What's Wrong with the New Biological Essentialism

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The received view in the philosophy of biology is that biological taxa (species and higher taxa) do not have essences. Recently, some philosophers (Boyd, Devitt, Griffiths, LaPorte, Okasha, and Wilson) have suggested new forms of biological essentialism. They argue that according to these new forms of essentialism, biological taxa do have essences. This article critically evaluates the new biological essentialism. This article's thesis is that the costs of adopting the new biological essentialism are many, yet the benefits are none, so there is no compelling reason to resurrect essentialism concerning biological taxa.

1. Introduction. The received view in the philosophy of biology and biology is that biological taxa (species and higher taxa) do not have essences. This view has been championed by Hull, Sober, Dupré, Mayr, Ghiselin, and many others (see Ereshefsky [2001] for discussion). Recently, the received view has come under fire. Some philosophers have countered that biological taxa do have essences (Griffiths 1997, 1999; Boyd 1999a, 1999b; Wilson 1999; Okasha 2002; LaPorte 2004; Devitt 2008). These philosophers offer new forms of essentialism that depart from traditional essentialism. They disagree on the nature of essentialism, so their arguments in favor of taxa having essences differ. Nevertheless, they concur that biological taxa have essences.

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In what follows, I will not discuss traditional essentialism.[1] Nor will I discuss why the majority of philosophers of biology believe that biological taxa do not have traditional essences. Instead, the focus of this article is the new biological essentialism. This article introduces several forms of the new biological essentialism and argues that they should be rejected. The thesis of this article is that the costs of adopting the new biological essentialism are many, yet the benefits are none. Therefore, there is no compelling reason to resurrect essentialism when it comes to biological taxa.

2. HPC Theory and Biological Taxa. Let's start with homeostatic property cluster (HPC) theory. Many have argued that biological taxa are HPC kinds (Boyd 1999a, 1999b; Griffiths 1999; Wilson 1999; Wilson, Barker, and Brigandt 2007; Brigandt 2009). Boyd is the originator and primary proponent of HPC theory. So this section will focus on his arguments.

HPC kinds have two components. First, the members of an HPC kind share a cluster of co-occurring similarities. No similarity is necessary for membership in an HPC kind, but such properties must be stable enough to allow for successful induction. Generally, the aim of HPC theory is to capture groups of entities that share similarities that are projectable and sustain successful induction. Furthermore, the co-occurrence of the similarities found among the members of an HPC kind is caused by that kind's homeostatic mechanisms. Suppose, for example, that *Canis familiaris* is an HPC kind. The members of *Canis familiaris* share many similar features, such that if you know that Sparky is a dog, you can predict with greater than chance probability that Sparky will have a tail. And, according to HPC theory, the similarities found among members of *Canis familiaris* are caused by that species' homeostatic mechanisms, such as interbreeding, shared ancestry, and common developmental mechanisms. Proponents of HPC theory see it as a form of essentialism because they believe that HPC kinds perform the inductive and explanatory roles of traditional essentialist kinds (without requiring that essential properties are intrinsic, or necessary and sufficient for kind membership).

Despite its virtues, HPC theory does not provide adequate grounds for resurrecting biological essentialism. There are three problems with treating biological taxa as HPC kinds: (1) HPC theory is inconsistent with bio-

1. In brief, traditional essentialism holds that essences in kinds have the following three features: (1) they occur in all and only the members of a kind, (2) they play a central role in explaining the properties typically associated with the members of a kind, and (3) they are intrinsic properties. As we shall see, each form of the new biological essentialism rejects one or more of these features of traditional essentialism.

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logical theory, (2) it does not provide a noncircular means for identifying taxon essences, and (3) it conflates the distinction between kinds and individuals. Let's consider each problem in turn.

2.1. HPC Theory Is Inconsistent with Biological Theory. Suppose we want to classify a group of organisms. We can classify them by shared significant similarities or by shared histories. Suppose these two ways of classifying those organisms result in conflicting classifications. The first problem with applying HPC theory to biological taxa is that when classifying by similarity and classifying by history conflict, Boyd sides with similarity, yet the major schools of biological taxonomy side with history.

To illustrate why similarity should trump history, Boyd offers a fictional case of a hybrid species. Hybrid species occur when organisms from two parental species interbreed and their descendants become reproductively isolated from either parental species. The result is a new species—a hybrid species. In Boyd's example, the new hybrid species has two separate speciation events: first, the hybrid species is formed and goes extinct, and then it forms again. The members of this hybrid species belong to two spatiotemporally distinct (historically disconnected) lineages. According to Boyd, the organisms in these lineages have "commonalities in evolutionary tendencies" and should be considered parts of one species despite their not belonging to a single continuous lineage (1999b, 80). Boyd writes, "I do not for better or worse, hold that HPC kinds are defined by historical relations rather than shared properties" (80). For Boyd, similarity trumps history: when classifying by similarity conflicts with classifying by historical continuity, we should opt for similarity.

However, the assumption that similarity trumps history puts HPC theory at odds with the two major schools of biological taxonomy–cladism and evolutionary taxonomy. These schools require that taxa are either monophyletic or paraphyletic. Monophyletic taxa contain all and only the organisms descended from a common ancestor. Paraphyletic taxa contain only but not all the organisms descended from a common ancestor. Paraphyletic and monophyletic taxa must be historically or spatiotemporally continuous entities. The point is that Boyd allows taxa to be noncontinuous entities, and that is at odds with biological taxonomy. Boyd sees HPC theory as a naturalistic philosophical theory that should be consistent with scientific theory. But it is not. The root of the problem is that HPC theory assumes that all scientific classification should capture similarity clusters. However, that is not the aim of biological taxonomy. Its aim is to capture history.

2.2. HPC Theory's Explanatory Circle. A virtue of HPC theory's characterization of biological taxa is that it is consistent with the diversity of

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properties and homeostatic mechanisms found among the organisms of a taxon. The members of an HPC kind can have a cluster of co-occurring similarities that vary at a time and over time. And HPC theory allows that the causal homeostatic mechanisms that cause such similarities can vary at a time and over time. Thus HPC theory is consistent with the variability found in species. But if the homeostatic mechanisms of an HPC kind vary at a time and over time, how do we decide which mechanisms are the mechanisms of a particular HPC kind? This is a pressing question, because if the essence of an HPC kind is a set of causal homeostatic mechanisms (Griffiths 1997, 212; 1999, 218), we would like to know how HPC theory determines which mechanisms are parts of an HPC kind's essence.

One way to answer this question is to consider the major motivation for positing HPC theory—namely, to highlight those clusters of covarying similarities that are used in successful induction and explanation. Perhaps when asking which mechanisms comprise the essence of a particular HPC kind, we should look for those mechanisms that cause the stable clusters of similarities associated with that kind. But recall that the similarities that make up the cluster of co-occurring similarities among the members of an HPC kind can vary at a time and over time. It seems that 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. Yet those similarities themselves vary over a time and at a time. 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?

When it comes to biological taxa, there is an answer that breaks out of this circle. To determine which organisms and homeostatic mechanisms are parts of a particular taxon, we need to determine which organisms and mechanisms are historically connected to a unique and common ancestor. Genealogy is the glue that binds the various organisms and their mechanisms within a particular taxon. Perhaps one can follow this line of reasoning and suggest that HPC theory should treat taxa as historically defined kinds: taxa as HPC kinds must be genealogically unique and continuous lineages. At least one supporter of HPC theory, Griffiths (1999, 220), makes this suggestion.

There are two problems with this suggestion. First, siding with history undermines the central motivation for positing HPC theory. The aim of HPC theory is to explain our successful inductive practices by highlighting kinds with similarities. Yet classifying by history and classifying by sim-

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ilarity can conflict, and if we side with history, then we give up a core aim of HPC theory, namely, to classify by similarity. Second, asserting that biological taxa are historical kinds conflates the distinction between kinds and individuals. 'Individual' here just means a historical or particular entity. Saying that taxa are historical kinds conflates the kind/individual distinction because a taxon is then both a kind and an individual. As I suggest below, there is a significant difference between being a kind and being an individual. Consequently, the third problem with HPC theory is that it conflates the kind/individual distinction.

2.3. HPC Theory Conflates the Kind/Individual Distinction. Boyd does not put much stock in the distinction between kinds and individuals. He writes, "We can see why the distinction between natural kinds and (natural) individuals is, in an important way, merely pragmatic" (Boyd 1999a, 163, also see 164). Boyd is not the only new biological essentialist to dismiss the kind/individual distinction (see Okasha 2002; LaPorte 2004).

There is a cost to denying the distinction between kinds and individuals. That cost is the conflation of two distinct ways in which scientists classify. Call these two different ways *kind thinking* and *individual thinking*. The aim of kind thinking is to find clusters of similarities that can be used in successful induction and explanation. To satisfy that aim, the members of a kind must have projectable similarities. The members of a kind need not causally interact in any particular way, so long as they have the appropriate similarities. In contrast, the parts of an individual need not be similar to be parts of that individual. Not even the relations among the parts of an individual must be similar. Instead the parts of an individual must be appropriately causally connected. Notice that there are two modal claims being made here. Parts of an individual *must* be appropriately causally connected. Members of a kind *must* be similar. It is true that in some instances the parts of an individual are similar and that in some instances the members of a kind are causally related. But if according to our best scientific theory the organisms of a species *must* be causally connected and they *can* be dissimilar, then species are individuals and not kinds.

One might respond, as Boyd, Okasha, and LaPorte do, that we can talk about a species as either a kind with members or as an individual with parts. But that linguistic move misses something significant. The kind/individual distinction highlights different causal features of the world. The parts of an individual must have certain causal relations to one another. There is no such causal requirement on members of a kind. Saying that one can treat a group of entities as either a kind or an individual misses that distinction. We can call a species a 'kind' or an 'individual', but doing so ignores the different ways in which the world

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is carved up. It is worth adding that we carve the world in two ways, and those two ways work together. We sort parts into individuals (via part-whole causal relations) and then individuals into kinds (via member-kind similarities).

In sum, Boyd and some proponents of the new biological essentialism propose that biological taxa are historical kinds, which are individuals with historical essences. For them, there is no distinction between kinds and individuals. I have argued that there is an important distinction between kinds and individuals. Consequently, any form of essentialism, including HPC theory, that conflates this distinction should be viewed with suspicion.

3. Relational Essentialism and Devitt's Challenge. Griffiths (1999), Okasha (2002), and LaPorte (2004) suggest a form of biological essentialism that can be called *relational essentialism*. According to relational essentialism, certain relations among organisms, or between organisms and the environment, are necessary and sufficient for membership in a taxon. Such relations, argue Griffiths, Okasha, and LaPorte, are taxon essences. For example, Griffiths and LaPorte suggest that being descended from a particular ancestor is necessary and sufficient for being a member of a taxon and thus a taxon's essence. Okasha (2002, 201) argues that prominent species concepts require that species have relational essences. Such relations include being descended from a particular ancestor, being part of a certain interbreeding population, or occupying a particular niche.

Devitt (2008) rejects relational essentialism. He argues that relational essentialism fails to answer two crucial questions. The taxon question asks, Why is organism O a member of species S? The trait question asks, Why do members of species S typically have trait T? Devitt suggests that to answer these questions, biological taxa need intrinsic essences, and because relational essentialism only posits relational essences, relational essentialism fails to answer these questions. Devitt's target is not merely to discredit relational essentialism but also to argue for a new form of intrinsic biological essentialism. According to Devitt (2008, 346), taxon essences consist of intrinsic properties and perhaps, but not necessarily, relational properties. More precisely, a taxon's essence for Devitt (2008, 352ff.) is the cluster of intrinsic properties and perhaps relations that cause and explain the typical traits of a taxon's members.

Let's look at Devitt's critique of relational essentialism. In doing so, we will see what is right and what is wrong with relational essentialism. Along the way, I will argue that Devitt's intrinsic biological essentialism should be rejected.

3.1. The Trait Question. Why do zebras have stripes? Devitt (2008,

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352ff.) argues that explanations that merely cite relations are insufficient to explain the traits typically found among zebras. We must cite intrinsic properties as well, and such properties are essential intrinsic properties of zebras. I am sympathetic to Devitt's claim that we need to cite more than relations to explain why zebras have stripes. Generally, to explain the occurrence of a homologue, such as stripes in zebras, we need to cite both relations among organisms and intrinsic factors within organisms (Ereshefsky 2009). More precisely, embryonic zebras have developmental mechanisms that cause zebras to have stripes. These mechanisms are intrinsic features of embryonic zebras. But those developmental mechanisms must be passed down from parent to offspring via genealogical relations. So a robust explanation of why zebras have stripes cites both the relations and intrinsic properties that cause stripes. Merely citing relations provides a relatively weak explanation of an organism's trait.

Given the observation that we should cite both genealogy and developmental mechanisms to understand why zebras have stripes, should we infer, as Devitt does, that the taxon Zebra has an intrinsic essence? I do not think so. Biologists explain the characters of organisms by citing other characters, without the added metaphysical claim that the character cited in the explanans is essential to membership in a taxon. Consider how a biologist explains the occurrence of stripes in a zebra. In its embryonic state, a zebra has an ontogenetic mechanism that causes it to develop stripes. That developmental mechanism is neither necessary nor sufficient for membership in Zebra. Some zebras lack that mechanism. Moreover, the developmental mechanism that causes stripes in zebras causes stripes in a variety of mammals, including cats (Carroll 2005, 238–40). Generally, the intrinsic properties that cause organismic traits do not coincide with taxonomic boundaries: they crosscut such boundaries. The belief that such intrinsic properties are essential for taxon membership is not part of biological theory. So while I agree with Devitt that relational essentialism offers a weak answer to the trait question, that does not imply that we should adopt intrinsic essentialism: biologists explain the traits of organisms by citing intrinsic properties of organisms without those properties being essential for taxon membership.

3.2. The Taxon Question. Let us turn to the taxon question: why are organisms $O_{1...n}$ members of species S? Relational essentialists argue that modern species concepts posit relational properties, such as interbreeding, genealogy, and occupying a specific niche, as the defining features of species. For example, being a descendant of a particular ancestor may be the defining relation for the members of a species (Griffiths 1999; LaPorte 2004). Or being able to successfully interbreed with other members of a species may be the defining relation (Okasha 2002). Relational essentialists

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tell us that biologists do not posit intrinsic properties as the defining features of species. They conclude that species have relational rather than intrinsic essences.

Devitt responds (2008, 365) that citing the relations among the organisms of a species does not explain why particular organisms are members of a certain species. According to Devitt, saying that O can interbreed with other *Homo sapiens* leaves unanswered why those other organisms are *Homo sapiens*. There's an unanswered regress: why are any of them *Homo sapiens*? According to Devitt, to answer that question we must cite the essential intrinsic properties in organisms.

Has Devitt made the case for intrinsic essentialism? I believe that the relational essentialists are right that citing relations, without positing intrinsic essences, sufficiently answers the taxon question. Once again, why are organisms $O_{1...n}$ members of species S? According to our best biological theory, if S is an interbreeding species, then O's have intrinsic reproductive mechanisms that allow them to interbreed with one another. Fine so far, but we do not have a satisfactory explanation because we do not know which intrinsic mechanisms are mechanisms that cause an organism to be a member of a particular species. We need some way of determining which mechanisms cause an organism to be a member of one species versus a member of another species—that's the taxon question. Here we must turn to relations: particular population and genealogical relations among organisms. The answer to why particular reproductive mechanisms are mechanisms of species S is that those mechanisms occur in organisms whose populations are genealogically connected in a single lineage.

The point I want to emphasize is that relations are explanatorily prior in explaining taxon identity, not intrinsic properties. To reinforce this point, consider which aspects of an organism can be changed while it remains a member of the same species and which aspects cannot be changed. The intrinsic reproductive mechanisms within the organisms of a species can be changed, but being part of the same lineage or gene pool cannot be changed. To make this more concrete, consider the case of ring species. A ring species consists of a geographic ring of populations such that organisms in contiguous populations can successfully mate, but organisms in populations at distant links in the ring cannot successfully mate. Interestingly, the organisms in distant populations of a ring species have different reproductive mechanisms (Mayr 1963, 512ff.). (The same is true of different generations of a single species: contemporary organisms within a species may have different reproductive mechanisms than those of organisms in earlier generations; Wu and Ting 2004.) Suppose Joe is a member of a ring species. Joe could have had a different intrinsic reproductive mechanism than the one he has. Imagine counterfactually that he is a member of a different population of his ring species, namely, one

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with different reproductive mechanisms than those found in his actual population. In this counterfactual situation, Joe is still a member of his species so long as we do not remove him from the lineage and gene pool of that ring species. Generally, an organism in a ring species can have a different reproductive mechanism and still be a part of that species. But an organism cannot be removed from his original lineage and be put in another lineage and remain part of the original species. Relations, I submit, are more fundamental for species (and taxon) membership than intrinsic properties are.

Still, Devitt could respond that I have not answered the taxon question because though I have bundled intrinsic reproductive mechanisms by citing relations, I have not explained why those relations are relations of a particular species. At this juncture, I suggest that we turn to the particular speciation event of a species. Why are organisms $O_{1...n}$ members of S? Because O's have certain intrinsic reproductive mechanisms that are bound by population and genealogical relations that are anchored to a particular speciation event. According to a standard model of speciation, allopatric speciation, a new interbreeding species must be reproductively isolated from other species, and there must be successful interbreeding within its founding population. No particular mechanisms are required: the particular mechanisms that the species' members have could have been different. But the particular relational properties they have—namely, of being reproductively isolated from neighboring species and being reproductively compatible among themselves—cannot be altered. A species' membership relations supervene on the intrinsic mechanisms of its organisms. When it comes to species membership, intrinsic mechanisms within the organisms of a species can vary, but certain relations among its organisms cannot.

To put it more starkly: the occurrence of certain relations *is* the species. It is the occurrence of those relations that makes the organisms engaged in them members of one species versus another species. In sum, intrinsic properties are not part of a taxon's membership conditions, and relational essentialists are right about how biologists individuate taxa.

4. Is Relational Essentialism a Form of Essentialism? Do the results of the previous section imply that we should accept relational essentialism? I do not think so. Consider two traditional requirements of essentialism that Okasha (2002, 202ff.) highlights. The membership requirement is that the essence of a kind provides the necessary and sufficient conditions for membership in that kind. The explanatory requirement is that citing a kind's essence is central in explaining the properties typically associated with the members of that kind. Given these two requirements, Okasha offers the following argument. Because certain relations are necessary and

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sufficient for membership in a species, such relations satisfy the membership requirement of essentialism. However, those relations do not satisfy the explanatory requirement. According to Okasha (2002, 204), relations such as genealogy and interbreeding fail to explain the traits typically found among the members of a species. Instead, we must cite the "genotype and its developmental environment" (204) to explain such traits. Despite failing to meet the explanatory requirement, Okasha still thinks that certain relations are taxon essences. Okasha writes that there is no a priori reason to retain the explanatory requirement of essentialism and suggests that it should be dropped (203). With the explanatory requirement out of the way and the membership requirement satisfied, Okasha concludes that species have relational essences.

In contrast to Okasha, I believe that the relations that serve as the identity conditions for a taxon play some role in explaining the typical traits among a taxon's members. But their role is nevertheless a weak one. As discussed earlier, such explanations are greatly enhanced when we know something about the developmental mechanisms that cause those traits. The problem with Okasha's relational essentialism is that if the relations that serve as the identity conditions for a taxon are not central in explaining the typical traits among a taxon's members, then such relations are not essences. Okasha too quickly jettisons a core feature of essentialism: that the essence of a kind plays a central role in explaining the typical features of a kind's members. Essentialists, from Aristotle to Locke and from Kripke to Boyd, believe that essences figure centrally in explaining the traits typically found among the members of a kind. If we give up that explanatory component of essentialism, we give up a core feature of essentialism, a feature that distinguishes real essences from nominal essences. Nominal essences demarcate membership in a kind, but they do not explain the typical traits of a kind. Arguably, any approach to natural kinds that aims to capture the kinds of science should preserve this explanatory feature of kinds.

So in the end, relational essentialism is not essentialism because it fails to satisfy a core aim of essentialism. The essence of a kind is supposed to bear the explanatory weight for understanding why the members of a kind have the typical traits they do. The relations that serve as the identity conditions of a taxon do not fulfill that explanatory role. Consequently, relational essentialism does not resurrect biological essentialism because it is not essentialism.

5. Conclusion. As a last-ditch effort, one could attempt to resurrect biological essentialism by asserting that the essence of a taxon is an open-ended disjunction of all the intrinsic and relational properties that cause the properties typically found in the members of a taxon, plus those

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phylogenetic and population relations that bound those properties. (It is an open-ended disjunction because a taxon can gain new properties and relations until it goes extinct.) One could assert that such disjunctions of properties and relations are taxon essences. But I do not see what is gained by arguing that biological taxa have such essences. Positing biological essences does not illuminate biological practice, nor does it help us understand how science works. As far as I can tell, it is no part of contemporary biological taxonomy.

Just as important, there are a number of costs to adopting any of the forms of the new biological essentialism. All such forms multiply entities beyond necessity. Biologists explain the traits of organisms and provide the identity conditions of taxa without positing taxon essences. No biologist I know of cites the sorts of disjunctions just mentioned to explain biological phenomena or taxon identity. There are also costs to adopting specific forms of the new biological essentialism. One cost is conflating two distinct modes of classifying in science—the sorting of parts into individuals and members into kinds. HPC theory and relational essentialism bear that cost. Another cost is positing a philosophical theory that is at odds with biological theory. Boyd's HPC theory is inconsistent with biological theory because it chooses similarity over history when classifying organisms. Devitt's essentialism is at odds with biological theory because it sides with intrinsic properties over relations in the membership conditions of taxa. Finally, relational essentialism bears the cost of abandoning the explanatory aim of essentialism, namely, to discover essences that are central in explaining the typical traits of a kind.

So, yes, we could adopt the new biological essentialism. But the costs of adopting the new biological essentialism are many, and the benefits are none. Thus, there is no compelling reason to resurrect essentialism when it comes to biological taxa.

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