**Molecular Phylogenetics 2018**

**Topics by Week**

1) Fundamentals and Parsimony #1

a) Characters, homology, alignment

b) Trees, rooting

c) Maximum parsimony methods #1

i) Justification and objections

ii) Algorithms: tree length, tree search

2) Parsimony #2

a) Consensus and Weighting

b) Support for phylogenetic inference: Decay index, Bootstrap, KH test

c) Accuracy of MP and long-branch attraction

3) Distance Methods

a) Defining and correcting pairwise distances

b) UPGMA

c) “Regression” methods

d) NJ and minimum evolution

e) Objections and rejoinders

4) Maximum likelihood #1

a) Why ML?

b) Likelihoods on trees

c) Markov models of sequence evolution

5) Maximum likelihood #2

a) Choosing models: LRT, AIC

b) Basic models

c) Heterogeneous models

d) Support: LRS, parametric bootstrap, SH/SOWH

6) ML #3/Bayesian Phylogenetics #1

a) Performance of ML, model violation, consistency, objections

b) Relationship between ML and MP

c) Bayesian phylogenetics: principles

c) Posterior probabilities on trees and parts thereof

7) Bayesian analysis #2

a) Bayesian phylogenetic algorithms

b) Choice of priors, impacts on inference

c) Model violation

8) Phylogenomics/incongruence

a) Separate or combined analysis of genes?

b) Incongruence, measures, tests

c) Supertrees and supermatrices

d) Choosing good data in a phylogenomic context

9) Ancestral sequence reconstruction

a) Alogrithms

b) Bias

c) Robustness and error

10) Molecular evolutionary analysis using phylogenetic methods

a) Adaptive evolution and codon models

b) Gene family evolution: duplication, changes in rates, etc

c) Rates, clocks, dating