



Introduction to Modern Phylogenetic Methods

with Brigid O'Donnell and Hilary McManus

May 30 - June 5, 2010

This seminar will provide participants with working knowledge to construct phylogenetic trees using modern methods. We will cover data sampling, construction of a data matrix (using morphological or molecular characters), alignment of molecular sequences, inference of phylogenetic trees (using parsimony, maximum likelihood and Bayesian approaches), estimation of support values, and interpretation and presentation of phylogenies. A recurrent theme in the course will focus on the multiple points in phylogenetic methodology that require critical thought: choice of characters and inference methods, alignment of molecular data, how to reconcile multiple robust trees, etc. In addition, we will cover applications of phylogenetic methods to modern biology, including, but not limited to: applications of phylogenetic information to a myriad of biological investigations, implications of phylogenetics for taxonomy (e.g. traditional versus molecular-based concepts of species), comparative methods and character evolution, inference of evolutionary dates, and more. Course content will include lectures, hands-on work with phylogenetic programs and roundtable discussions of journal articles relevant to the topics at hand. Participants are strongly encouraged to bring a personal laptop (PC or Mac) and to download or purchase the following programs prior to their arrival at Eagle Hill. Participants can elect to bring their own dataset or work with a dataset provided by the instructors.

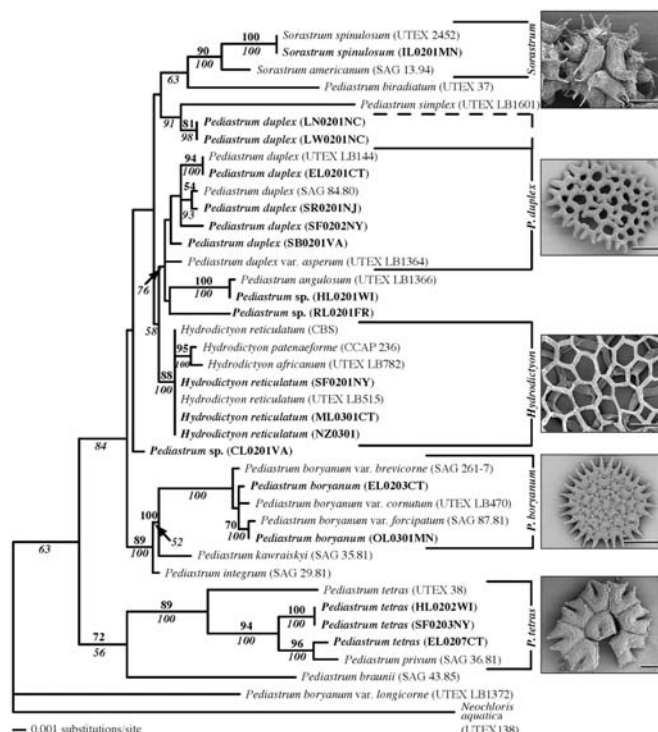
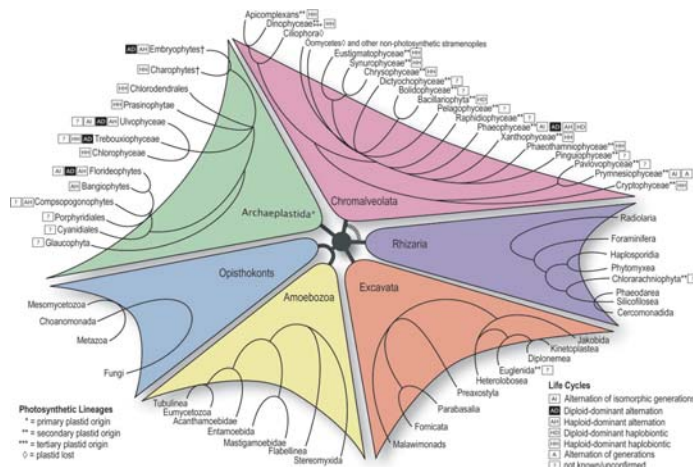
- 1) Alignment programs: ClustalX (PC) (free): <http://www.clustal.org/>, or MacClade (Mac) (at a cost): <http://macclade.org/macclade.html>
- 2) PAUP* (at a cost): <http://paup.csit.fsu.edu/> AND GARLI (free): https://www.nescent.org/wg_garli/
- 3) MrBayes (free): <http://mrbayes.csit.fsu.edu/>
- 4) TreeView (free): <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>.

Brigid C. O'Donnell (bcodonnell@mail.plymouth.edu) is an assistant professor and researcher at Plymouth State University, NH and studies mayfly phylogenetics with an emphasis upon leptophlebiid mayflies. She studies the development of mayflies of the eastern U.S., with an emphasis on embryonic and early nymphal stages of Ephoron leukon.

Dr. Hilary McManus (hilarymcmanus@gmail.com) is an assistant professor at Le Moyne College, NY and studies green algal evolution and taxonomy. She utilizes molecular phylogenetics and landmark-based morphometrics to explore questions regarding morphological evolution and species boundaries, with a focus on the freshwater green alga

Pediastrum and related genera. Dr. McManus is also interested in the evolution of land plants and the traits that allowed them to diversify in a terrestrial habitat, as well as life cycle evolution in the photosynthetic eukaryotes and the multiple independent origins of alternation of generations.

Guest lecturers who study phylogenetic methods will be announced.



Information is available on . . .

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