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Phylogenetics Final Project Proposal Outline

**Introduction:**

There are many inconsistencies within the cnidarian tree of life, and recently many in siphonophores. There are new findings in siphonophore biology that enable us to help resolve them such as ROVs and data extraction technology. Using this, new relationships can be uncovered. This, in parallel with modern phylogenetic analysis programs, allows us to ask these questions. After taking this class, I am compelled to understand the decisions these top scientists have made in this field to uncover the new phylogeny of siphonophores.

**Phylogenetic Question:**

To explore how different models of evolution impact the phylogeny outcome by performing maximum likelihood, parsimony, and Bayesian (can I do this yet?) approaches. Evaluate them at the end by looking at the log likelihood and AIC scores. Also explore the impacts of bipartitions at different parts of the phylogeny. I want to understand the decisions the scientists made by making phylogenies and understanding the impact of making said decisions. I hope to come to the same conclusions and reproduce the same tree from the paper with the same certainty.

**Proposed Methods:**

Use RAxML to do maximum likelihood analysis and the class server to run bootstrap replicates of different modes of evolution. Use MrBayes for Bayesian analysis (?). Use morphological characters and sequencing data to help resolve the tree (can I do this?).

**Sources of Data:**

<https://www.sciencedirect.com/science/article/pii/S1055790318300460>

Munro, C., Siebert S., Zapata, F., Howison, M., Damian-Serrano, A., Church S.H., Goetz F.E., Pugh, P.R., Haddock, S.H.D., Dunn C.W. *Improved phylogenetic resolution within Siphonphore (Cnidaria) with implications for trait evolution.* Molecular Phylogenetics and Evolution