

nice element of MacClade is its compatibility with other programs. MacClade reads data files as output by PAUP, PHYLIP, HENNIG86, CLUSTAL V, as well as the common National Biomedical Research Foundation (NBRF) format. Reciprocally, it can provide output to be read by these same programs.

Once the data have been input, you can move to the "tree window" and examine the most-parsimonious distribution of character changes on your tree topology of choice. A variety of "tools" are available that allow you to customize a graphical representation of a tree and then see how those changes affect tree length, tree statistics, and distribution of particular characters. You can reposition branches and taxa, reroot trees, and variously include or exclude taxa or characters. For example, if you wanted to know the number of additional steps required, and the particular characters involved, to support a sister relationship not found in the shortest tree, you could simply reposition the taxa as necessary.

A variety of bar charts, bubble charts, or tables can be calculated summarizing for one or more characters, consistency indices, retention indices, rescaled consistency indices, or numbers of changes by type. This can be done for one or more trees, including stored trees and randomly generated trees. For molecular data, tables may be obtained listing the frequency of possible changes between various nucleotide base pairs, the numbers of transitions and transversions by base position, and the number of changes per codon position, based on any particular tree topology. Another feature compares two trees for the number of steps required for each of the characters. These and additional features not mentioned will be useful in seeing how multiple equally-parsimonious trees differ in their implications about character evolution.

You may readily reweight characters in order to assess potential changes in support for trees when different sets of characters or types of character change are allotted more weight in phylogenetic analyses. For example, measures of congruence among characters, such as the consistency, retention and rescaled consistency indices mentioned above, may be used to

reweight characters, enabling use of a "successive approximations" approach in parsimony analyses.

MacClade has several tools allowing users to compare tree topologies and distributions of character change. It can calculate test statistics between trees based on the observed data and those based on randomized data. Character data may be randomly shuffled preserving the observed frequency of different character states, or data may be randomly generated. You also may specify parameters (probabilities for change from one character state to another) for a stochastic model of character evolution, and allow MacClade to generate change along different branches of a tree at different rates. The relevance of randomization schemes to studies of phylogeny is unclear, as the process of evolution, including functional constraints on characters and numerous forms of character nonindependence (due to phenomena such as pleiotropy and polygeny) is decidedly nonrandom. Nonetheless, MacClade provides the tools to assess the variable degree of departure from random change for characters.

The book accompanying MacClade describes the program's features in detail, and provides an overview of issues and problems in phylogenetic theory. The latter is essential reading for users in seeking to understand the authors' particular approach and to interpret results of analyses using MacClade. Though the authors provide numerous caveats regarding assumptions inherent in various analyses and potential misapplications of the program, users will benefit from consulting the primary literature.

MacClade has been admirably developed since its first release in 1986, and evolutionary biologists will hope that the authors continue to support and upgrade the program. The real significance of MacClade lies in its ability to foster new research, as it is the development of new tools, providing new perspectives, that leads most consistently over time to progress in scientific inquiry.—DAVID P. MINDELL, *Department of Biology and Museum of Zoology, University of Michigan, Ann Arbor, Michigan 48109, USA.*

Announcement



Recent Ornithological Literature Supplement.—Due to the untimely death of Marion Jenkinson Mengel, there is no Recent Ornithological Literature Supplement

with the October issues of the *Auk*, *Ibis*, and *Emu*. Instead, this Supplement will accompany the January issues of the three journals.