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A Student-Friendly Tool for Phylogenetic Analysis

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The desire to engage introductory biology students in phylogenetic analysis 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. In this hands-on demonstration, participants will address evolutionary questions regarding the relationships among primates using actual data. They will 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. They will identify where relationships are well-resolved and where additional lines of evidence are needed. Molecular data from GenBank is then added to give an increasingly clear 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.

Mission, Review Process & Disclaimer

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