

Tree Thinking and Reasoning about Change Over Deep Time

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Introduction

Evolutionary theory is used by scientists to account for a wide range of biological phenomena. Like all scientific theory, evolution provides an explanatory lens through which one can make sense of patterns observed in the natural world. More specifically, evolutionary theory is made up of models that describe various mechanisms of change and the view that all life is genealogically linked such that new species arise by descent with modification from existing species. Evolutionary models are generally grouped into those addressing changes within species and those addressing changes between species—often referred to as micro- and macroevolution respectively. If the goal of evolution education is to teach students to make sense of the richness of life from an evolutionary perspective, then students should learn to use a variety of evolutionary models and ideas about descent with modification to account for the unity and diversity present in the living world.

A great effort has already gone into understanding students' reasoning about microevolutionary phenomena and models. Research on students' thinking about natural selection has highlighted the consistent use of teleological explanations for change and a focus on individuals instead of population-level thinking (Bishop & Anderson, 1990). With a detailed awareness of these and other potential conceptual difficulties that students face when learning about microevolution, it is possible to develop instruction aimed specifically at addressing these misconceptions. There have also been efforts to characterize the nature of scientific reasoning about microevolution. This approach emphasizes features of disciplinary inquiry including the range of phenomena that can be addressed, the types of data used, and norms for developing and defending explanations. A close analysis of the discipline makes it possible to engage students with realistic scientific problems and help them develop a deep understanding of natural selection as an explanatory model (Passmore & Stewart, 2002). The issues associated with teaching microevolution effectively are by no means fully resolved. Nonetheless, the existing research base on both the nature of disciplinary reasoning and on students' ideas about the causes of microevolution phenomena provide a foundation for addressing teaching and learning issues in a systematic way.

However, there is much more to understanding evolutionary theory than studying changes within species. Explaining patterns of similarity and difference among species and broader taxonomic groups requires a different kind of reasoning that invokes the consequences of speciation, descent with modification, and extinction. Over the last 40 years, biologists have increasingly used tree thinking to refine their understanding of biodiversity, guide their research efforts, and solve applied problems (O'Hara, 1997). Even more recently, growing access to genetic sequence data has helped integrate the use of phylogenetic information—details about the historical relationships between groups of organisms—across biological subdisciplines from ecology and behavior, to cellular physiology (Avice, 2004). Unfortunately, at this point we know very little about how students make sense of phylogenetic trees or how they use information about the historical relationships between species to reason about patterns in biological data.

Existing instruction in macroevolution often focuses on methods of historical reconstruction used to develop evolutionary trees. Understanding the assumptions and inferences involved in tree building is clearly an important aspect of understanding macroevolutionary theory. However, it is not clear that students are gaining a deep appreciation for the implications of speciation, descent with modification, and extinction from these experiences. I believe that additional emphasis needs to be placed on teaching tree reasoning skills so students can take advantage of phylogenies to make sense of macroevolutionary patterns. Evolutionary biologists think about the unity and diversity of life in terms of how their observations fit within the branching structure of genealogical relationships between species. They recognize the roles of descent from common ancestry and evolutionary modification in establishing patterns of similarity and difference among groups of organisms. In short, they see biology through the perspective of phylogeny. Emphasizing the interpretation and use of evolutionary trees can connect the conceptual and representational conventions biologists use with rich real-world examples, helping students understand the explanatory power of a tree thinking perspective. Adopting a tree thinking perspective could support

- understanding how to read and interpret a phylogenetic tree, including how to make inferences about missing data, describing more- and less-inclusive groups, discussing most recent common ancestors, and tracing character evolution;
- understanding the scientific rationale underlying comparative analyses, including the use of model organisms and many bioinformatics techniques;
- a more sophisticated view of the strengths and weaknesses of different approaches to biological classification;
- associating patterns of similarity and difference observed across organisms with important biological concepts like homology, analogy, adaptive radiation, gradualism, and punctuated change;
- the development of scientific explanations for phenomena using macroevolutionary models, including speciation, descent with modification, and extinction;
- understanding the evidentiary basis for phylogenetic inference, including the nature of phylogenetic claims, the types of data used to support them, and how disagreements are resolved;
- overcoming misconceptions about macroevolution level phenomena, such as the ideas that humans evolved from chimps, that evolution involves progress toward a predetermined goal, and that species are types defined by their characteristics; and
- viewing biodiversity in a phylogenetic context.

Evolutionary trees have already begun to play a more prominent role in biology textbooks, but very little is known about how students make sense of them. Early work on students' interpretations of tree diagrams points to difficulties they have describing relationships between groups in trees and relating biological concepts like homology to tree figures. These problems are likely due to insufficient experience working with trees as tools for evolutionary reasoning. The differences between students' everyday experiences with living organisms and biologists' theoretically

informed perspective on the relationships between species is a potential source of many misconceptions. Our direct experience with organisms leads us to group them into distinct types that do not appear to be changing. This ahistorical perspective can lead to an overemphasis on ecological adaptation in explanations of similarities and differences among species. While this may be a fruitful way to organize our personal knowledge, it does not provide the same explanatory power that biologists gain from macroevolutionary theory.

Medicine, bioinformatics, agriculture, conservation, and basic biological research are all being shaped by what we know about the history of relationships between species. Phylogenetic reasoning is an important aspect of our ability to bring an evolutionary perspective to our understanding of life on Earth. Without additional research into students' misconceptions about macroevolution and careful analysis of the nature of phylogenetic reasoning it will be difficult to systematically improve evolution education.

Brief Description of the Resources

The following section introduces two collections of resources that share a common commitment to biology education that emphasizes the importance of understanding evolutionary trees.

Details of the Resources

Title	Author	Medium	Grade Level	Publisher	Copyright	Cost/Ordering Information
The Tree Thinking Group	Various	Web site	Primarily 9–12 and undergraduate			Free http://www.tree-thinking.org
Description: A collaborative community that you can join						
The BEDROCK Bioinformatics Education Project	Various	Web site	Primarily undergraduate majors and nonmajors			Free http://bioquest.org/bedrock/
Description: A collaborative community that you can join						

Extended Description of the Resources

The **Tree Thinking Group** Web site, <http://www.tree-thinking.org>, is the Web space for a community of scientists and educators who are interested in phylogeny and other macroevolution topics in evolution education. The members of this group share an interest in understanding the ways that students reason about evolutionary trees and in developing curricula and assessments that support the adoption of a tree thinking perspective. The site compiles instructional materials, conceptual discussions, and research resources related to tree thinking in evolution education. The overarching goals include advancing research into how students learn about tree thinking and to improving instructional practice in evolution education.

The **BEDROCK Bioinformatics Education Project**, <http://bioquest.org/bedrock/>, is the Web home of a National Science Foundation funded professional development effort aimed at integrating bioinformatics into undergraduate biology education. The project is built on the premise that an evolutionary framework can be used to link bioinformatics analyses with many disciplinary research

questions throughout the undergraduate biology curriculum. The site emphasizes instruction that uses an inquiry approach, allowing students to learn through engagement in research activities.

The resources available at this site include bioinformatics curricular materials, workshop participant projects, and links to a variety of bioinformatics tools and other teaching resources. Of particular interest are the “problem spaces,” which provide data sets, curricula, and background materials that make it possible to engage students in researchlike experiences using bioinformatics analysis tools. The existing problem spaces include HIV sequence evolution, Galápagos finch classification, whale origins, chimpanzee conservation, epidemiology of the West Nile virus, and a case study of protein structure and function using Trp-cage. Also be sure to check the list of upcoming workshops and join us for a hands-on introduction to teaching biology using bioinformatics.

References

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