

# A Student-Friendly Tool for Phylogenetic Analyses

Joshua Povich<sup>1</sup>, Tania Bettis, and Tamara Mau

<sup>1</sup>University of California, Berkeley Department of Integrative Biology, 3040 Valley Life Sciences Bldg.  
#3140, Berkeley CA 94720 USA  
([povich@berkeley.edu](mailto:povich@berkeley.edu))

The desire to engage introductory biology students in phylogenetic analyses using real data and current research methods can be inhibited by the complexity and multitude of command line- driven programs typically used for these analyses. We have developed a graphical user interface (GUI) that combines the components of phylogenetic analysis into one student-friendly application, RevBayes. Here we present a lab activity in which students address evolutionary questions regarding the relationships among primates using morphological and molecular data. In this activity, students begin by making observations of primate skeletons from an interactive online database (eSkeletons.org) and then evaluate hypotheses about evolutionary relationships using RevBayes to generate the most parsimonious phylogenetic trees. Students are able to identify where relationships are well-resolved and where additional lines of evidence are needed. Molecular data from GenBank is then added to give a more resolved hypothesis about relationships within the group. RevBayes allows students to focus on the central concepts of phylogenetic analysis and interpretation by simplifying the interface with sophisticated analytical tools.

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## Citing This Article

Povich, J., T. Bettis, and T. Mau. 2016. A Student-Friendly Tool for Phylogenetic Analyses. Article 84 in *Tested Studies for Laboratory Teaching*, Volume 37 (K. McMahon, Editor). Proceedings of the 37th Conference of the Association for Biology Laboratory Education (ABLE). <http://www.ableweb.org/volumes/vol-37/?art=84>  
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