Van Valen’s ESC, species have both a historical and an ecological component; a species forms a common lineage and inhabits an adaptive zone “minimally different” from other nearby lineages.

It is worth noting that ESC does not exclude the possibility of species being reproductively isolated, and of isolating mechanisms playing a role in maintaining the existence of a species. However, for a promoter of ESC, the existence of a distinct selective regime—due to

⁶ According to Van Valen’s concept of adaptive zones, they can exist independently from their inhabitants. In this regard, his notion of adaptive zones contrasts with Lewontin’s view that there can be no environment without organism. For Lewontin, “[a]n *environment* is something that surrounds or encircles, but for there to be a surrounding there must be something at the centre to be surrounded” (Lewontin, 2000, p. 48). For further details about Lewontin’s view, see Lewontin (2000, section 2). See Coyne and Orr (2004, p. 458) for the view that defining adaptive zones independently of their inhabitants makes Van Valen’s ESC questionable.

different niche occupation—is the ultimate cause for the origin of species; if isolating mechanisms arise, then they are a product of ecological factors (L. Andersson, 1990). In contrast, for a promoter of BSC, niche differences are relevant for the persistence rather than the origin of species (Coyne and Orr, 2004, p. 35). Thus, promoters of both BSC and ESC agree that reproductive isolation and ecological factors are relevant for species evolution. However, they have different hypotheses on what is necessary for the existence of sympatric species. According to BSC, reproductive isolation is necessary for the sympatric coexistence of (sexual) species; for ESC, species' coexistence requires niche differences. Another important point of contrast between ESC and BSC is their application to asexual species. Since both sexual and asexual organisms can occupy different niches, ESC can be applied to nonsexual organisms as well.⁷ In contrast, BSC is only applicable to sexual organisms.⁸

4.1.3 The Phylogenetic Species Concept (PSC)

There is a family of species concepts under the heading 'Phylogenetic Species Concept' (PSC). Following Baum and Donoghue (1995), I will distinguish two versions of PSC: character-based and history-based PSC. According to the *character-based* PSC, species are defined in terms of a combination of characters, without taking into consideration whether these characters are ancestral or derived. For the *history-based* PSC, species are defined by historical relations (i.e., ancestor-descendant relations). I start with a character-based PSC

⁷ See Cohan (2002) for an example of an ecology-based species concept for bacteria.

⁸ It's worth noting, however, that Dykhuizen and Green (1991) propose a BSC-like definition of bacterial species by taking into account homologous recombination between bacterial strains.

proposed by Cracraft (1992).

As described earlier, Mayr and Van Valen believed that the species concept should be defined in terms of the processes that are responsible for the evolution of species. Cracraft (1992) holds a different view. According to him, the species concept is best described in terms of the *results* of evolution (patterns) rather than the processes that are responsible for species evolution. Cracraft summarizes his position in this quote:

Biologists have now come to believe that these processes [that produce species] are highly variable and often depend upon the group being studied. To have a number of species concepts, each possibly applying to a different group, obscures the potential discovery of common phylogenetic and evolutionary patterns from one taxon to another. The results of evolution appear to be more or less the same in all groups. . . . Thus, by defining species in terms of the resulting *pattern*, it allows us to investigate these processes, unbiased by a species concept that is derived from our preconceptions of those processes (*ibid.*, pp. 102–103).

As opposed to Mayr and Van Valen, Cracraft does not believe that there is a single type of process that is responsible for the evolution of every single species. Cracraft's point is that we can overcome this problem if we define species in terms of evolutionary patterns—since there is a *single* evolutionary pattern. More specifically, Cracraft proposes the following species definition: “[a] species is the smallest diagnosable clusters of individual organisms within which there is a parental pattern of ancestry and descent” (*ibid.*, p. 103). And for Cracraft, these “diagnosable clusters” are delimited via “unique combinations of primitive

and derived characters” (*ibid.*, p. 103).⁹

A more recent version of a character-based PSC has been proposed by Wheeler and Platnick (2000). Like Cracraft (1992), they believe that species should be defined in terms of patterns rather than the evolutionary processes that shaped such patterns. According to them, “[a]s phylogeneticists divorced the discovery of historical patterns of cladistic relationships from unnecessary assumptions about evolutionary processes (Platnick, 1979), it became apparent that modes of speciation need not be confounded with criteria used to distinguish among species” (Wheeler and Platnick, 2000, p. 55). Moreover, Wheeler and Platnick maintain that whereas “evolutionary patterns are the cumulative result of countless kinds of processes acting singly and in combination” (*ibid.*, p. 62), there is a single resulting pattern from the confluence of these many processes.¹⁰ For this reason, their character-based definition of species is compatible with different speciation theories.¹¹ Wheeler and Platnick’s

⁹ Even though he grants that many species will be defined by uniquely derived characters, he does not think that species should be defined in terms of derived characters. The reason is that derived characters alone are not sufficient to recognize ancestral species—for ancestral species should have ancestral characters in relation to their descendants.

¹⁰ Wheeler and Platnick elaborate this point in the passage: “[t]he process of evolution’ has become an unfortunate cliché in biology textbooks, perpetuating a sloppiness in the use of the word *evolution* that contributes to semantic confusion. Textbooks definitions about changes in gene frequency notwithstanding, there is no ‘process of evolution.’ Instead, evolutionary patterns are the cumulative result of countless kinds of processes acting singly and in combination” (Wheeler and Platnick, 2000, p. 62).

¹¹ Other examples of character-based PSC include Eldredge and Cracraft (1980), Nelson and Platnick (1981) and Nixon and Wheeler (1990).

species definition is similar to Cracraft's. Species for them are "the smallest aggregation of (sexual) populations or (asexual) lineages diagnosable by a unique combination of character states" (*ibid.*, p. 58).¹² Different from Cracraft's definition, Wheeler and Platnick employ the notion of lineages when referring to asexual organisms. The reason is that, different from the notion of a 'lineage', populations are typically defined in terms of interbreeding.¹³

Like the promoters of the character-based PSC, Mishler and Brandon (1987) share the belief that there is no single causal process that is responsible for the evolution of every single species. However, instead of proposing a character-based species definition, Mishler and Brandon advance a process-based PSC coupled with a certain type of pluralism. In order to articulate their version of PSC, Mishler and Brandon distinguish two components of a species concept, *grouping* and *ranking* criteria. Grouping criteria provide membership conditions for taxa; ranking criteria determine whether a taxon belongs to the rank of species. They illustrate this distinction with this example:

Taking the biological species concept as an example, its grouping component is "organisms that interbreed." But since such groups are found at many levels of inclusiveness, especially if "potentially interbreeding" is added to the grouping criterion, a ranking component is needed which usually is something like "the

¹² Like Cracraft, they employ both ancestral and derived characters to define species: "for the purposes of distinguishing among species, reference is made to character states without regard to polarity" (Wheeler and Platnick, 2000, p. 59). That's because under Wheeler and Platnick's species concept, species are distinguished before taking into consideration cladistic analysis.

¹³ See Baum and Donoghue (1995, p. 561ff.) for further discussion.

largest grouping in which effective interbreeding occurs in nature” (*ibid.*, p. 404).

Mishler and Brandon’s idea is that a grouping criterion only fixes the extension of a taxon, without telling us whether this taxon belongs to the rank of, say, species or subspecies. For instance, interbreeding groups can be found both in the species and subspecies ranks. Hence, in addition to a grouping criterion, a species concept must also contain a ranking criterion. A ranking is required to determine how inclusive a taxon needs to be in order to belong to the species rank.

According to Mishler and Brandon’s PSC, species should have a single grouping criterion: all taxa must be monophyletic. But species for them can have different ranking criteria. According to them, “[t]he ranking concept to be used in each case should be based on the causal agent judged to be most important in producing and maintaining distinct lineages in the group in question” (*ibid.*, p. 406). Examples of such processes include “breeding barriers”, “selective constraints” and “the action of strong developmental canalization” (*ibid.*, p. 406). Thus, Mishler and Brandon are pluralistic with respect to ranking criteria but monist concerning grouping criteria.

A potential problem with Mishler and Brandon’s grouping criterion is that monophyly is typically defined in terms of species; viz., monophyletic taxa are groups that contain all and only the descendants of a single ancestral species. For instance, Hennig (1966) adopted an interbreeding species concept and only considered higher taxa as being monophyletic. Accordingly, species cannot be monophyletic unless we modify the definition of monophyly. Mishler and Brandon (1987) provide the following alternative definition: “[a] monophyletic taxon is a group that contains all and only descendants of a common ancestor, originating in

a single event” (*ibid.*, p. 409). In order to apply the above definition, we need to determine the meaning of the expression “common ancestor”. A “common ancestor” cannot be a monophyletic group because monophyletic groups do not have descendants by definition (section 2.3.1). Instead, Mishler and Brandon define “common ancestor” as follows:

“Ancestor” here refers, not to an ancestral species, but to a single individual. By “individual” here, we do not necessarily mean a single organism, but rather an entity (*less inclusive than the species level*) with spatiotemporal localization and with either cohesion or integration or both (as defined above). In particular cases this ancestral individual could be a single organism, a kin group, or a local population (*ibid.*, p. 409, emphasis added).

According to Mishler and Brandon, a drawback of Cracraft’s PSC is that even though it has a grouping criterion (i.e., unique combination of primitive and derived characters), it does not have a ranking criterion: “[i]t is not sufficient to say that a species is the smallest diagnosable cluster (Cracraft, 1992) or even monophyletic group, because such groups occur at all levels, even *within* organisms (e.g., cell lineages). Some judgment of the significance of discontinuities is needed” (Mishler and Brandon, 1987, p. 408). One of Cracraft’s (1992) concerns with pluralist views like Mishler and Brandon’s is that species taxa from different groups may be non-comparable (because different species for Mishler and Brandon can be defined by different processes). Mishler and Brandon do not see this as a problem though. Rather than being a shortcoming of their species definition, Mishler and Brandon (1987) maintain that the non-comparability of species taxa is an unavoidable “fact of nature” (see *ibid.*, p. 407, for further details).

Ridley proposes another variant of PSC. According to him, a species is a “set of organisms between two speciation events, or between one speciation event and one extinction event, or that are descended from a speciation event” (Ridley, 1989, p. 3). Roughly speaking, species for Ridley are sets of organisms between two nodes of a phylogenetic tree. Like Mishler and Brandon (1987), Ridley also thinks that species are monophyletic, but he articulates the notion of monophyly of species in an alternative way. Instead of appealing to the idea that the origin of species is an “individual”, Ridley thinks that “species are monophyletic in the sense of including all the descendants from a speciation event, up to the next speciation event, when the cladistic species comes to an end” (Ridley, 1989, p. 4).

Ridley’s (1989) species concept depends on the notions of “speciation” and “lineage.” But, as he acknowledges, his species definition does not provide an account of these two notions. For Ridley, his species concept should be complemented with the biological and the ecological species concepts in order to provide an account of these two notions. BSC and ESC are thus subsidiary theories of Ridley’s PSC (*ibid.*, pp. 7–8). However, Ridley does not think that this turns him into a species pluralist like Mishler and Brandon (1987). Instead, Ridley insists that his pluralism is restricted to the notion of lineages:

Once the priority of the cladistic concept is accepted, however, the dispute becomes secondary. Maybe shared selection pressures are more important in some species, and interbreeding in others: the controversy does not affect the cladistic concept. The ‘pluralism’ is only a multiplicity of (extremely-formulated) explanations of the cladistic lineage; it is not a pluralism in the cladistic species concept itself (Ridley, 1989, p. 8).

Meier and Willman articulate a process-based PSC similar to Ridley's. According to them, "[s]pecies are reproductively isolated natural populations or groups of natural populations. They originate via the dissolution of the stem species in a speciation event and cease to exist either through extinction or speciation" (Meier and Willman, 2000, p. 31).¹⁴ Like Ridley, they define a species as a lineage between two speciation events (or a speciation event and a extinction event). But unlike Ridley's concept, Meier and Willman are not pluralists concerning the notion of speciation because for them species must be reproductively isolated groups.

In short, we can identify two major versions of PSC, character- and history-based PSC (Baum and Donoghue, 1995). According to the character-based PSC, species are groups of organisms that exhibit unique combinations of characters (primitive and derived) (e.g., Cracraft, 1992; Wheeler and Platnick, 2000). The character-based PSC defines species in terms of the results of evolution, evolutionary patterns, rather than the evolutionary processes that produce them. History-based PSCs follow a different approach. According to them, species should be both monophyletic (in some sense) and defined in terms of evolutionary processes. Yet, history-based PSCs disagree over which processes produce species. For Meier and Willman (2000) reproductive isolation is necessary, while Mishler and Brandon (1987) and Ridley (1989) allow that different types of processes can produce and maintain species.

This ends my preliminary discussion of species concepts. I now turn to some recent arguments for species essentialism, starting with Okasha's (2002) essentialism.

¹⁴ This definition is also proposed by Willmann (1986).

4.2 Okasha's relational essentialism

4.2.1 Okasha on species concepts and essentialism

Okasha's essentialism is based on the distinction between intrinsic and relational properties. Intuitively, *intrinsic* properties are features that something has regardless of what is going on outside of it, such as an organism's genotype. Alternatively, an organism's fitness is a *relational* property because the same organism can be more or less fit depending on the environment it is in. According to Okasha (2002), Kripke and Putnam maintain that species essences are *intrinsic* properties of organisms. As opposed to Putnam and Kripke, Okasha (2002) argues that species taxa contain *relational* essences:

Kripke's and Putnam's account of natural kinds *can* be applied to biological species, simply by replacing their "hidden structure" with whatever relational property we take to determine species membership ... Kripke and Putnam are not wrong to regard morphological criteria as indicative of something deeper; their error lies only in a mistaken view of what that "something deeper" is (*ibid.*, pp. 202–203).

Like Kripke and Putnam, Okasha believes that species contain essences. But instead of being intrinsic, Okasha contends that biological essences should be relational properties. For Okasha "[t]wo molecule-for-molecule identical organisms could in principle be members of different species" (Okasha, 2002, p. 201).¹⁵ Let us consider Okasha's arguments for relational

¹⁵ Williams (2011) does not think that Okasha's interpretation of Putnam is correct. According to Williams, Putnam did not take essences to always be intrinsic. In particular,

essentialism.

In Okasha's reading, the gist of the classical anti-essentialist arguments (e.g., Sober, 1980; Hull, 1965) is that "modern biology offers no grounds whatever for supposing that intra-specific variation is confined to some particular set of 'accidental' traits, leaving an invariant shared essence" (Okasha, 2002, p. 197). Okasha adds that these anti-essentialist arguments are neutralized once we define species essences as relational properties. The traditional anti-essentialist arguments for him "only show that species cannot be defined in terms of essential properties, if those properties are meant to be *intrinsic* properties of the species' members" (*ibid.*, p. 199). So rather than showing that species taxa do not have essences, what the anti-essentialist arguments show is that species taxa do not contain *intrinsic* essences.

Okasha claims that species contain relational essences because contemporary species concepts define species taxa in terms of relational properties such as "being able to interbreed successfully with one group of organisms and not another" (BSC); "occupying a particular ecological niche" (ESC); and "being a member of a particular segment of the genealogical

Williams argues that Putnam assigned relational essences to disease kinds such as tuberculosis. A different reading of Putnam's theory of natural kinds is articulated by Hacking (2007). According to Hacking, "hidden structures" for Putnam were not essences but properties we choose according to our interests. Hacking also notes that Putnam later rejects the idea of metaphysical necessity as going beyond physical necessity. As Putnam says in 1990, "I now think that the question, 'What is the necessary and sufficient condition for being water *in all possible worlds?*' makes no sense at all. And this means that I now reject 'metaphysical necessity' " (Putnam, 1990, p. 70).

nexus” (PSC) (*ibid.*, p. 201). Okasha’s proposal is thus that current species concepts warrant relational essentialism. His essentialism would then be a consequence of how species taxa are defined in contemporary systematics.

According to Okasha, species essences have two roles in the Kripke/Putnam model: (a) fix the extension of species names; and (b) causally explain some of the morphological features of intraspecific organisms.¹⁶ Okasha contends that there is no *a priori* reason to suppose that the same property satisfies both (a) and (b). A property may satisfy (a) without satisfying (b)—and vice-versa. According to Okasha (2002), the notion of relational essences he proposes satisfies (a) but not (b). That is, relational essences determine the extension of species names, but they do not explain why conspecific organisms share certain traits. The reason is that species concepts do not provide proximal explanations for an organism’s traits. Okasha explains his view by focusing on BSC, the biological species concept:

Now clearly, the causal explanation of why an organism has the particular morphological traits it does will cite its genotype and its developmental environment,

¹⁶ Okasha describes (a) and (b) as follows:

For in the Kripke/Putnam model, the concept of hidden structure in fact plays two quite distinct roles. On the one hand, “hidden structure” is what users of a natural kind term are “really” trying to refer to, i.e., what they hope their superficial characteristics are reliable indicators of. On the other hand, “hidden structure” is meant to be causally responsible for the presence of those superficial characteristics (or in some versions, to constitute their supervenience base) (Okasha, 2002, p. 203).

not its ability to interbreed with certain other organisms. Morphology is indicative of that ability, but not the causal outcome of it (*ibid.*, p. 204).

Okasha makes the same point concerning PSC, the phylogenetic species concept. According to him, sharing a “particular chunk of genealogical nexus” provides no proximal explanation of why a certain organism contains certain traits (*ibid.*, p. 204). Thus, in Okasha’s view, species’ essences do not causally explain why conspecific organisms share certain traits.

Nevertheless, one might object that classifications in science are valuable only if they produce groupings that we can make successful inductions about. But since Okasha’s essentialism does not guarantee that, the objection continues, his essentialism is unsatisfactory. In response to this objection, Okasha argues that this view about the role of classifications in scientific theories is simply wrongheaded in the case of biology. As an alternative, Okasha thinks that the species concepts are valuable because of other reasons:

What then *does* make the species category a scientifically valuable one? ...

The answer is straightforward. ... Interbreeding concepts pick out groups of organisms bound together by gene flow, ecological concepts pick out groups of organisms adapted to similar environmental conditions, and phylogenetic concepts pick out groups related to common ancestry. ... Classification in biology, unlike in chemistry, is not concerned with causal generalisations, but rather with identifying those units that play a fundamental role in the evolutionary process (*ibid.*, p. 209).

To sum up, the main views defended by Okasha are the following. The classical anti-essentialist arguments are only effective against *intrinsic* essences, not relational essences.

Species concepts warrant the claim that species contain relational essences. Relational essences do not play the same role as Kripke and Putnam’s essences. For Kripke and Putnam, essences have both a semantic role and a causal-explanatory role. Okasha’s essences only satisfy the semantic role. With an understanding of Okasha’s position in hand, I now turn to some difficulties in Okasha’s argument.

4.2.2 Evaluating Okasha’s argument

Okasha’s argument for species essentialism is based on the assumption that species concepts fix the extension of species *taxa*. Nonetheless, species concepts are primarily definitions of the species *category* (section 4.1). That is, species concepts specify why a taxon belongs to the species rank—rather than the genus or the subspecies ranks. Species concepts certainly play a prominent role in fixing the extension of species taxa (Sites and Marshall, 2003, 2004; Wiley and Lieberman, 2011). However, it is worth noting that Okasha advances a specific account of how species concepts determine the extension of species taxa. More specifically, Okasha’s argument for species essentialism relies on the following premises: (i) “all modern species concepts” make use of *relational*—rather than *intrinsic*—properties for determining the membership conditions of species taxa (Okasha, 2002, p. 201); and (ii) species concepts fix the extension of species taxa by ascribing *essences* to species taxa. The thesis (i) alone does not imply (ii). For instance, Mayr and Ashlock contend that “the word ‘species’ in biology is a relational term” without endorsing species essentialism (Mayr and Ashlock, 1991, p. 27). My goal in this section is to challenge these two premises. My position is that Okasha’s (2002) essentialism relies on an incorrect account of how the modern species

concepts fix the membership conditions of species taxa. I now turn to my criticisms. I start off with Okasha's claim that the modern species concepts define species in terms of relational properties.

Criticism 1: not all “modern” species concepts define species in terms of *relational* properties

In contrast to what Okasha (2002) says, some modern species concepts define species in terms of intrinsic properties.¹⁷ In section 4.1.3 I introduced a family of species concepts, the character-based PSC, that defines species in terms of intrinsic rather than relational properties. According to these species concepts, species are the smallest diagnosable clusters of organisms (e.g., Cracraft, 1992; Wheeler and Platnick, 2000). Another example of a character-based species concept is Mallet's (1995) genotypic cluster species concept. This species concept defines species in terms of genotypic similarity. Let us consider Mallet's concept in detail.

Like promoters of the character-based PSC, Mallet claims that a species concept should not contain assumptions of how new species evolve. Instead, Mallet contends that a species should be defined in terms of how species are recognized. Specifically, in opposition to Mayr's BSC, Mallet says: “it has never been clear why we need to improve on a good taxonomist's or naturalist's definition. Viewing species as anything other than definable groups of individual organisms risks weaving hidden evolutionary constraints into the definition, just as the

¹⁷ The view that species concepts define species taxa in terms of ‘relational’ properties has also been assumed by others. See e.g., Barker, 2010; Sterelny and Griffiths, 1999; Wilson, 1999.

creationist concept of species made it hard to imagine evolution” (Mallet, 1995, p. 296). For Mallet, a species concept should not contain specific assumptions about how species evolve. To that end, Mallet claims that species should be thought of as genotypic clusters:

[W]e see two species rather than one if there are two identifiable genotypic clusters. These clusters are recognized by a deficit of intermediates, both at single loci (heterozygote deficits) and at multiple loci (strong correlations or disequilibria between loci that are divergent between clusters) (*ibid.*, p. 296).

In brief, we can identify two general approaches to the species problem. Some like Mayr and Van Valen think that the species concept should specify the process responsible for species evolution, such as reproductive isolation. Others such as Mallet, Cracraft, Wheeler, and Platnick disagree. According to them, defining the species category in terms of evolutionary processes adds an unwelcome bias to the species concept. My point here is not to defend character-based species concepts. Rather, my position is that Okasha’s depiction of the current species concepts is incorrect. In current biological systematics, some prominent species concepts define species in terms of intrinsic properties. Moreover, as Lewens (2012) points out, the use of character-based species definitions are not exceptional in current biology. Character-based species definitions are used in different fields of biology such as microbiology (Ereshefsky, 2010a), botany (Stuessy, 2009) and protistology (Finlay, 2004; Harper et al., 2009). Thus, my criticism of Okasha (2002) is that his argument relies on a false premise; viz., that the modern species concepts define species taxa in terms of relational properties. Not only are some prominent species concepts character-based, but also character-based species definitions are widely used in current biology. Accordingly, an argu-

ment for relational essentialism cannot be neutral concerning the species problem: Okasha's argument for relational essences can only take off if complemented with an argument against every non-relational species concept, such as Mallet's (1995). Nevertheless, even if complemented with such an argument, I think there are further difficulties with Okasha's argument.

Criticism 2: relational essentialism and population thinking

In this section I argue that, while Okasha's essences are relations between *organisms*, BSC (and ESC) delimits species taxa via relations between *populations*. In what follows, I first describe in which sense BSC is a population-based concept, and then explain why that affects Okasha's essentialism.

Earlier attempts of defining species in terms of interbreeding did not use the notion of 'population' (Mayr, 1982, pp. 270–271). For instance, at the beginning of the Modern Synthesis, Dobzhansky (1935) formulates reproductive isolation as a property of individual organisms: "a species is a group of individuals fully fertile inter se, but barred from interbreeding with other similar groups by its physiological properties (producing either incompatibility of parents, or sterility of hybrids, or both)" (*ibid.*, p. 353). However, his definition has the drawback of implying that interspecific organisms do not exchange genes (Coyne and Orr, 2004, p. 28). Even though Dobzhansky acknowledges that reproductive isolation is not an all-or-none device, the possibility of species hybridization is not built-in to his species definition. The same is not true about Mayr's definition. According to him, "[s]pecies status is the property of populations, not of individuals. A population does not lose its species status when occasionally an individual belonging to it makes a mistake and hybridizes with another species" (Mayr, 2004, p. 178). So, reproductive isolation is a population-level phenomenon:

two populations can be said to be reproductively isolated while individual organisms belonging to those different populations hybridize with each other.¹⁸ Furthermore, current formulations of BSC follow Mayr’s lead in understanding reproductive isolation as a relation between populations (see e.g., Coyne and Orr, 2004; Ghiselin, 1997; Johnson, 2006; Sober, 2000).¹⁹

Returning to Okasha’s account, essences for him are relations between individual organisms. As Okasha phrases it, a pet dog belongs to the species *Canis lupus* because of how this dog relates “to other organisms and/or to the environment” (Okasha, 2002, p. 199). Relational essences are thus what ties an individual organism to its species. Okasha claims that this view about species membership is justified by the current species concepts, including BSC. In what follows, I suggest a non-essentialist interpretation of how BSC fixes the

¹⁸ Like BSC, ESC is also concerned with populations. Recall that for Van Valen (1976) species are *lineages* that occupy a certain adaptive zone, and a lineage is “a clone or an ancestral-descendant sequence of populations” (*ibid.*, p. 233). And similar to Mayr, Van Valen understands populations as groups in which individuals inside the population exchange genes “more frequently than with individuals outside the population” (*ibid.*, p. 234). So, like in BSC, there can be gene flow between different ESC-species.

¹⁹ As Ghiselin puts it: “Interbreeding is a property of populations as wholes, not of organisms, and it makes a great difference. For one thing, organisms of different sizes or the same sex could exist within a single species. Domesticated dogs are all parts of the same species, even though a Chihuahua cannot mate with a Great Dane. A similar situation can exist upon a geographical basis, and in the case of ‘ring species’ two local populations behave as if they were two different species in a region of local overlap” (Ghiselin, 1997, p. 95).

membership conditions of species. Here is my suggestion in a nutshell. The relation “is able to interbreed with” applies to populations rather than individual organisms. This means that two populations can be reproductively isolated while some individual members of these populations interbreed with each other. But if “being able to interbreed” is a property that conspecific organisms can have or lack, then this property is not essential but an *accidental* property of conspecific organisms. In this way, what binds a pet dog to *C. lupus* is not an essence, but an accidental property.

One potential concern with the above suggestion is that cross-species hybridization within BSC-species might be exceptional. In what follows, I argue otherwise. To begin with, to expect total reproductive isolation in BSC-species is unreasonable given what we know about species evolution. In particular, because speciation is a gradual process (with exception of cases of speciation by polyploidy), species are expected to exhibit different degrees of reproductive isolation. In fact, many well-established species that BSC applies to do not show total reproductive isolation, such as Darwin’s finches (Grant, 1993) and warbler species (Secondi et al., 2003; Secondi, Faivre, and Bensch, 2006). Another group of examples that illustrates cross-species hybridization is *hybrid zones* (Barton, 2001; Barton and Hewitt, 1985). A remarkable feature of hybrid zones is that they can be responsible for interspecies ‘introgression’, where genes of one species are permanently incorporated into another species (Currat et al., 2008). Thus, species differences are not only compatible with gene flow, but with introgression of some genes from one species to another. The above examples illustrate that, under BSC, what is relevant for species status is not hybridization per se, but the consequences of such hybridization events. Interbreeding between two populations

only indicates that they belong to the same species if the gene pools become fused.²⁰ Species status is thus compatible with different degrees of species hybridization, including cross-species introgression. Coyne and Orr (2004) nicely summarize this feature of BSC:

Our notion of species status, then, involves a sliding scale. . . . As reproductive barriers become stronger, taxa become more and more “species-like,” and when reproductive isolation is complete we consider taxa to be “good species.” This view obviously requires some subjective decisions about species status (*ibid.*, p. 34).

The “sliding scale” conceptualization of species is well-suited for understanding speciation given that speciation is mostly a gradual process. Hence, if we are interested in how new species evolve, then allowing species hybridization is a virtue rather than a limitation of BSC. In contrast, in order to satisfy the International Codes of Nomenclature (e.g., ICZN and ICBN), taxonomists must decide about the species status of taxa with intermediary reproductive isolation. So whereas BSC brings to the fore the gradual process of species formation, the codes are designed to omit this fact. Mayr draws attention to that fact in the quote:

The rigidity of zoological nomenclature forces the taxonomist to record borderline

²⁰ Ghiselin makes this point in the quote: “[w]hat matters is not that all gene flow be cut off, but that it be cut off to a sufficient degree that the species can continue to diverge instead of fusing back together into a single populational individual” (*ibid.*, p. 96). In a similar fashion, Hull says: “[c]ontrary to popular opinion, the production of an occasional fertile hybrid is not enough for biologists to consider two species one. What matters is how extensive the introgression is” (Hull, 1978, p. 349).

forms either as subspecies or as species. An outsider would never realize how many interesting cases of evolutionary intermediacy are concealed by the seeming definiteness of the species and subspecies designations (Mayr, 1963, p. 499).

BSC is designed to understand the origin of new species and, for this reason, this concept should make room for taxa to be more or less species-like. That's not true about the codes. Since the codes are designed to provide guidelines for taxon designation, taxa have to be thought as having more definite boundaries.²¹ While species designation abstracts away the difference between good and not-so-good species, this difference is a central focus of BSC. My view is that Okasha's essentialism overlooks this contrast. Viewing 'capacity of interbreeding' as a species essence treats BSC as a criterion for taxon designation rather than an account of species status at different stages of evolution.

In short, Okasha's essentialism is an account of what ties an individual organism to a particular species. According to him, the species an organism belongs to is fixed by a relational essence, set by the modern species concepts such as Mayr's BSC. My point in this section is that this argument is not correct. The relation "being able to interbreed with" is an *accidental*—rather than an essential—feature of conspecific organisms in a BSC-species: conspecific organisms can fail to satisfy this relation, and organisms of different species can have this property. Furthermore, species hybridization is not exceptional among BSC-species. There are many species that BSC applies to that do not exhibit total reproductive isolation.

²¹ In order to characterize evolutionary intermediaries, concepts not employed by the current codes have been proposed such as *superspecies* and *semispecies*. For further details about these concepts, see Mayr and Ashlock (1991, pp. 53–54). See also Mayr and Ashlock (1991) for a list of recommendations for assigning species status to incipient species.

And, given that BSC is supposed to account for how species evolve, BSC alone provides a “sliding scale” conception of species rather than an account of species designation for any given organism. Thus supposing that “being able to interbreed with” is a species’ essence goes both against how BSC has been applied in nature and the theoretical motivations behind BSC.

Stepping back from these details, here is an outline of this section. One of the appealing features of Okasha’s essentialism is its purported neutrality with respect to the species problem debate. That is, no matter which of the current species concept one chooses, relational essentialism is supposed to hold. Okasha attempts to accomplish that by defending a general thesis of how the modern species concepts fix the extension of species taxa. For Okasha, species concepts fix the members of species taxa by ascribing relational essences to them. My point in this section is that this view is incorrect. Some prominent species concepts define species in terms of intrinsic instead of relational properties, such as genotypic similarity (Mallet) or apomorphies (Cracraft). And population-based species concepts such as BSC do not delimit species by assigning essential properties to conspecific organisms but accidental properties. Therefore, Okasha’s essentialism is not grounded by current species concepts.

4.3 Boyd's HPC theory

4.3.1 Biological taxa as HPC kinds

Boyd (1991, 1999a,b, 2010) and others (e.g., Rieppel, 2005; Wilson, Barker, and Brigandt, 2007) have proposed a theory of natural kinds called *Homeostatic Property Cluster* (henceforth, HPC theory). Natural kinds as defined by HPC theory are called *HPC kinds*. For Boyd and others biological species are paradigmatic HPC kinds. HPC kinds as defined as having two components: a cluster of properties, and “homeostatic” mechanisms. In the case of species, “shared phenotypic characters” form an HPC cluster, and “gene flow” is a homeostatic mechanism (Boyd, 1991, p. 142). The properties within a cluster should “co-occur in an important number of cases” (Boyd, 1999a, p. 143). In other words, the instantiation of a property in an HPC cluster tends to be followed by the instantiation of other properties in the same cluster. If species are HPC kinds, then one can infer with better than chance prediction that members of the same species look like. Also, according to HPC theory, the properties in a cluster tend to co-occur because of homeostatic mechanisms. For example, in the case of species, gene flow could be a homeostatic mechanism responsible for maintaining shared similarities among conspecific organisms. In short, HPC kinds have two distinguishing features. Firstly, there is a cluster of properties that tend to co-instantiate. Moreover, the co-instantiation of these properties has a causal underpinning, provided by homeostatic mechanisms.

There are two features that set HPC theory apart from intrinsic essentialism. In Boyd's theory, membership conditions for natural kinds may contain relational properties. For instance, Boyd considers “capacity of interbreeding”, a relational property, to be an example

of a homeostatic mechanism for species. Furthermore, unlike intrinsic essentialism, HPC theorists do not think that there is a set of properties that is jointly sufficient and necessary for kind membership. For them, different members of an HPC kind can satisfy different subsets of the HPC cluster. Yet, like intrinsic essentialists, HPC theorists claim that the shared similarities within a taxon are robust enough to warrant successful induction.

If biological taxa are HPC kinds, then we should be able to break taxon definitions into two components, property clusters and homeostatic mechanisms. Promoters of HPC theory have proposed different ways to accomplish this (Boyd, 1999a; Brigandt, 2009; Wilson, Barker, and Brigandt, 2007). In the case of species, HPC theorists suggest that the cluster of properties contain the phenotypic features that typically occur within a species.²² With respect to the homeostatic mechanisms, they can be mechanisms described by the species concepts, such as reproductive isolation, ecological factors, and common descent (Boyd, 1999a; Brigandt, 2009; Wilson, Barker, and Brigandt, 2007). In order to motivate how HPC theory could be applied to finches, Wilson, Barker, and Brigandt (2007) observe that “[f]inches may tend to have beaks of a certain size and shape because of selective regimes their ancestors faced in deep past and because of gene flow that distributed the traits that

²² According to Boyd:

All of the standard sorts of evolutionary explanations, either for speciation or for the phenotypic properties species exhibit, tacitly (if not explicitly) presuppose that members of each of the various species in question exhibit a very wide range of shared phenotypic characters of the sort sustained by mechanisms of property homeostasis (Boyd, 1999a, p. 167).

were selected for under those regimes” (*ibid.*, p. 15). According to them, the size and shape of the beak of finches belongs to the property cluster. “Selective regimes” and “gene flow” are homeostatic mechanisms that explain why finches have a specific type of beak.

In the case of higher taxa, HPC theorists suggest that the property cluster of a taxon is its shared synapomorphies, whereas its homeostatic mechanism is common descent.²³ Brigandt makes this suggestion:

The fact that in each taxon member these characters [synapomorphies] tend to occur together and that each character is shared by most members is explained by common descent from a founding species, so that common descent is the causal process (‘homeostatic mechanisms’) determining the identity and boundary of this higher taxon (Brigandt, 2009, p. 80).

HPC theorists make the empirical claim that biological taxa satisfy Boyd’s definition of HPC kinds. According to them, biological taxa can be factored into a cluster of co-occurring properties caused by homeostatic mechanisms. In what follows, I discuss some shortcomings of HPC theory. My overall suggestion is that the proposed arguments for species being HPC kinds are incomplete at best. Consequently, HPC theory represents a potential account, rather than a definitive view about species taxa.

²³ However, in addition to synapomorphies, plesiomorphies should also be part of a property cluster. Otherwise, ancestral groups would be excluded.

4.3.2 HPC kinds, variability, and induction

Members of the same species can exhibit a wide range of phenotypes. Consider for instance alternation of generations in ferns, in which parents and their offspring can look very unlike each other (Godfrey-Smith, 2009, pp. 78–79). Variation within species is in turn caused by a wide range of evolutionary processes: gene flow, interspecies competition, epistatic interactions, development and sexual selection, to name a few. This prompts the following question: from all the processes that shape the evolution of a species, which of them should we pick as a species’ homeostatic mechanism? Boyd describes species concepts as assigning particular homeostatic mechanisms to species (Boyd, 1999a). For him different species concepts disagree over the sort of homeostatic mechanism that maintains the integrity of a species.²⁴ In this way, one might think that defining species in terms of homeostatic mechanisms is already present in the modern species concepts. If a species is better characterized by, say, the ecological species concept, then the homeostatic mechanism of this species will include selective forces stemming from the species’ niche. Nevertheless, as I shall argue below, different from what Boyd claims, species concepts do not ascribe homeostatic mechanisms to species.

Okasha (2002) makes the point that (process-based) species concepts such as BSC and

²⁴ For instance, according to Boyd “the dispute between defenders of Mayr’s biological species concept and theorists who hold that the species category properly includes asexually reproducing organisms is just a dispute over the relative power of these sorts of homeostatic mechanisms in sustaining the sort of homeostatic integrity characteristic of biological species” (Boyd, 1999a, p. 165).

ESC do not explain why conspecific organisms tend to share certain traits.²⁵ Referring to BSC, Okasha says: “[n]ow clearly, the causal explanation of why an organism has the particular morphological traits it does will cite its genotype and its developmental environment, not its ability to interbreed with certain organisms” (*ibid.*, p. 204). A way of articulating Okasha’s point is with Mayr’s distinction between *ultimate* and *proximal* explanations:

Organisms . . . have two different sets of causes because organisms have a genetic program. Proximate causes have to do with the decoding of the program of a given individual; evolutionary causes have to do with the changes of genetic programs through time, and with the reasons for these changes (Mayr, 1982, p. 68).²⁶

For instance, there are two types of causal explanations one might propose for sexual dimorphism: “the proximate causation of sexual dimorphism might be hormonal or some genetic growth factors, while sexual selection or a selective advantage of differential utilization of the food niche might be the ultimate causation” (*ibid.*, p. 68). BSC is designed to help explain how isolated gene pools evolved. Accordingly, BSC is in the business of providing ultimate explanations. Yet, BSC is silent about the particular diagnostic traits of, say, finches. For in order to explain the traits of a species, we need to refer not only to the genotype of its organisms but also to how its members respond to immediate factors from the environment. For instance, in order to explain the beak shape of a finch species, we have to refer to factors

²⁵ As discussed in section 4.2, Okasha does not believe that species concepts can have an explanatory role. Instead, he thinks that species have a semantic role (i.e., species concepts fix the extension of species taxa).

²⁶ See also Mayr (1961).

like food supply and the particular selective forces at play. In short, while process-based species concepts such as BSC yield ultimate explanations, Boyd's homeostatic mechanisms provide proximal explanations. Consequently, it is not evident how species concepts can be used to determine the homeostatic mechanisms of species. We are then back to our original question: from all the processes that shape species evolution, which of them are homeostatic mechanisms? But before I re-consider this question, let me pause for a moment to discuss other features of Boyd's HPC theory.

The proximal causes of a species' traits are likely to be very variable, such as food supply and selection strength. And like some fern species, conspecific organisms may look very unlike each other. HPC theorists acknowledge that species are imperfectly similar, and they have proposed ways to accommodate that in their model. To begin with, no phenotypic feature in a property cluster has to occur in all and only members of an HPC kind (see above). And in order to accommodate species' polymorphism such as sexual dimorphism, Boyd suggests a further refinement:

[Species polymorphisms] require that we characterize the homeostatic property cluster associated with a biological species as containing lots of conditionally specified dispositional properties for which canonical descriptions might be something like, "if male and in the first mold, *P*," or "if female and in the aquatic stage, *Q*" (Boyd, 1999a, p. 165).

So, Boyd deploys two strategies to accommodate the variability of species: no feature in the property cluster is sufficient and/or necessary for species membership; and the properties in a property cluster can be conditional statements. Even though these remarks are about

property clusters, I suppose that a promoter of HPC theory could apply the same strategies to homeostatic mechanisms. However, there is the concern that these strategies make HPC kinds too liberal. This type of criticism has been raised by Ereshefsky and Matthen (2005). In particular, they worry that Boyd's use of conditional statements makes HPC kinds too permissive to model species.²⁷ Summarizing, the point I want to emphasize is this. Because of species heterogeneity, promoters of HPC theory typically stress that HPC kinds are very flexible since it allows the use of conditional statements as suggested by Boyd (e.g., Wilson, Barker, and Brigandt, 2007, p. 211). Still, I do not think that this is enough. For there is the need of an additional argument showing that a species and the HPC kind that corresponds to that species have the same boundaries. Otherwise HPC kinds run the risk of being more inclusive than the species that they are supposed to model in the first place.

So far I have discussed ways Boyd has suggested to accommodate species' variability. But it is worth noting that HPC theory is not compatible with any range of variation within a species either. Variability within species should stay within certain limits for it to warrant successful induction. Species are HPC kinds only if the following thesis is true: “[i]t is also true of biological species . . . that their members are often *pretty* uniform, so that studying a relatively small sample from a species gets information about (almost) all of its members” (Boyd, 1999b, p. 82). If true, Boyd's quote can only be true about *certain* traits within a species. For species do not appear to be uniform with respect to any trait. For instance,

²⁷ As Ereshefsky and Matthen (2005) note: “[o]ne needs, however, to be careful how one uses such powerful logical tools: they can become a universal solvent that makes all variation disappear and collapses the entire biological domain into a single morpho-clump” (*ibid.*, p. 9).

domestic dogs do not appear to be uniform with respect to size. But what sort of traits is Boyd referring to? More generally, for a given species, how can we determine its property cluster? As discussed previously, a similar problem applies to homeostatic mechanisms. There is a constellation of processes that shape the evolution of species and it is not evident which of them should be homeostatic mechanisms (and species concepts will not help). As Ereshefsky (2010c) puts it, HPC theory leaves us in an “explanatory circle”:

In searching for which mechanisms are parts of an HPC kind’s essence, we look for those mechanisms that cause that kind’s covarying similarities. . . . We then need a way to identify which covarying similarities are similarities of the kind in question. The only avenue that HPC theory offers for determining which similarities are those of a particular kind is to investigate which similarities are caused by that kind’s homeostatic mechanisms. But then we are back to our original question: which mechanisms are parts of a kind’s essence? (*ibid.*, p. 677).

An HPC theorist might claim that the homeostatic mechanisms and the property cluster of a species is an empirical matter. I disagree, however. Even if we had exhaustive empirical data about a species, the points raised above would still stand. HPC theory, as formulated, does not specify how one could model this species as HPC kinds. My view is thus that HPC is an incomplete position (at best). Different from what Boyd claims, HPC theory as it stands fails to show the existence of any link between conspecificity and induction in species.

4.4 Devitt’s hybrid essentialism

Devitt advances the following notion of essence:

A property P is an *essential property* of being an F iff anything is an F partly in virtue of having P . A property P is *the essence* of being an F iff anything is an F in virtue of having P . The essence of being F is the sum of its essential properties (Devitt, 2008, p. 345).

Devitt (2008) argues that species taxa and higher taxa contain essences as defined above. Devitt's essentialism is a 'hybrid' brand of essentialism in the following sense. Unlike intrinsic essentialists such as Kitts and Kitts (1979), Devitt (2008) allows relational properties to be part of species' essences. However, as opposed to relational essentialists such as Okasha (2002), Devitt does not think that species essences can only contain relational properties. In brief, for Devitt species essences should be at least partially intrinsic.

The goal of this section is to introduce Devitt's hybrid essentialism. I begin discussing Devitt's argument for species essentialism in section 4.4.1. After that, I move to the issue of whether Devitt's hybrid essentialism is compatible with some of the current species concepts (section 4.4.2). I end with Devitt's view about what the intrinsic features for species are (section 4.4.3).

4.4.1 Devitt's argument for species essentialism

Devitt's argument hinges on a particular view of why we classify organisms:

We group organisms together under what seem, at least, to be the names of species or other taxa and make generalizations about the morphology, physiology, and behavior of the members of these groups: about what they look like, about what they eat, about where they live, about what they prey on and are prey to,

about their signals, about their mating habits, and so on (Devitt, 2008, p. 351).

According to Devitt we classify organisms into species because we can make reliable generalizations about conspecific organisms. Devitt adds, the existence of such generalizations demands an explanation. Since there are reliable generalizations about the members of a species, there must exist some connection between species membership and their observable attributes. Devitt claims that we can only specify this connection if we take into account the intrinsic properties of species:

Explanations will make some appeal to the environment but they cannot appeal only to that. There has to be something about the very nature of the group—a group that appears to be a species or other taxon of some sort—that, given its environment, determines the truth of the generalization. That something is an intrinsic underlying, probably largely genetic, property that is part of the essence of the group. Indeed, what else could it be? (*ibid.*, p. 352).

Devitt's suggestion is that one can make reliable generalization about a species in part because of the intrinsic properties of its members. However, this conclusion does not show that species contain intrinsic essences. For instance, maybe the same set of intrinsic properties could account for the same trait across different species. In order to complete his argument for essentialism, Devitt adds:

Suppose that the generalization is 'All F s are P ' and that the explanatory intrinsic property is G . So it is agreed that, ultimately, it is because F s have G that they have P . *The question asks why we must take G to be an essential*

property of F's. My answer rests on the just argued claim that the generalization is law-like (ibid., p. 378, emphasis added).

So Devitt thinks that the intrinsic features used to explain reliable generalizations over species should be essences because such generalizations are law-like. However, as opposed to Devitt, one might protest that biological generalizations cannot be law-like because generalizations about species may contain exceptions. In response to this, Devitt points out that there are different accounts of laws that can make sense of the idea that biological generalizations are law-like even though they are not true about *every* member of a species. In particular, Devitt suggests three ways in which biological generalizations can be law-like:

(w₁) They are *ceteris paribus laws*.

(w₂) They are *statistical laws*.²⁸

(w₃) They are law-like “but there is some indeterminacy about precisely which organisms they would cover”.

Thus, Devitt believes that the “purported exceptions” to biological generalizations can be accommodated if we choose an appropriate conception of law. A biological generalization does not have to be true about every member of a species in order to be law-like. And for Devitt there are at least three ways of guaranteeing that: either biological generalizations only hold in certain conditions (i.e., (w₁)); or they are true just to a certain parcel of a species

²⁸ Here is an example of statistical law according to Devitt: “the claim that, say, 90% of *F*'s are *P* can be lawlike: it can sustain the subjunctive conditional that if something were an *F* it would very likely be *P*” (Devitt, 2008, p. 377).

(i.e., (w_2) and (w_3)). Note that establishing that there are law-like generalizations about species is a crucial step in Devitt's argument. It is based on this step that he concludes that species contain intrinsic essences.

In short, Devitt's argument for his hybrid essentialism comprises the following steps. The reason we classify organisms into species is because we can make reliable generalizations about the traits of conspecific organisms. In order to account for such generalizations, we should cite intrinsic features of organisms. Finally, these intrinsic features should be species essences because generalizations about species are law-like. With an understanding of Devitt's argument in hand, I now discuss some difficulties in his argument.

Devitt's argument depends on the premise that generalizations over species are law-like. As Devitt acknowledges, generalizations over species are known to contain exceptions. For instance, having one horn is a diagnostic trait of Indian rhinos (Laurie, Lang, and Groves, 1983). Still, that does not prevent an Indian rhino from lacking this feature (e.g., a young Indian rhino may not have a fully developed horn). Devitt suggests ways in which we can accommodate these exceptions while still maintaining that there are reliable generalizations over conspecific organisms. As he suggests, generalizations over species can be thought of as statistical laws for instance (see above). Nonetheless, Devitt does not provide an account of how we can assess whether a generalization about species is law-like (Barker, 2010, p. 85). More specifically, Devitt does not provide a *positive* argument showing why generalizations in biology are law-like in any of the senses he proposes—i.e., (w_1) , (w_2) and (w_3) . Devitt seems to only show that generalization over species could in principle be law-like. But if it is not established that generalizations over species are law-like, Devitt's argument for essentialism cannot take off.

Another difficulty in Devitt’s argument is his claim that the intrinsic features used to explain shared traits in a species have to be species-specific. This criticism has been raised by Ereshefsky (2010c). For instance, consider stripes in zebras. Zebras’ stripes are explained by specific ontogenetic mechanisms (Carroll, 2005). But even though these ontogenetic mechanisms refer to intrinsic features of zebras, these mechanisms also occur in other mammals such as cats (Ereshefsky, 2010c, p. 680). Ereshefsky’s point is that although Devitt may be right that we must cite intrinsic properties to explain an organism’s trait, there is no reason for thinking that these intrinsic properties only occur in members of a certain species.²⁹ Thus, even if we assume that generalizations over species are law-like, Devitt’s conclusion that species contain intrinsic essences does not follow.

A further issue with Devitt’s essentialism is whether it is consistent with the species concepts. As we shall see in the next section, Devitt’s essentialism is not compatible with phylogenetic definitions of species.

4.4.2 Devitt on species concepts

One potential objection to Devitt’s essentialism is that species concepts define species taxa without postulating intrinsic essences. In this way, to assign intrinsic essences to species seems to unnecessarily inflate our ontology. Devitt’s answer to this objection starts with the observation that there are two ways of interpreting the question “What is a species?”:

The Taxon Question: What are the necessary and sufficient conditions for an organism to belong to a species?

²⁹ This type of criticism of Devitt (2008) has also been proposed by Barker (2010, p. 85ff.).

The Categorical Question: Why is a group of organisms a species rather than a subspecies, a genus, etc.?

The Taxon Question is about the relation between individual organisms and species taxa. The Categorical Question is about the relation between species taxa and the species category.

Although Devitt grants that the species concepts may serve as an answer to the Categorical Question, he contends that they are not sufficient to answer the Taxon Question. Regarding BSC and ESC, Devitt says: “[t]hey [BSC and ESC] do not tell us what property makes an organism a member of the group of *F*’s *in particular*. Indeed, they do not even tell us *what sort* of property that must be” (Devitt, 2008, p. 360). So, since BSC and ESC are not designed to answer the same question as his hybrid essentialism, Devitt concludes that these two species concepts can be wedded to his hybrid essentialism. However, as he acknowledges, the same line of reasoning does not apply to the Phylogenetic Species Concept (PSC).

According to Devitt, his hybrid essentialism is not compatible with (history-based) versions of PSC. The reason is that his hybrid essentialism is in disagreement with two assumptions congenial to PSC. These two assumptions are:

- (1) Species are only formed via a branching phenomenon. Consequently, speciation may not occur by anagenesis.
- (2) A species may form a new species without changing the intrinsic properties of its members.³⁰

³⁰ This view has been defended by Okasha (2002).

Devitt cannot accept (1) because, if true, there is no limit to the variation of intrinsic characteristics among conspecific organisms. Because, according to (1), in absence of a branching phenomenon, the species members may undergo any intrinsic change. And (2) is incompatible with intrinsic essentialism since (2) allows speciation without variation among the organisms' intrinsic features. Thus, Devitt's essentialism is incompatible with both (1) and (2). Hence, while Devitt's hybrid essentialism is compatible with BSC and ESC, his essentialism is inconsistent with PSC.

So far I considered Devitt's argument for essentialism, and how his essentialism relates to species concepts. But I did not consider Devitt's view about what an intrinsic essence is. This is done in the next section.

4.4.3 Devitt's appeal to clusters of intrinsic properties

For Devitt (2008), species essences are at least partly intrinsic. But what kind of intrinsic properties should be part of a species essence? Devitt suggests that they are "largely genetic":

In sexual organisms the intrinsic underlying properties in question are to be found among the properties of zygotes; in asexual ones, among those of propagules and the like. For most organisms the essential intrinsic properties are probably largely, although not entirely, genetic (*ibid.*, p. 347).

A central theme in the criticism against intrinsic essentialism is that species do not have any genetic property essentially. As Okasha (2002) makes this point, "species taxa are distinguished by clusters of covarying [chromosomal and genetic] traits, not by shared essences" (*ibid.*, p. 197). Devitt (2008) does not think that this is a problem for his hybrid

essentialism. After quoting the aforementioned passage from Okasha (2002), Devitt adds:

Great! So the clusters are the essences!! On the strength of these remarks, it seems as if the consensus should be simply that the crude idea that there is, say, “a tiger gene” is wrong. But to reject that crudity is not to reject the idea that a certain cluster or pattern of underlying, largely genetic, properties is common and peculiar to tigers (Devitt, 2008, p. 371).

Like Boyd’s HPC, Devitt also relies on the idea that we can define species in terms of clusters of properties. This brings the same sort of challenges I raised against HPC theory (section 4.3.2). First of all, there is the problem of specifying which subset of intrinsic features should belong to a species cluster. Also, for Devitt the variability within a species cluster should stay within certain limits—because species for him can evolve by anagenesis (section 4.4.2). Nevertheless, Devitt does not indicate how much variation there can be within a species’ intrinsic cluster before the evolution of a new species happens. In short, Devitt does not mark out how inclusive these clusters of intrinsic properties are. And this is relevant for Devitt’s argument because, without this information, we cannot evaluate whether any species satisfies Devitt’s account.

Summarizing so far. Devitt’s argument relies on the premise that generalizations are lawlike. However, Devitt does not provide a positive reason for thinking that generalizations over species are lawlike. But even if we suppose that such generalizations are lawlike, it is not evident why the intrinsic properties one might use to explain these generalizations are essences. It seems that the same intrinsic properties could be used to explain a generalization across different species. And finally, Devitt’s appeal to the notion of properties clusters

introduces new difficulties in his argument. In particular, Devitt does not give enough details concerning which intrinsic properties should belong to a species' cluster.

Next chapter: so far I have argued against modern versions of biological essentialism, such as historical essentialism and HPC theory. However, one might object that by simply rejecting essentialism we are left with unanswered questions that essentialism was designed to solve, such as explaining the presence of certain traits among conspecific organisms. For this reason, the objection continues, even if some of the current essentialist theories are not satisfactory, this does not show that developing an essentialist theory is not a desirable program to be pursued in philosophy of biology. The difficulties with essentialism may simply indicate how we can improve our essentialist theories rather than showing that we have to reject essentialist theories (about biological taxa) altogether. The goal of the next chapter is to engage with this objection. More precisely, I will motivate the view that we can satisfy the rationale for essentialism in non-essentialist ways.

Chapter 5

Biological taxa without essences

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As discussed in the previous chapters, essences have been thought to satisfy at least one of the following roles: (1) to explain shared similarities within a taxon (Boyd, 1999a; Devitt, 2008; Griffiths, 1999); and (2) to provide membership conditions for taxa (LaPorte, 2004; Okasha, 2002). In the previous chapters I have argued against different versions of modern essentialism. But if biological essentialism is unjustified, how can we account for (1) and (2)?

My goal in this chapter is to introduce non-essentialist ways of satisfying these two roles. In section 5.1, I consider a non-essentialist view about membership conditions for taxa proposed by Moore (2003). Moore's proposal is that, in order to increase taxonomic stability, membership conditions should not fix all potential members of a taxon like essentialist theories do. The reason is that essentialist membership conditions are not flexible enough to prevent drastic revisions of our current classifications as our knowledge about biodiversity updates. In section 5.2, I assess the argument that postulating essences is required to explain shared features among members of the same taxon. Based on Sober's (1984) distinction between group and individual explanations, I suggest that we can explain a taxon's shared similarities in non-essentialist ways. Hence, the argument that we should postulate essences because of its explanatory power is not cogent. Therefore, my conclusion in this chapter is that the two main rationales for essentialism, membership conditions and explanatory power, are not compelling reasons for adopting biological essentialism.

5.1 Membership conditions without essences

An account of the membership conditions for biological taxa is supposed to show the relation that ties a taxon name to its referents. In other words, such an account provides a hypothesis about what fixes the extension of taxon names. The discussion about membership conditions for taxa has gained some prominence in recent philosophy and biology literature due to criticisms of commonly used principles by modern codes of nomenclature, such as the use of taxonomic ranks (e.g., de Queiroz and Gauthier, 1994; Ereshefsky, 2001). Arguments for and against the current codes are typically associated with a particular view about

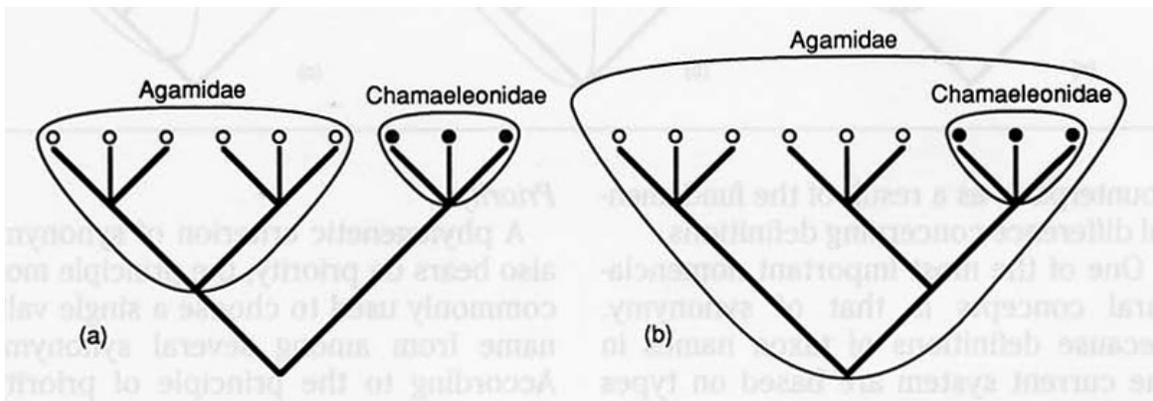


Figure 5.1: Agamidae and Chamaeleonidae under different phylogenetic hypotheses. From de Queiroz and Gauthier (1994, p. 30).

how the extension of taxon names should be fixed. For instance, de Queiroz and Gauthier (1990, 1994) argue that fixing the extension of biological taxa via common ancestry relations yields a more stable system of classification. Against de Queiroz and Gauthier, Ghiselin (1995) argues that biological taxa should be defined ostensively. In this section I describe different accounts for taxon membership and motivate a non-essentialist alternative proposed by Moore (2003). According to Moore, membership conditions for taxa should be partial—i.e., they should not fix all potential members of a taxon in advance. But before I introduce his view, I discuss what a satisfactory account of taxon membership is supposed to accomplish in section 5.1.1. As I elaborate in that section, membership conditions for taxa should yield stable classifications. In section 5.1.2, I turn to the question of whether essentialist theories can guarantee stable classifications.

5.1.1 Membership conditions and stability

Membership conditions for taxa are supposed to foster *taxonomic stability* (Jeffrey, 1989, sec. 4). In other words, as we update our knowledge about biodiversity, our current classifi-

cations are not expected to change drastically. To make an analogy with chemistry, it would be undesirable to have a system of classification in which the definition of most elements are revised every month due to new chemical findings. In a stable taxonomic system, our classifications are somehow buffered against the influx of new information, such as phylogenetic revisions and the discovery of new species. To mention an example, de Queiroz and Gauthier (1994, p. 30) argue that the following definitions yield a stable classification:

“Agamidae” =_{df} the clade stemming from the most recent common ancestor of the species represented by open circles (see Figure 5.1).

“Chamaeleonidae” =_{df} the clade stemming from the most recent common ancestor of the species represented by filled circles (see Figure 5.1).

Figure 5.1 shows how the extension of Agamidae and Chamaeleonidae change under different phylogenetic hypotheses. For de Queiroz and Gauthier (1994), these definitions ensure stability since the taxon names “Agamidae” and “Chamaeleonidae” refer to the same clade (i.e., branches with the same ancestor) under different phylogenetic hypotheses.¹ The definitions of Agamidae and Chamaeleonidae dictate how we should change the extension of these taxa as our knowledge about phylogeny updates. Stability is thus a function of how we define taxa. Moreover, de Queiroz and Gauthier do not think that the above definitions yield stable

¹ De Queiroz’ and Gauthier’s (1990; 1992; 1994) conception of stability has been criticized. For instance, according to Nixon and Carpenter (2000) the number of species within a taxon is what determines if a system is stable. So, in Nixon and Carpenter’s view, a taxon can refer to the same clade in different scenarios and, yet, the taxon’s definition may produce instability because there are big shifts in number of species referred to the taxon.

classifications because their definitions are explanatory. Stability has to do with the denotation of a taxon under different phylogenetic hypotheses. Stability is thereby a constraint that taxon definitions should satisfy which is distinct from the capacity of explaining shared similarities among members of a taxon.

Thus essentialism can provide satisfactory membership conditions for taxa only if the resulting classification is stable. In the next section I discuss how the current taxonomic codes attempt to ensure stability. As I shall discuss, the current codes ensure stability by preventing taxa from having essentialist membership conditions. Accordingly, counter to what biological essentialists have claimed, essentialist membership conditions are in disagreement with contemporary taxonomy.

5.1.2 The idea of partial membership conditions

Current views about membership conditions for taxa rely on principles used by the current codes of nomenclature (e.g., Hull, 1978), or on criticisms of these codes (e.g., de Queiroz and Gauthier, 1990). The main currently used codes are the International Code of Zoological Nomenclature (ICZN), the International Code of Botanical Nomenclature (ICBN), and the International Code of Nomenclature of Bacteria (ICNB).² Such codes regulate taxon names by a series of rules (or articles) plus recommendations for specific circumstances (Winston, 1999, p. 23). Despite variations among these codes, there are some common principles used by such codes. For instance, taxon names in the current codes convey information about

² For a history of the current codes, see Ereshefsky (2001, ch. 6) and Winston (1999, ch. 2). A description of the differences between the zoological and the botanical codes is given by Winston (1999, pp. 31-35).

ranks. Binomials are used for taxa ranked as species; and suffixes are added to the names of higher taxa to indicate their rank. Another important principle used by the current codes is the ‘principle of priority’ according to which the first published name for a particular organism is the correct one to use. But despite the extensive coverage of the current codes, the rules are not explicit about how taxon names are *defined*. And, there has been some disagreement concerning how these codes define taxon names or even if it is correct to think that the current codes define taxon names at all (Moore, 2003). Then there are those that have proposed that we should define biological taxa phylogenetically (de Queiroz and Gauthier, 1990).

The goal of this section is to introduce and evaluate different accounts of membership conditions for biological taxa. Following Moore (2003) I argue that, for the current codes, biological taxa contain *partial* membership conditions. That is, such membership conditions specify some but not all potential members of a taxon. An important motivation for proposing partial membership conditions is to ensure stability. But before I describe this view, I should mention some additional features of the current codes.

In addition to the use of taxonomic rankings and the principle of priority, the current codes also contain principles governing the use of *diagnoses* and *descriptions*. Diagnoses are characters that are useful to tell the described taxon from other taxa. Descriptions state the characters of the taxon without special emphasis being placed upon those characters that distinguish the described taxon from other taxa.³ A further principle, the ‘principle

³ Further references on the difference between diagnoses and descriptions: Wiley and Lieberman (2011, pp. 340-341), Mayr and Ashlock (1991, 352ff) and Winston (1999), chapters 10 and 11.

of typification’, describes the use of *types*.⁴ Types are not used to provide a description of the range of variation within the taxon. Rather, the importance of using a type is that when there is a dispute regarding a name, the type can be used as a starting point by the describer (Wiley and Lieberman, 2011, pp. 347-348).⁵ Based on these different principles, different interpretations about how the current codes specify membership conditions have been proposed. I begin with de Queiroz’ view.

In a paper criticizing the current codes of nomenclature, de Queiroz claims that most contemporary biologists “formulate taxonomic definitions as lists of organismal traits or characters”, meaning that organismal traits are traditionally seen as being both sufficient and necessary conditions for membership in a taxon (de Queiroz, 1994, p. 501).⁶ For instance,

⁴ For instance, one of the articles in ICBN reads: “[t]he application of names of taxa of the rank of family or below is determined by means of nomenclatural types (types of names of taxa)” (ICBN, Vienna Art 7.1).

⁵ Species are typified by specimens. A type for a higher taxon is a subordinate taxon rather than a type specimen. But in the end all names are ultimately attached to type specimens. Moore illustrates this point with the example: “[i]n order for a name to be properly typified a nomenclatural ‘cascade’ must be present that ‘flows’ in one direction to a specimen (an ultimate type). Thus, the name *Magnoliaceae* ‘flow’ to *Magnolia* L., thence to its type *M. virginiana* L., and finally to the type specimen of *M. virginiana* L.” (Moore, 1998, p. 566).

⁶ This view that the current codes is character-based also appears in de Queiroz and Gauthier (1990) and de Queiroz (1992). But in de Queiroz and Gauthier (1994, p. 28) the current codes are described as being based on nomenclatural types and Linnaean categories rather than character-based. Additionally, in some passages, instead of criticizing how traditional taxonomy defines taxa, de Queiroz claims that traditional taxonomy is unsatisfactory because it does not distinguish definition from diagnoses (de Queiroz, 1992,

according to de Queiroz, biologists typically define ‘Mammalia’ in terms of organismal traits such as hair, mammary glands, and endothermy. De Queiroz (1994) further adds that these character-based definitions constitute a form of essentialism that predates Linnaeus. This way of characterizing how taxa are defined in the current codes has been criticized on different fronts. Winsor (2003, 2006) argues that this description of the history of taxonomy is inaccurate. According to her, Linnaeus was not an essentialist. But most importantly, de Queiroz’ view has also been criticized for being a misunderstanding of the current codes since characters are used in the current codes for diagnosing rather than for defining taxa (see e.g., Moore, 1998; Wiley and Lieberman, 2011, 250ff). Moreover, Ghiselin and Hull have articulated membership conditions for biological taxa rooted in the current codes that are not character-based. Such a view is described in the next paragraph.

Hull’s (1978) account of how taxa are defined is based on the principle of typification used by the current codes:

A taxonomist in the field sees a specimen of what he takes to be a new species.
... The taxonomist could not possibly select a typical specimen, even if the notion made any sense, because he has not begun to study the full range of the species’ variation. He selects a specimen, any specimen, and names it. Thereafter, if he turns out to have been the first to name the species of which this specimen is part, that name will remain firmly attached to that species. A taxon has the

pp. 296-297). However, the claim that traditional definitions for taxa are character-based seems central in de Queiroz’ and Gauthier’s (1990) argument, since an important theme in their paper is that phylogenetic definitions provide an alternative to character-based definitions of biological taxa.

name it has *in virtue of* the naming ceremony, not *in virtue of* any trait or traits it might have (Hull, 1978, p. 352).

In Hull's view, a species taxon is married to a specific type specimen. But since this type specimen may not contain the typical features of the species taxon, the membership of a species taxon is not fixed by traits but by ostensibly referring to a type specimen. This view is also proposed by Ghiselin. Like Hull, Ghiselin (1995) thinks that names of taxa are defined ostensibly by type designation without defining properties.⁷ However, there is a potential concern with Hull and Ghiselin's view I'd like to consider. In particular, there is the question of whether understanding taxon definitions as ostensive definitions is sufficient to account for how a taxon's extension is fixed.

Hull and Ghiselin's view of taxa is similar to Kripke and Putnam's view on natural kinds. But in contrast to Hull and Ghiselin, Kripke and Putnam do not think that ostension alone is sufficient to fix a kind's extension. Essential features are also required. In their view, an object belongs to a kind because it shares an essential feature with an ostensively given

⁷ As Ghiselin describes it (in the case of species taxa):

Definition of a species by type designation involves showing a component, which is understood to be component of the species that is named. Similarly, when defining the name of an organism, we might "point at" just a part of it, for example a beard. But in neither case do we find any property of an individual species or organism that is logically necessary, in the sense that things could not have been otherwise (Ghiselin, 1995, p. 221).

sample.⁸ But most important, even though Hull and Ghiselin might have compelling reasons to reject (biological) essentialism, ostension alone is not sufficient to fix the members of a taxon. For given that the same type specimen can belong to taxa from different ranks, fixing a type specimen will not be sufficient to pick out a particular taxon. For instance, a type specimen alone does not distinguish whether the taxon containing it belongs to the class or to the family ranks. That is, a type specimen cannot determine how inclusive a taxon is.⁹ A type specimen can only establish whether an organism belongs to a taxon if we also supply a same-kind relation. With such a relation, we could say that an organism would belong to a taxon if this organism is related to the type specimen in a certain way. Kripke and Putnam provide an account of the same-kind relation applicable to natural kind terms; for them, it is the property of sharing the same essential feature. So, apparently, a viable alternative to Kripke/Putnam essentialism should provide a non-essentialist replacement for this same-kind relation.

A possible choice for the same-kind relation is the property of belonging to a certain rank (e.g., genus and family). In this view, the extension of taxon names is determined not only by a type specimen but also by designating a rank. For instance, the genus *Homo* would

⁸ See Matthen (1998, 113ff) for a discussion.

⁹ This problem can be understood as a version of the *qua-problem* as described in Devitt and Sterelny (1999, 91ff) applied to biological taxa. Devitt and Sterelny characterize this problem (with respect to natural kind terms) as stemming from the fact that “[t]he term is applied to the sample not only *qua* member of a natural kind but also *qua* member of one particular natural kind. Any sample of a natural kind is likely to be a sample of many natural kinds” (*ibid.*, p. 90).

be defined as “the taxon including the type species *Homo sapiens* that is assigned to the rank of genus” (Lee and Skinner, 2007, p. 644). The intuition here is that, whereas the specification of a type guarantees that *Homo* includes at least the species *Homo sapiens*, the information that *Homo* is a genus would tell us how inclusive this taxon is. However, ranks cannot perform such a role.

Following Hennig (1966), one might suppose that taxa belonging to the same rank should have originated at the same time.¹⁰ If combined with the assumption that taxa are clades, that seems enough to delimit taxa since the rank would indirectly fix the clade that the type specimen belongs to.¹¹ However, ranks cannot perform such a role since taxa of a particular rank are not comparable with respect to time. In a recent paper Avise and Liu (2011) review publications describing evolutionary ages of higher taxa of different groups of organisms. The conclusion of this review is that the taxa at the same level are not consistent with respect to the time of origin:

Within mammals, for example, some extant genera provisionally date back only 100 000 years, whereas others are as old as 40 Myr; and, within, reptiles, coalescent points for extant members of various genera range from approximately 7-160 Mya. Similar statements apply to the taxonomic ranks of families and orders. For example, the provisional evolutionary ages of amphibian families range from 43-226 Myr, and dates for mammalian families range from 7-80 Myr (*ibid.*, p. 710).

¹⁰ See Ereshefsky (2001, 219ff) for a discussion.

¹¹ Not all taxonomists agree that taxa are clades. See for instance Brummitt (2002) and Sosef (1997).

This inconsistency with respect to evolutionary time is a product of the fact that the implementation of the codes to date do not attempt to standardize taxonomic ranks (Avisé and Liu, 2011; Ereshefsky, 2001). As mentioned in the above quote, even within mammals, genera can drastically vary with respect to time of origin. Moreover, recent defenses of the use of taxonomic ranks typically assume that those ranks are conventional in the sense that they do not represent any biological phenomena (e.g., Moore, 1998; Schuh, 2003). Hence, the information that a taxon belongs to a certain rank gives one no yardstick to determine how inclusive a taxon is. Consequently, complementing Hull/Ghiselin ostensive definitions with information about ranking will not provide complete membership conditions for biological taxa.

Here is the situation so far. I described different views about membership conditions for biological taxa based on the current codes. The first candidate was that taxa are defined via organismal characters. This is not a satisfactory view given that the descriptions used in the current codes are not defining features. Alternatively, we could think that taxa are defined ostensively via a type specimen as suggested by Hull and Ghiselin. However, this approach is problematic given that ostension alone is not sufficient to determine how inclusive a taxon is; the same type can belong to taxa of different ranks. Also, adding information about ranks is not enough since ranks are not comparable and, accordingly, they do not provide a basis for deciding which taxon an organism belongs to. We can thus distinguish two general approaches to membership conditions about biological taxa. On one side, there is the Kripke/Putnam approach in which we can distinguish two components: ostension and essentialism. On the other side, we have a stripped down version of Kripke and Putnam's approach proposed by Hull and Ghiselin in which taxa are defined ostensively

with no essential feature. A drawback of Hull/Ghiselin position is that it does not seem to provide a complete account of the membership conditions for biological taxa. In this way, it might seem that essentialism is the only viable account to membership conditions. Nonetheless, in what follows, I suggest a non-essentialist route.

The above discussion about membership conditions rests on the assumption that membership conditions for biological taxa should fix every potential member of a taxon in advance. This view has been criticized by Moore (2003). As he states in his position, the names of biological taxa should not be *defined*.¹² As I shall discuss, the central motivation for his view is that, in not defining the names of biological taxa, the current codes deliver a more stable system of classification. Consequently, rather than being a positive feature, the fact that essences fix any potential member of a taxon constitutes a reason against biological

¹² An alternative way of defending that taxon names are not defined is proposed by Stuessy (2000). But Stuessy's point is different from Moore's. For Stuessy neither the PhyloCode nor the current codes *define* taxon names but rather they are different "methods or concepts for *taxon* circumscription". Rather than being defined, for Stuessy names are associated with taxa by christening or baptism. Stuessy thinks the PhyloCode should be couched in different terms: "[o]ne can go through the *PhyloCode* and substitute the words 'circumscribe' for 'define' and 'taxa' for 'taxon names' to remove most of the confusion; in fact, the *PhyloCode* should, in my opinion, be rewritten toward that end" (Stuessy, 2001, p. 186). These considerations are tangential to my main point. My focus is on different types of membership conditions one might assign to taxa. Thereby, my thesis is compatible with Stuessy's view that such membership conditions are better thought as "methods for taxon circumscription"—rather than defining biological taxa. See Queiroz (2000) for a criticism of Stuessy's view. Stuessy (2001) provides a response to de Queiroz. For further references, see Stuessy (2009, 133ff) and Queiroz and Cantino (2001).

essentialism. The fact that Hull and Ghiselin's approach does not define taxa (in Moore's sense) does not imply that their view is necessarily mistaken. Below I motivate Moore's view by contrasting it with de Queiroz' conception of stability.

Although phylogenetic definitions proposed by the PhyloCode guarantee that a taxon name will always refer to the same clade, PhyloCode critics contend that phylogenetic definitions allow the content of a taxon to change very drastically (e.g., Nixon and Carpenter, 2000). Moore (2003, pp. 10-11) illustrates this point with the following example. Suppose we define the taxon 'Delta' as the least inclusive clade containing species *E* and *F* and that we originally thought that Delta comprised the three species *E*, *F*, and *G*. However, we later find out that the species *F* is actually not closely related to *E* and *G*. In such a case, even though Delta is always married to the same clade by definition (i.e., the least inclusive clade containing *E* and *F*), the number of species within Delta could drastically change as we revise our phylogeny. Phylogenetic definitions guarantee that taxon names will always refer to the same clade by allowing the referred taxa to change in content. Membership conditions in the current codes are less specific. They do not fix the extension of a taxon in advance like phylogenetic definitions do. But in being less specific, the current codes allow revisions to take into consideration extensions and characters previously associated with a taxon (e.g., Angiospermae is typically associated with plants with flowers). And, in doing so, the current codes prevent drastic shifts in a taxon's extension. Moore illustrates this point by describing how a taxonomist would handle Delta's revision under the current codes:

Let us say that the name *Delta* was typified by species *E* and was originally circumscribed to include species *E*, *F*, and *G*. Once species *F* was found to be

far more distantly related to species E and G than originally thought, it would simply be removed from *Delta*, which would now consist of species E and G. Under the traditional approach less is attached to the name, and this provides the taxonomist with much greater flexibility when applying the name under revised phylogenetic hypotheses (*ibid.*, p. 11).

In brief, phylogenetic definitions handle revisions by stipulating that taxon names will always refer to the same clade. Proponents of the PhyloCode see that as showing that the use of phylogenetic definitions produces a more stable system than the current system. Critics of the PhyloCode maintain that this type of stability (i.e., referring to the same clade) is not the relevant one because phylogenetic definitions are compatible with drastic shifts in the number of species within a taxon. PhyloCoders and their critics then have competitive ways of understanding stability. But most importantly, the current codes and the PhyloCode use different types of membership conditions in order to guarantee their respective conceptions of stability.

Phylogenetic definitions provide *complete* membership conditions; an organism belongs to Delta just in case it belongs to the least inclusive clade containing *E* and *G*. In this way, phylogenetically defined taxa are guaranteed to always refer to the same thing. For the current codes, the type constitutes the ‘minimal’ membership of a taxon; i.e., Delta contains at least its type, the species *E*. However, the current codes do not fix any potential member of a taxon. So even though the current codes provide some membership conditions, unlike phylogenetic definitions, they are *partial*. Moreover, being partial is a way of preventing drastic shifts in the number of species within a taxon. For since we cannot anticipate which

changes in our knowledge about biodiversity will take place, any attempt at specifying the boundaries for biological taxa beforehand is liable to produce drastic shifts in the content of taxa.¹³

Returning to essentialism, like the PhyloCode, essentialist membership conditions fix all members of a taxon, whether they are actual or not. For essentialists, membership conditions should be capable of fixing any potential member of a taxon. To use Moore's terminology, biological essentialism provides 'complete' rather than 'partial' membership conditions for biological taxa. But in providing complete membership conditions, essentialism faces the same challenge as the PhyloCode: it is not flexible enough to prevent drastic revisions in our current classifications. That is, my point is that Moore's criticism of the PhyloCode also applies to biological essentialism. In this way, Moore's notion of partial membership conditions provides an alternative to essentialist membership conditions. Further, Moore's position is based on the current taxonomic codes. This goes against another important thesis defended by biological essentialists; namely, that biological essentialism is the default position concerning membership conditions in contemporary taxonomy. Therefore, essentialist membership conditions are neither inevitable nor are they a consequence of current biological taxonomy.

¹³ As one might note, the classification of chemical elements is stable without using partial membership conditions. That might raise the concern of whether the use of partial membership conditions is the best way of guaranteeing stability. One possible reply is to say that, unlike other scientific disciplines like chemistry, biological classification is more apt to change. See Moore (2003, pp. 12-13) for a defense of such a view.

5.2 Explanations without essences

The view that essences have some explanatory import implies that some explanations in biology follow a specific pattern: it is because organisms in a taxon share the same essence that they typically exhibit certain features. For instance Griffiths (1999) argues that, because all the members of a taxon share the same most recent common ancestor, we can understand why some traits exhibit “strong phylogenetic inertia,” such as the presence of pentadactyl limbs in tetrapods (Griffiths, 1996, S2). HPC theorists appeal to “homeostatic mechanisms” to explain why finches’ beaks have a certain size and shape (Wilson, Barker, and Brigandt, 2007, p. 15). One type of argument employed in favor of essentialism is that postulating essences is required for explaining such shared similarities. Devitt (2008) deploys this type of argument in favor of his brand of intrinsic essentialism:

Why, for instance, is there this difference between the Indian and African rhinos?
... Regardless of the history of its coming to be true, in virtue of what is it now true? What are the mechanisms? ... There has to be something about the very nature of the group ... that, given its environment, determines the truth of the generalization. That something is an intrinsic underlying, probably largely genetic, property that is part of the essence of the group. Indeed, *what else could it be?* (*ibid.*, p. 352, emphasis added).

This argument for essentialism takes the shape of an inference to the best explanation: essences exist because they are the best explanation of why members of the same taxon share certain similarities. Accordingly, this argument for essentialism is only cogent if non-essentialist alternatives are worse off than essentialist explanations. My goal in this section

is to undermine this type of argument for essentialism by suggesting non-essentialist ways of explaining same taxon similarities. In other words, I offer a possible answer to Devitt's question "what else could it be?" The conclusion of this section is that the argument that we should postulate essences due to their explanatory role is not cogent.

The general suggestion in this section is that we can explain shared similarities within a taxon by citing features of *populations* rather than *individual* organisms. But for that suggestion to work we need an account of what distinguishes population- from organismal-level explanations. I believe that Sober's (1984) distinction between group and individual explanations provides such an account. I discuss Sober's distinction in the next section.

5.2.1 Group versus individual explanations

In order to explain an event, one has to show why this event, rather than a *contrasting alternative*, happened. As Sober (1986, p. 145) illustrates, what counts as an explanation of why tigers exist depends on the contrasting alternatives we choose:

- Given that there were ancestral felines, why are there tigers?
- Given that there were mammals, why are there tigers?
- Given that there were animals, why are there tigers?

Sober's point is that the question "why are there tigers?" alone does not specify how the answer to this question should begin. It is only by considering a particular contrasting alternative that we can specify what we can take for granted in our explanation.

A further example is presented in Sober (1984). Suppose that all the children in a third grade class know how to read. One might propose two types of explanations as to why these

children know how to read:

Group Explanation: there is a rule in the school according to which the students are only admitted to the third grade if they can read.

Individual Explanation: for each individual child, there is a series of events that explains how she learned to read.

We can formulate the distinction between Group and Individual Explanations as follows: they are different explanations because they make use of different contrasting alternatives. For the first explanation, the contrasting alternative is ‘not all the children in the third grade class know how to read’; in contrast, the second explanation describes why a certain child rather than a different one knows how to read. The contrasting alternatives for the first explanation are groups of children; in the second explanation, the contrasting alternatives are individual children such as Mary and John.¹⁴

¹⁴ A related distinction is Lewontin’s contrast between two types of “evolving systems”, *transformational* (or developmental) and *variational* systems. Lewontin makes this distinction in the quote: “[t]here are two basic dynamic forms for evolving systems. One is *transformational*, in which the collection of objects evolves because every individual element in the collection undergoes a similar transformation. (...) The alternative evolutionary dynamic, unique as far as we know to the organic world (...) is *variational evolution*. (...) Variational evolution occurs by the change of frequency of different variants, rather than by a set of developmental transformations of every individual” (Lewontin, 2001, pp. 53-54). Given Lewontin’s distinction, it seems reasonable to say that while Individual explanations describe transformational systems, Group explanations describe variational systems.

Lamarck's theory of evolution explains traits of whole populations via Individual Explanations. More precisely, Lamarck's mechanism for explaining evolution can be broken down into two components (Gould, 2002, pp. 178-179):

Environment-habit-form causal chain: environment changes slowly and continuously. To match such changes, organisms change their habits. These altered habits can in turn change the organism's morphology and physiology.¹⁵

Inheritance: an organism's acquired characteristics, due to change in habits, can be passed down to this organism's offspring.

Lamarck's theory provides an explanation of why a group of organisms acquired a certain feature via changes in the habit of each *individual* organism. In this sense Lamarck's theory explains properties of whole populations by aggregating Individual Explanations. In contrast, Darwin's theory of natural selection can explain population-level features via Group Explanations, without ascribing a set of transformations for each individual (e.g., changes in each individual's habit). For instance, the selection against light peppered moths during the industrial revolution is a case of Group Explanation where the contrasting alternatives

¹⁵ According to Lamarck's theory, a change in an organism's habit is not consequence of the organism's desires or willingness to change. Gould elaborates this point in the quote:

But a fair assessment of Lamarck's actual words shows that he advocated no ineffable willing, but only the commonplace idea that a change in environment can, in an almost mechanical way, elicit response in terms of altered habits (Gould, 2002, p. 179).

are populations, the light- and the dark-colored peppered moth populations. So a distinguishing feature of natural selection explanations is that they show how we can explain population-level features (e.g., frequency of light peppered moths) without aggregating Individual Explanation as in Lamarck's theory. Now, based on the distinction between Individual and Group Explanations, I turn to our original discussion about essentialism.

5.2.2 Non-essentialist explanations

Essentialist explanations are Individual Explanations—instead of Group Explanations. According to essentialist theories, members of the same taxon tend to share certain features because every member of that taxon shares the same essence. Essences provide a causal explanation of certain similarities shared by a taxon. Similar to Lamarck's theory of evolution, essentialist explanations explain features of populations by aggregating Individual Explanations. In this section I suggest that there is no compelling reason to think that in order to explain taxon similarities we must resort to Individual Explanations and, consequently, to essentialism.

Consider Devitt's rhino example once again. One of the shared features of the Indian rhinoceros is 'having one horn'. Incidentally, this character is part of the diagnosis of the Indian rhinoceros (Laurie, Lang, and Groves, 1983). And in being part of its diagnosis, this character does not have to be constant for all Indian rhinos (Wiley and Lieberman, 2011; Winston, 1999). That is, an individual Indian rhino may lack its horn.¹⁶ Hence, in order to

¹⁶ And members of other species can also be singled-horned, such as the unicorn beetle (*Dynastes tityus*).

explain why Indian rhinos are similar with respect to the number of horns we have to explain the frequency of this feature in populations—instead of explaining why each individual rhino has this feature. The gaps between species reflect differences in the frequencies of traits in populations, not of differences between individual organisms (Matthen, 2009; Mayr, 1942; Sober, 1980).¹⁷ As discussed earlier, natural selection explanations show that we explain frequency of traits in populations without resorting to Individual Explanations. Accordingly, there is nothing about the task of explaining shared similarities that makes essentialist explanation the best alternative. Natural selection explanations, an example of a Group Explanation, seem equally suited for the job.

However, one might object that essences provide a type of explanation that natural selection cannot offer. More specifically, essences can explain why a particular member of a species tends to have certain traits. In contrast, while natural selection can explain why individuals with a certain trait exist (as opposed to some other individuals), it cannot explain why an individual rhino has the trait it has (as opposed to another trait). In other words, natural selection is a sorting mechanism, which distributes the frequencies of variants of a population that already exist. In this way, an essentialist might claim that, even though natural selection may explain why, say, 80% of Indian rhinos have one horn, it cannot

¹⁷ Mayr makes this point in the quote: “[i]t is only rarely possible to say that this or that individual of a population is “more typical” than some others. The characters of a population are determined by the characters of the sum total of the individuals of which it is composed. If we want to compare a form or species with another one, we compare samples (“series” of the taxonomist), we do not compare individuals; this is one of the basic principles of modern systematics” (Mayr, 1942, p. 25).

explain why a particular Indian rhino has one horn. But because essentialists like Devitt are concerned with explaining why a particular rhino has the particular features it has, one might think that natural selection explanations are not a suitable alternative to essentialist explanations. In what follows, I argue otherwise. Natural selection can explain the traits of individual organisms and, accordingly, it constitutes a viable alternative to essentialist explanations. Following Neander (1995b), I suggest below that natural selection can explain features of individual organisms by considering changes in populations.

As Neander (1995b) argues, natural selection can explain the traits of individual organisms because of cumulative selection. In order to motivate her view, Neander (1995b, pp. 62-63) distinguishes two readings to the question “Does natural selection explain our opposable thumb?”:

The Persistence Question: how or why did the genetic plan for an opposable thumb prosper and persist in the human population, once it arose?

The Creation Question: how did the genetic plan for an opposable thumb originate in the human species (or its ancestors)?

For Neander, natural selection answers Creation Questions by answering Persistence Questions (Neander, 1995b, p. 67). In order to argue for that, Neander draws attention to two types of selection processes:

Single-step selection: the probable outcome of any random/select sequence is not influenced by the results of the preceding selection process.

Cumulative selection: the probable outcome of future sequences depends on the results of previous sequences.

In both single-step and cumulative selection there is random generation of possible outcomes and selection of those outcomes. As Neander points out, the difference between single-step and cumulative selection is not the number of repetitions of random/select sequences but the *relation* between the repetitions ([ibid.](#), p. 72). Unlike the case of single-step selection, in cumulative selection a random/select sequence can alter the probable outcome of future sequences. In order to illustrate this point, she considers the following example ([ibid.](#), p. 74).

Consider a lottery machine consisting of a cage with 30 balls with seven holes into which the balls fall. A winning ticket should match the holes in the same order. The chance of someone winning in this lottery is the same for every round (i.e., $23!/30!$). So this example counts as a case of single-step selection: earlier rounds of this lottery do not alter your chance of winning in the future. However, suppose we change the rules of this lottery so that after each try, the balls that match with your ticket stay in the hole and are not tossed in subsequent rounds. Now your chance of winning this lottery may increase at each round. This modified lottery is thus a case of cumulative selection: every time you match a ball, your chance of winning the lottery increases. So, unlike single-step selection, the distinguishing feature of cumulative selection is that the history of previous random/selection sequences matter for determining the probability of a future outcome. For Neander natural selection is cumulative in the same way as the latter lottery case: “[s]election does more than merely distribute genotypes and phenotypes, therefore: *by* distributing existing genotypes and phenotypes it plays a critical causal role in determining which new genotypes and phenotypes arise” (Neander, [1995a](#), p. 585). In other words, cumulative selection has a creative role because it affects what may evolve downstream.

Another example illustrating how cumulative selection can have a ‘creative’ role is intro-

duced by Godfrey-Smith:

Building the genotype underlying the human eye involved bringing together many alleles, each of them originally the product of local mutation processes. . . . Consider a collection of genetic material, \mathbf{Y} , that has everything needed, as far as genes go, to make a human eye, except for one final mutation. So this background \mathbf{Y} is such that *if* new mutation \mathbf{M} arises against \mathbf{Y} , it will finalize the evolution of the human eye (Godfrey-Smith, 2009, p. 50).

Godfrey-Smith's idea is that cumulative selection can make the appearance of the eye more likely by producing \mathbf{Y} , which would be very unlikely to arise by immediate sources of variation. Like Neander, his view is that (cumulative) "selection affects the production of new traits by changing the background against which the 'proximal' sources of variation operate" (*ibid.*, p. 50).

An important consequence of Neander's view is that it shows that we can explain the features of individual organisms by considering the frequency of traits in populations. In Neander's words, "[e]ven if natural selection does not explain change in a population by explaining changes to individuals, it can still explain why individuals have the properties they do by explaining changes in populations" (Neander, 1995b, pp. 71–72). Thus, one might explain the traits of individual organisms without having to resort to Individual Explanations and, consequently, to essentialist explanations. Moreover, as discussed earlier, same-taxon similarities can also be construed as frequencies in a population—because such similarities are not (usually) invariant within a taxon. But in doing that, postulating essences becomes unnecessary. Therefore, it is not evident that essentialist explanations are the only and best

option for explaining same-taxon similarities.

5.3 Summary

There are two motivations for postulating essences: to account for how the extension of taxa are fixed, and to explain shared traits among members of the same taxon. I argued that these two motivations can be satisfied in non-essentialist ways. With respect to membership conditions, essentialist membership conditions seem conducive to taxonomic instability. With respect to the explanatory role of essences, I argued against the view that we should postulate essences in order to explain shared similarities within a taxon. In my view, we can explain such similarities in terms of features of populations—instead of individual organisms. Then, neither explanation nor membership conditions are convincing reasons to resurrect biological essentialism.

The arguments in this section also suggest that biological work on membership conditions and explanation are more subtle than recent essentialists have assumed. In the section about membership conditions, I mentioned the fact that an important constraint for taxon's membership conditions is stability. But essentialist theories are not equipped to deal with this issue. A similar situation is true about essentialist explanations. Many essentialists argue that the best way of explaining why conspecific organisms are alike is by assigning essences to all and only members of that species. This argument seems motivated by the assumption that, in order to explain shared similarities within a species, we need to aggregate Individual Explanations. However, this is not the only available alternative. Cumulative selection can both explain the distribution of traits within a population and why an organism has a certain

trait. Different from what essentialists claim, it is not evident that biological essentialism is the most appropriate type of explanation for same-taxon similarities.

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