"Validating the Tree of Life"

**Term Project Part 1 -- HW6** (due Nov 14)
Multiple sequence alignment of mitochondrial cytochrome C oxidase exonic sequences from 10 closely related species, with bootstrap values. Kimura distance matrix.

**Term Project Part 2 -- HW7** (due Nov 28)
A program to calculate branch distances using the least squares method, and to calculate the S score.

**Term Project Part 3.** (due Dec 1) Work in teams. You choose whose species to use.

1) Starting with your tree and your MSA distances from HW6, modify the branch with the **worst bootstrap value**, using NNI. Evaluate three alternative trees (two NNI variants and the original) by calculating the S score using your program from HW7.

2) Find your species in the tree of life using OneZoom (http://www.onezoom.org/). Create a tree in Newick format for your species from the OneZoom tree. If the tree based on OneZoom is not one of the trees you evaluated in (2), evaluate it using least squares and your Kimura distances.

3) Study your species set. Show a complete Linnean classification with a lineage of phenotypic characteristics. Discuss the phenotypic differences that correlate with one or more branch points in the tree, especially the branch points you evaluated in (1). Would you overrule the best scoring tree in favor of a different tree, based on phenotypic differences?