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Testable but not falsifiable?

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Abstract

We are puzzled by a recent comment that suggested that historical hypotheses can be tested but are unfalsifiable. We argue that phylogenetic hypotheses are falsifiable without the aid of a time machine and that they are like any other hypothesis: they are tentative knowledge propositions capable of falsification with character evidence.

> Although evolutionary hypotheses can be tested they cannot be falsified, as they are historical hypotheses about singular events, and, in fact, we are unable to come back to the past to check whether they are true or false. Assis (2014: 240)

Assis (2014) cited Vogt (2008, 2014) for this statement, and we are puzzled by this view of science, this supposed epistemological pursuit, as a way of learning. If all hypotheses are valid because none can be falsified, how is new knowledge discovered? In fact, under this framework, knowledge (and thus epistemology) dissipates because the relativism between knowledge and a sea of statements crumbles. We see the philosophy of science as seeking to address the question, how do we know when we know something? In the formulation of Assis and Vogt, we do not see how the question can be answered, and not only for historical sciences.

What does it mean to be able to test something yet not be able to falsify that same something? Is that the same as everyone gets a ribbon for competing in a race, and therefore no one loses? Is 5 min 10 s less than 5 min 20 s? Or are they both the same after the test of the run?

If we have competing phylogenetic hypotheses A, B, and C, and there are data to test these hypotheses, and the data fit tree A significantly better by any metric than they fit on B and C, have B and C not been falsified? Or is there some other outcome that we are unaware of? Should we still entertain B and/or C as a viable hypothesis? We would answer no. We have advanced our understanding via falsification of B and C. We admit that we do not know if A is true, but given the data, we do know that A is the least discomfirmed hypothesis of the three. Importantly, falsification of phylogenetic hypotheses is not a simple either/or proposition because there can be varying levels of falsification, and thus A may have a single disconfirming character while B and C have 10 and 12 each. Farris (1983), among many others, noted that variable abundance of homoplasy is expected among competing phylogenetic hypotheses based on the same data. Although we cannot know the truth, we can know what is not the truth, and it is through this "positive power of negative thinking" (Gattei, 2002) that we obtain new knowledge. Rieppel (2008: 268) viewed this position of falsificationism as "extreme skepticism" and while it certainly is skepticism (Watkins, 1984; Gattei, 2002), we do not think Rieppel's label detracts from its effectiveness in phylogenetic hypothesis testing (e.g. Kluge, 1997).

Has the hypothesis that the endotherm groups Mammalia and Aves are sister taxa been falsified? Or should we continue to entertain the Haemothermia as a viable alternative simply because we do not have a

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time machine? Or how about the Amphibia of Linnaeus that included reptiles, amphibians, lampreys, rays, sharks, and sturgeons? Should that grouping still be considered a viable alternative hypothesis? To both we would answer no, they are no longer competing hypotheses. They have been falsified by repeated tests of character state distributions.

Hypotheses can be formulated where they are testable but seemingly not falsifiable. The hypothesis[1] "there is life on other planets in the universe" is easily accepted if life is found, but what do we say after 50 planets are sampled and nothing is found? Have we rejected the hypothesis? We could answer yes, temporarily, as even this claim is falsifiable with subsets of planets despite the impossible task of sampling every planet in the universe. This extreme hypothesis is falsifiable and testable solely because falsification rejects the utility of law-like generalizations that lack complete testability: induction.

The same argument can be made for phylogenetics, and perhaps this is the point of Assis (2014) and Vogt (2008, 2014). Until we have sampled the universe of characters for life we cannot generalize any set of relationships. As potentially troubling as that sounds, samples of characters and character states provide us with data to identify least disconfirmed hypotheses and recognize them as the most corroborated given the data, until such time that new data infer a rival hypothesis that is more highly corroborated than any other previous inference, hence falsifying the previous one (e.g. Gaffney, 1979; Kluge, 1999).

We recognize that all hypotheses are tentative knowledge propositions, but we also recognize that among the competing hypotheses some will be more tentative than others because they have been refuted more times than others, i.e. they have been falsified. We also believe that the tentative nature of a successful hypothesis is not confined to historical inferences, but to any hypothesis in science. Does a frequentist or Bayesian approach to a sample of experimental results somehow remove the "tentative" nature of the hypothesis that succeeds the tests? We do not see how and answer no. To us, all hypotheses are tentative and subject to further test, thus falsification.

To remove falsifiability from phylogenetics is, in essence, to remove the process from empiricism and allow metaphysical interpretation. Popper's criterion for demarcation called for an ability to experience (Popper, 1959). To that end, Popper asserted that within an empirical scientific system, refutation by experience must be possible. To claim that a time machine is required to falsify evolutionary hypotheses is to collapse the value of its data (characters) and defy homology altogether. If a coyote kills a coop full of chickens tonight and tomorrow we hypothesize that all of the chickens were white, although having never seen them, would this hypothesis not be falsified by the presence of a black feather? Is the finding of this black feather not an experience? If we cannot agree that synapomorphies, improved character quantification, and better taxon sampling can be black feathers then we cannot agree on the existence of relation by descent.

[1]We could have posed the hypothesis as "there is no life on other planets in the universe" to make it simple to falsify and difficult to verify. We chose not to do so in order to mimic the situation Assis described, a hypothesis that is testable but difficult to falsify.

References

Assis, L., 2014. Testing evolutionary hypotheses: from Willi Hennig to Angiosperm Phylogeny Group. Cladistics 30, 240–242.
Farris, J.S., 1983. The logical basis of phylogenetic analysis. In: Platnick, N.I., Funk, V.A. (Eds.), Advances in Cladistics. Proceedings of the Willi Hennig Society. Columbia University Press, New York, Vol. 2, pp. 7–32.
Gaffney, E.S., 1979. An introduction to the logic of phylogeny reconstruction. In: Cracraft, J., Eldredge, N. (Eds.), Phylogenetic Analysis and Paleontology. Columbia University Press, New York, pp. 78–111.
Gattei, S., 2002. The positive power of negative thinking. Cladistics 18, 446–452.
Kluge, A.G., 1997. Testability and the refutation and corroboration of cladistic hypotheses. Cladistics 13, 81–96.
Kluge, A.G., 1999. The science of phylogenetic systematics: explanation, prediction, and test. Cladistics 15, 429–436.
Popper, K.R., 1959. The Logic of Scientific Discovery. Hutchinson, London.
Rieppel, O., 2008. Hypothetico-deductivism in systematics: fact or fiction? Pap. Avulsos. Zool. 48, 263–273.
Vogt, L., 2008. The unfalsifiability of cladograms and its consequences. Cladistics 24, 62–73.
Vogt, L., 2014. Why phylogeneticists should care less about Popper's falsificationism. Cladistics 30, 1–4.
Watkins, J.W.N., 1984. Science and Scepticism. Princeton University Press, Princeton.