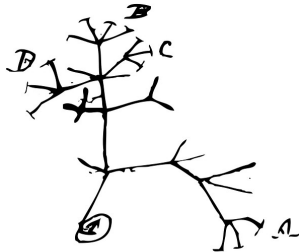


Outline 2 hours weekly plus home exercises

Greg Rouse grouse@ucsd.edu

Eckart room 139, Thursdays 10-1150

I think



sciencemarch

We will review some of the tremendous variety of methods for constructing phylogenetic trees using morphological and molecular data. The various options are outlined and critically examined, along with a set of relevant free software. There will be a lectures on a series of relevant topics followed by a series of exercises. The uses of the resulting phylogenetic trees (e.g., evolutionary transformations,, biogeography, systematics and taxonomy) are examined. At the end you should be able to access DNA data from GenBank use your own, and potentially use multiple genes and analyze from a phylogenetic perspective, as well as issues like species delimitation.

Week 1 Jan 9

Introduction to systematics, tree-thinking, basic terminology; current nomenclature

Week 2 Jan 16

Parsimony, tree searching, multiple equally parsimonious trees & consensus (**PAUP***)

Week Jan 23

Molecular sequence data 1. Acquisition and Alignment, (**Mesquite and MAFFT**)

Week 4 Jan 30

Uncorrected pairwise distance and generating a tree in **Mesquite (via RaxML NG)**

Week 5 Feb 6

Combining datasets with **Sequence Matrix (or Geneious)**. Model selections and Maximum Likelihood via **RaxML NG**.

Take Home Midterm, due Feb 11.

Week 6 Feb 13

Maximum Likelihood; bootstrapping **RaxML NG**

Week 7 Feb 20

Bayesian methods **MrBayes**

Week 8 Feb 27

Hypothesis testing

Week 9 March 6

Species delimitation, DNA barcoding, Networks **ABGD, PopArt, ASAP**

Week 10 March 13

Tracing the history of character evolution with **Mesquite** Fossils, molecular clocks and dating on trees. **BEAST Introduction**

Take Home Final, due March 18.