

**Philosophy and the Tree of Life:
The Metaphysics and Epistemology of Phylogenetic Systematics**

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Dissertation abstract**

This dissertation examines the foundations of phylogenetic systematics which involves both the construction of phylogenetic trees to represent evolutionary history and the use of those trees to study various aspects of that history. I begin by defending a genealogy-based view of biological taxonomy: the view that all taxa—the formal groups in our classification system—must be monophyletic, i.e., they must consist of an ancestor and all of its descendants. Furthermore, I argue that, contrary to current practice, these taxa should not be assigned ranks (such as genus, family, and order).

I then proceed by applying these principles to the debate about species. I argue that non-genealogically based species concepts (such as the popular “biological species concept”) are unacceptable. Instead, a species concept must delimit species so that they form genealogically exclusive groups – groups of organisms more closely related to each other than to any organisms outside the group. With this in mind, I develop two distinct phylogenetic species concepts. Each treats a species as a genealogically exclusive group of organisms. The first determines genealogical relatedness in terms of recency of common ancestry; the second understands genealogy as a composite of gene histories. Finally, I argue that there can be no objective ranking criteria for species and therefore biologists can either keep the species rank, while acknowledging that which taxa are ranked as species is arbitrary, or alternatively, can simply get rid of the rank of species.

Having carefully described what phylogenies represent, I move to the epistemological problem of inferring phylogenetic trees and argue that a Bayesian methodology is appropriate. I then focus on one common objection to Bayesian inference – “the problem of prior probabilities.” I argue that this problem has been misunderstood in some cases, which leads to the failure of a variety of objections in the literature. I then develop the beginnings of a solution to this problem within phylogenetics, describe just what has been achieved, and acknowledge what has yet to be accomplished.