

Essentialism, History, and Biological Taxa

Makmiller Pedroso

Abstract

Recent writers are committed to a new brand of essentialism called “historical essentialism” [Griffiths, 1999; LaPorte, 2004]. According to this brand of essentialism, relations of common ancestry are essential features of biological taxa. The main argument used for this version of essentialism is that the dominant school of classification, the cladistic school, defines biological taxa in terms of common ancestry. The goal of this paper is to show that this argument for historical essentialism is unsatisfactory: cladistics provides membership conditions for biological taxa without assuming that relations of common ancestry are essential attributes of biological taxa.

Keywords: historical essentialism - cladistics - biological taxa - natural kinds

1 Introduction

Different versions of essentialism are distinguished by the kind of properties allowed to count as a taxon’s essence. According to a particular brand of essentialism, *intrinsic essentialism*, essences are intrinsic properties, such as genotype and morphological traits. However, due to the incompatibility between intrinsic essentialism and contemporary biology, the view that biological taxa do not contain intrinsic essences has become the predominant view among philosophers of biology [Ereshefsky, 2001]. As an alternative to intrinsic essentialism, some have proposed a version of essentialism, called *historical essentialism*, according to which certain ancestor-descendant relationships are essential

features of biological taxa [Griffiths, 1999; LaPorte, 2004]. The goal of this paper is to raise some objections to historical essentialism.

The main argument used in favor of historical essentialism is that the dominant school of classification, the cladistic school, defines biological taxa in terms of ancestor-descendant relations. Section 2 of this paper outlines this argument for historical essentialism, and introduces the definition of historical essences as formulated by both Griffiths [1999] and LaPorte [2004]. In the Sections 3 and 4 I present objections to historical essentialism.

2 Biological Taxa and Historical Essences

2.1 Historical Essences: The LaPorte Way

According to LaPorte, cladistically defined taxa contain historical essences. His notion of historical essence is stated in the quote:

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, 12].

LaPorte’s idea is that the specifiers of Mammalia (i.e. horses and echidnas) do not have to be same across possible worlds. Rather, the invariant feature of Mammalia is the property of having *G* as the most recent ancestor. Horses and echidnas are only necessary to fix the most recent ancestor of Mammalia in the actual world. Thus, given a taxon *x* where *G* is the most recent ancestor of the specifiers of *x* in the actual world, we can extract the following notion of historical essence from LaPorte’s quote:

(L) For all y , y is a member of x if and only if y descends from G .

2.2 Historical Essences: The Griffiths Way

According to Griffiths [1999], biological taxa contain historical essences because they are defined by relations of common ancestry. For him, “Nothing that does not share *the historical origin* of the kind can be a member of the kind” [Griffiths, 1999, 219, my emphasis]. Griffiths thus seems to endorse the following notion of historical essence:

(G) All and only the members of a taxon share the same “historical origin.”

Griffiths’ formulation of historical essence appeals to the notion of “historical origin.” Griffiths [1999] does not provide an account of what the expression “historical origin” means, or specify the conditions under which two organisms have the same “historical origin.” A plausible interpretation is to suppose that two organisms have the same “historical origin” just in case they have the same most recent ancestor. In this interpretation, Griffiths’ historical essentialism is the same as LaPorte’s. Consequently, any criticism against LaPorte’s essentialism will apply to Griffiths’ essentialism as well.

3 Is evolution a necessary assumption of cladistics?

In this section, I provide an outline of cladistic methods and distinguish two schools within cladistics: process cladistics (subsection 3.1) and pattern cladistics (subsection 3.2). As mentioned earlier, 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 that pattern cladistics does not support historical essentialism. Hence, citing cladistics 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 cladistics and reject pattern cladistics.

3.1 Hennig's System

In order to describe his system of classification, Hennig [1966] distinguishes two groups based on their ancestry and descent. A *monophyletic group* contains the common ancestor and all of its descendants; a *paraphyletic group* contains the common ancestor and some but not all of its descendants. According to Hennig, every higher taxon must be monophyletic.

Hennig's system is a viable option for classifying organisms only if we have the necessary methods for discovering phylogenetic relations among biological taxa. Although the existence of taxa being hierarchically arranged is a consequence of evolution, evolutionary theory alone does not show how we can discover monophyletic groups. Such methods were first articulated by Hennig, about one hundred years after Darwin's *Origin*.

In cladistics, the characters used are discrete (e.g. "DNA sequences") as opposed to characters that vary continuously (e.g. "leaf length"). Each character in cladistic analysis has exclusive "states." For instance, the character "mode of reproduction" has the states "viviparity" and "oviparity." However, not every character provides reliable evidence for inferring phylogenetic relations. For two taxa may be very alike even though they don't share the most recent ancestor. It is thus necessary to provide a criterion to distinguishing reliable characters from the unreliable ones.

Reliable character states should be shared between two or more taxa and also be present in their common ancestor. Otherwise stated, reliable characters must be *homologies*. Character states shared between two or more species that are not present in their common ancestor are called *homoplasies*. Thus, a first step in cladistic analysis is to distinguish homologies from homoplasies. Homologies can be of two types: *ancestral homology* (or *symplesiomorphy*) are homologies that are present in the common ancestor of the group of species under study; *derived homologies* (or *synapomorphies*) are homologies that evolved after the common ancestor, within the group of species under study. Only derived homologies (or synapomorphies) are useful for inferring phylogenetic relations.

To sum up, in the Hennigian system, higher taxa have to be monophyletic. Cladistics provide the methods necessary for distinguishing reliable from unreliable traits for dis-

covering monophyletic groups. To this end, cladistic analysis proceeds in two states: (1) distinguish homologies from homoplasies; and (2) distinguish derived homologies from ancestral homologies.

3.2 Cladistics after Hennig

In Hennig’s system, evolutionary theory is what provides the justification for the cladistic analysis: the distinction between derived and ancestral homology is a consequence of how evolutionary history proceeded. However, some cladists after Hennig have argued that not only is the assumption of evolution unnecessary for justifying cladistic methods, but also that cladistics is better off if formulated independently of evolutionary theory [Platnick, 1979; Nelson and Platnick, 1981; Brower, 2000]. In this way of understanding cladistics, systematics is supposed to provide evidence for evolution – rather than the opposite. This version of cladistics is usually referred in the literature as “pattern cladistics” – as opposed to “process cladistics” which includes Hennig and others sharing the assumption that evolution is necessary to justifying cladistics.

An important motivation for pattern cladistics is the claim that the evolutionary models used to justify cladistics involve contentious claims. 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 a number of branches strictly greater than two. In order to justify this methodology, Hennig argues for a specific speciation model, according to which speciation events only happen via splitting of an ancestral species into two new species [Hennig, 1966, 207–11]. As observed by Platnick [1979], Hennig’s model of speciation 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, 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 models of evolution.

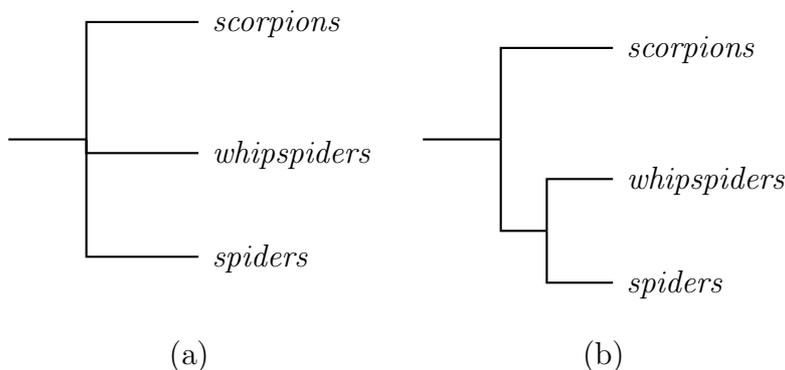
Alternatively Platnick [1979] proposes a justification for Hennig's commitment to dichotomous trees without relying on any theory about speciation. For Platnick dichotomous trees should be favored not because of any assumption about evolution, but because dichotomous trees contain higher information 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. 1. The trichotomous tree in Fig. 1a predicts that, if we take a sample of the terminal taxa, then we will find the presence of:

1. synapomorphies shared by all three terminal taxa; and
2. synapomorphies unique to each terminal taxa.

In addition to 1. and 2., the dichotomous tree in Fig. 1b also predicts the presence of:

3. synapomorphies only shared by whipspiders and spiders.

Figure 1: Examples of a trichotomous (a) and dichotomous (b) tree. From Platnick [1979, 540].



Based on this difference between the trees in Fig. 1a and Fig. 1b, Platnick argues that dichotomous trees are preferable to trichotomous trees because they allow us to test an

additional hypothesis (i.e., 3.). No specific theory of speciation is therefore necessary to justify the preference for dichotomous trees.

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. Nevertheless, as opposed to pattern cladistics, the process cladists follow Hennig's lead justifying cladistic methods using evolutionary theory. For instance, Wiley [1981] argues that cladistic analysis should contain evolutionary information but, as opposed to 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, 105].

The question of whether evolution should rely on evolutionary theory is still a matter of ongoing debate [e.g. Brower, 2000; Kluge, 2001]. My intention in highlighting this dispute between pattern and process cladists is that of elucidating the type of “cladistic practice” relevant in the argument for historical essentialism. Both process and pattern cladistics define biological taxa in terms of synapomorphies, but only the first type of cladism connects synapomorphies with ancestor-descendant relations.

Arguments that appeal to consensus of a group of scientists – like the cladistic school – are convincing only if there is evidence of such a consensus. We have discussed some disputes about the relation between cladistic classification and evolutionary theory, such as the relation between cladistics and speciation models. These disputes show that, although cladists agree in terms of methods for classifying taxa (e.g. outgroup comparison), the relation between cladistics and evolutionary theory is disputed. To argue for historical essentialism on the basis of cladism falsely suggests that every version of cladistics defines biological taxa in terms of evolutionary theory. Hence, if cladistics supports historical essentialism, then additional premises must be provided. In particular, the essentialists need to argue that process cladism is right; pattern cladism is wrong.

However, one may object, pattern cladists can define biological taxa without relying on genealogical relations, they still believe that common ancestry is an essential attribute to biological taxa. I agree that this might be the case; pattern cladists can 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. Nevertheless, in the next section, I also argue that process cladism by itself provides inadequate justification for historical essentialism.

4 The notion of “ancestor” in cladistics

In Section 2, I distinguished two conceptions of historical essence:

The Griffiths Way [Griffiths, 1999]: all and only the members of a taxon share the same “historical origin.”

The LaPorte Way [LaPorte, 2004]: given a clade x with G as the most recent ancestor of the specifiers of x , for all y , y is a member of x if and only if y descends from G .

I also argued that, according to a plausible interpretation of what the expression “historical origin” means, Griffiths’ and LaPorte’s conceptions of essence are equivalent.

LaPorte [2004] defines Mammalia as necessarily having the same most recent ancestor across different possible worlds – rather than having the same specifiers “horses” and “echidnas.” However, as I will argue below, LaPorte’s notion of historical essence is not grounded by cladistic practice, even if we stick to process cladistics.

If cladistics legitimizes historical essentialism, then this is supposed to be a consequence of how cladists specify the membership conditions for biological taxa. In cladistics, the members of a taxon are established via synapomorphies (or derived homology). For instance, tortoises do not belong to the monophyletic group Amniotes since they lack the synapomorphy “viviparity.” Thus, if cladistically defined taxa provides evidence for the existence of historical essences *sensu* LaPorte [2004], then the following statement is true:

(L1) The synapomorphies used to provide membership conditions for higher taxa provide evidence for the view that biological taxa contain historical essences in the LaPorte Way.

According to LaPorte's conception of historical essence, a taxon t contains a historical essence only if t has the same most recent ancestor across different possible worlds (in which t exists). Hence, (L1) implies that:

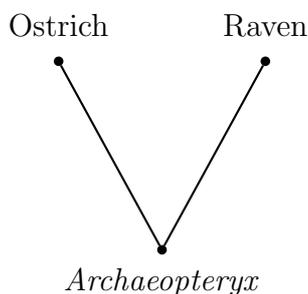
(L2) The synapomorphies used to give membership conditions for higher taxa provide evidence for the view that all and only the members of a taxon have the same most recent ancestor.

For process cladists, synapomorphies count as evidence of common ancestry among different taxa. Nevertheless, as I will argue below, the synapomorphies used to define biological taxa do not distinguish the most recent ancestor of a clade. Hence synapomorphies alone do not justify (L2).

Consider the following example mentioned in Kitching et al. [1998, 13-14]. Suppose the clade containing the taxa *Archaeopteryx*, ostrich and raven, drawn in Fig. 2. If (L2) is true, then synapomorphies alone can guarantee that the clade formed by ostrich + raven + *Archaeopteryx* must have *Archaeopteryx* as its most recent ancestor. However, this is not the case. *Although synapomorphies provide evidence for thinking that Archaeopteryx belongs to the clade in question, synapomorphies alone cannot show that Archaeopteryx is the most recent ancestor of this clade.*

The three taxa in Fig. 2 belong to the same clade because they possess the same synapomorphy; in this case, that of having feathers. In order to determine whether *Archaeopteryx* is the ancestor of the clade, *Archaeopteryx* must have a feature not shared by the other two taxa (i.e. ostrich and raven). Thus, there are only two cases in which synapomorphies can be used to show that *Archaeopteryx* is the most recent ancestor of the clade in Fig. 2: (I) there is a synapomorphy shared by ostrich + raven but absent in *Archaeopteryx*; and (II) *Archaeopteryx* contains an "autapomorphy," a synapomorphy not shared by the other taxa.

Figure 2: A tree representing the ancestor-descendant relations between *Archaeopteryx*, ostrich, and raven. From Kitching et al. [1998, 12].



Concerning (I), ostrich + raven contain the synapomorphy of having a pygostyle not shared by *Archaeopteryx*. Nevertheless, there are many animals that do not have a pygostyle. The property of not having a pygostyle then fails to show that *Archaeopteryx* is the most recent ancestor of the clade. Because of this, (I) fails to guarantee (L2). 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 synapomorphies unique to *Homo sapiens* do not make humans the ancestral species of other taxa in the Hominidae group. It is because of this reason that, if *Archaeopteryx* has an autapomorphy, then cladists would consider *Archaeopteryx* as the sister-group of the group ostrich + raven (instead of being their ancestor). Hence, autapomorphies cannot be used to justify LaPorte's historical essentialism.

Therefore, (L2) is false: even though synapomorphies provide membership conditions for a clade, they do not distinguish which taxon is the the most recent ancestor of the clade. An alternative way of making this point is in terms of the difference between sister-group and ancestor-descendant relations. Synapomorphies provide evidence for the existence of sister-groups – in showing that two taxa are more related to each other than a third taxon. However, as Hull observes, the sister-group relation is collateral, not ancestral-descendant [Hull, 2001, 223-24]. In short, historical essentialism defines biological taxa in terms of ancestral-descendant relations; however, cladistic methods

define biological taxa solely in terms of sister-group relations.¹ Because of this, cladistic methods do not show that biological taxa contain historical essences in the LaPorte Way. And since Griffiths' essentialism boils down to LaPorte's essentialism (section 2), the same critique applies to the notion of historical essences in the Griffiths Way.

5 Conclusion

One might assume that biological taxa are historical entities without embracing historical essentialism. For instance, Ghiselin [1974] and Hull [1978] both claim that species are spatiotemporally limited, but that historical features of species are contingent (rather than necessary) properties of species. Accordingly, the mere fact that genealogy is constantly used in contemporary systematics cannot serve as evidence for historical essentialism; an additional argument must be provided. Griffiths [1999] and LaPorte [2004] propose such an additional argument. In both Griffiths [1999] and LaPorte [2004] we find the argument that cladism supports essentialism. Given that cladistics is the dominant school in taxonomy, this seems to be a powerful argument for historical essentialism. In this paper, however, I presented two reasons showing why cladistics does not justify historical essentialism: (1) arguments that appeal to a consensus of a group are convincing only if such a consensus in fact exists. I argued that the consensus necessary to warrant historical essentialism is absent (Sec. 3); (2) cladistic methods alone cannot provide any evidence for historical essentialism (Sec. 4). If sound, these two arguments show that historical essentialism, as proposed by Griffiths [1999] and LaPorte [2004], is false.

References

Brower, A. [2000], 'Evolution is not a necessary assumption of cladistics', *Cladistics* **16**, 143–54.

¹For further references about the impossibility of using synapomorphies to identify ancestral taxa see: Engelmann and Wiley [1977], Wiley [1981, 105-107], Kitching et al. [1998, 13-14], and Schuh [2000, 84-86].

- Engelmann, G. and Wiley, E. [1977], ‘The place of ancestor-descendant relationships in phylogeny reconstruction’, *Systematic Zoology* **26**, 1–11.
- Ereshefsky, M. [2001], *The poverty of the Linnaean hierarchy: a philosophical study of biological taxonomy*, Cambridge University Press, Cambridge.
- Ghiselin, M. [1974], ‘A radical solution to the species problem’, *Systematic Zoology* **23**, 536–44.
- Griffiths, P. [1999], Squaring the circle: natural kinds with historical essences, in R. A. Wilson, ed., ‘Species: new interdisciplinary essays’, MIT Press, Cambridge, pp. 208–228.
- Hennig, W. [1966], *Phylogenetic Systematics*, University of Illinois Press, Chicago.
- Hull, D. [1978], ‘A matter of individuality’, *Philosophy of Science* **45**, 335–360.
- Hull, D. [2001], ‘The role of theories in biological systematics’, *Studies in History and Philosophy of Biological and Biomedical Sciences* **32**, 221–38.
- Kitching, I. J., Forey, P. L., Humphries, C. J. and Williams, D. M. [1998], *Cladistics: the theory and practice of parsimony analysis*, Oxford University Press, Oxford.
- Kluge, A. [2001], ‘Parsimony with and without scientific justification’, *Cladistics* **17**, 199–210.
- LaPorte, J. [2004], *Natural kinds and conceptual change*, Cambridge University Press, Cambridge.
- Nelson, G. and Platnick, N. [1981], *Systematics and Biogeography: Cladistics and Vicariance*, Columbia University Press, New York.
- Platnick, N. [1979], ‘Philosophy and the transformation of cladistics’, *Systematic Zoology* **28**, 537–46.
- Schuh, R. [2000], *Biological systematics: principles and applications*, Comstock Publishing, New York.

Wiley, E. [1981], *Phylogenetics: The Theory and Practice of Phylogenetic Systematics*,
John Wiley & Sons, New York.