

On The Impossibility of Monophyletic Linnaean Classification for Fossil and Extant Species

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A biological classification system should be as principled as possible. In recent years, proponents of phylogenetic taxonomy [2, 3] have argued that a taxon must be monophyletic. The monophyletic condition would define the content of a taxon as a single ancestor and all descendants of that ancestor. However, this is incompatible with a Linnaean taxonomy that covers both fossils and extant species. The intuitive idea that the incompatibility exists [5, 2] and that fossils play a role is not new [4, 1]. Nevertheless, the nature of this incompatibility has never been made precise. The aim of this paper is to present a counter model. A model that demonstrates this incompatibility and highlight reasons for its existence.

The contradiction between Linnaean and monophyletic classification lies in a tacit assumption. Overwhelmingly, phylogenetic trees in the literature only have labelled leaves¹ – typically labelled with the names of species. The assumption is that every species can be represented by a leaf in a phylogenetic tree. Yet, consider the phylogenetic tree depicted in Figure 1(a) and species y and z . Let x denote the most recent common ancestor of y and z . A serious problem arises if we wish to classify x – as may well occur if x is represented by fossil specimens. Consider the smallest clade containing x , y and z . Call this clade T . If T is to be part of

¹The term ‘leaf’ is used here in its mathematical sense. Intuitively, it refers to a dead end point in a tree.

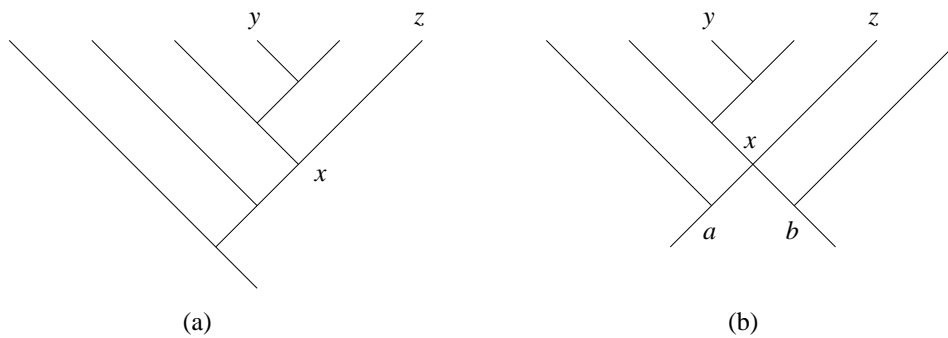


Figure 1: Two phylogenetic hypotheses. In (a), x is the most recent common ancestor of y and z . In (b), a phylogenetic network, a and b produce x through hybridization or endosymbiosis.

a Linnaean taxonomy then T must be placed at some rank. Suppose that T is identified as a family. Under a Linnaean taxonomy, x will also be placed in some genus and some species; taxonomic ranks subordinate to family. However, under a monophyletic system it is impossible to consider x in isolation. Since every clade that contains x must contain all descendants of x , there are no clades that contain x and are smaller than T – a taxon recognised as a family. It is possible to place x with a genus. This genus will necessarily be the only genus in the family. Moreover, the species contained within the genus are exactly those contained in T . The contradiction between monophyletic and Linnaean classification shows itself at the species rank. Under Linnaean classification, x must be placed alone at the species rank. However, T is still the smallest clade containing x , and that also contains y and z . Therefore, no clade containing x can correspond to the species x in a Linnaean taxonomy. The problem extends to all ancestors of x .

The incompatibility between Linnaean and phylogenetic classification is exacerbated with phylogenetic networks caused by hybridisation. Consider some species x that is contained in two Linnaean taxonomic groups S and T . Since the Linnaean system is hierarchical, it will always be the case that either S is contained in T or T is contained in S . For example, S could be an order that contains family T which, in turn, contains x . However, this containment property can be violated under a phylogenetic system. Consider Figure 1(b). Define clade S as a and all descendants of a . Also, define clade T as b and all descendants of b . Species x is contained in both clade S and clade T . However, it is not the case that one clade is contained within the other.

A possible solution to this incompatibility is to place all species in the leaves

of a phylogenetic tree. Under such circumstances, a Linnaean taxonomy can be monophyletic. This is achieved by imposing the restriction that if a sub-tree in a phylogenetic hypothesis is placed at a certain rank, then a *sibling* sub-tree must also be placed at the same rank. However, surely not every fossil is a dead end?

References

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