

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

- Assigned: Nikaido et al 1999, Wheeler et al. 1995, Farris 1983.
- Supplemental: Thompson et al. 1994; Edgar. 2006; Lloytnoja and Goldman 2008
- Textbook: Tree Thinking, chs 3-4;

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

- Hillis and Bull 1993; Wenzel and Siddall 1999; Hillis 1998
- Discussion: Huelsenbeck 1997 / Whiting 1998 (Supplementary recent analysis of this classic problem: Boussau et al. 2014; Niehuis et al 2012)
- Strongly recommended: Felsenstein 1978; Mindell and Thacker 1996; These are important, but there's a lot of reading already for this week.
- Textbook: Felsenstein chs. 3-5, 20-21, pp 81-87
- Due: Problem set 1: Trees homology and alignment

3) Distance Methods

- a) Defining and correcting pairwise distances
- b) UPGMA
- c) "Regression" methods
- d) NJ and minimum evolution
- e) Objections and rejoinders

- Assigned: Hillis, Huelsenbeck and Cunningham 1994; (Also: read leftovers Felsenstein 1978 and Mindell and Thacker 1996 from week 2)
- Discussion: Aguinaldo et al. 1997 / Blair 2002
- Textbook: Felsenstein ch 11
- Due: Problem set 2: Maximum Parsimony

4) Maximum likelihood #1

- a) Why ML?
 - b) Likelihoods on trees
 - c) Markov models of sequence evolution
- Assigned: Foster 1991; Le and Gascuel 2008
 - Discussion: Zanis 2003
 - Textbook: Felsenstein ch. 16;
 - Due: Problem set 3: Long branch attraction

5) Maximum likelihood #2

- a) Choosing models: LRT, AIC
 - b) Basic models
 - c) Heterogeneous models
 - d) Support: LRS, parametric bootstrap, SH/SOWH
- Assigned: Cunningham et al. 1998; Lartillot and Phillipe 2007; Le and Gascuel 2010;
 - Discussion: Nardi et al 2003 / Delsuc et al. 2003
 - Supplementary: Anisomova and Gascuel 2011; Le and Gascuel 2012
 - Textbook support: Felsenstein 13-14
 - Due: Problem set 4: ML #1
 - Due: 1 paragraph prospectus

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
- Assigned: ML: Siddall and Kluge 1999; Kolaczkowski and Thornton 2004; Huelsenbeck et al. 2002
 - Discussion: Phillippe et al 2005
 - Supplementary: Zhou, Shin, Hittinger and Rokas et al 2017
 - Due: Problem set 5: ML #2
 - Due: Specific aims

7) Bayesian analysis #2

- a) Bayesian phylogenetic algorithms
 - b) Choice of priors, impacts on inference
 - c) Model violation
- Assigned: Kolaczkowski and Thornton 2007; Nascimento et al. 2017
 - Discussion: Murphy et al. 2001; Delsuc et al 2006 / Boullat et al. 2006
 - Supplementary: Kolaczkowski and Thornton 2009
 - Due: Midterm

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

- Assigned: Dequeiroz et al. 1995; Farris et al. 1995; Shen, Hittinger and Rokas 2017
- Discussion: Rokas 2003 / Jeffroy 2006;
- Due: Problem set 6 Bayesian phylogenetics

9) Ancestral sequence reconstruction

- a) Algorithms
- b) Bias
- c) Robustness and error

- Assigned: Hanson-Smith et al. 2010; Williams et al. 2012; Eick et al. 2016;
- Discussion: Whelan et al. 2015; Pisani et al. 2015 ; Simon et al. Curr Biol 2017
- Supplementary: Yang et al 1995, Thornton NRG 2004
- Due: Nothing. Work on your project.

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

- Assigned: Yang and Nielsen 2002; Venkat et al. 2017;
- Discussion: Dehal and Boore 2005
- Supplementary: Zhang et al. 2005
- Due Monday: Proposal draft for peer workshop

- Read Guoy: rooting the tree of life: the phylogenetic jury is still out. Systematic error. Heterogeneity.
- Suppl: Philippe's essay on data quality