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Abstract

The formal structure of the inference of a phylogenetic hypothesis is analyzed in the context of the different classes of reasoning applied in all fields of science. Rather than making the traditional distinction between deductive and inductive reasoning, it is shown that phylogenetic hypotheses are derived from a form of non-deductive inference commonly known as abduction. In making distinctions between abductive, deductive, and inductive inferences, the relationships between the origins of hypotheses and their testing become apparent. Abduction serves to provide explanatory hypotheses as tentative answers to specifiable causal questions. It is by way of deduction that specific potential test consequences are determined, whereas induction *sensu stricto* characterizes the act of carrying out a particular test. The formal structure of phylogenetic inference as a form of abduction is presented. Significant implications arise in recognizing that phylogenetic hypotheses are the products of abductive inference. The most apparent of these are that the distinctions between parsimony and likelihood as methodological criteria are unfounded. Parsimony refers to the relation between a causal question(s) and the hypothesis that serves as an answer for that question(s), whereas likelihood refers to the relation between the evidence as premises and the hypothesis allowed by those premises. The consequence is that parsimony has logical priority over likelihood in abduction, such that the likelihood of any hypothesis is maximized in the event that a causal theory of descent with modification is applied as fully as possible to observed shared similarities. In contrast, the application of rate-dependent theories, under the guise of maximum likelihood, are at odds with observations of shared similarities among two or more species and the causal questions regarding such observations; any rate-dependent theory only pertains to effects that are only tokogenetic in scope, not phylogenetic (*sensu* Hennig 1966). In recognizing phylogenetic hypotheses as answers to causal questions, the popular conception of testing such hypotheses by the introduction of new characters is incorrect. New character distributions cannot be deduced from a cladogram since such a structure only has causal relevance to the characters for which the hypothesis was inferred. The proper testing of a phylogenetic hypothesis requires the deduction of specific consequences as closely related as possible to the specified causal events of character origins and fixation, and subsequent speciation events. Such consequences must be effects that are independent of the class of effects the hypothesis was intended to explain, i.e., character data. As a result, effects that stand as legitimate potential test evidence are those effects that best support the different sets of causal events presented in the hypothesis. Problems with the popular applications of support indices, as offered by the bootstrap, jackknife, and permutation tests, are discussed. The main problem with these techniques is that they are only useful for testing statistical hypotheses, not explanatory hypotheses. Similarly, Bremer support analysis cannot provide indications of clade support because it is empirically meaningless to compare cladograms of different length, as each hypothesis only has relevance to the respective observations it explains.