Ideas for student presentations

If you are not sure what to do for your presentation, please feel free to consider any of the following topics, all of which would be amenable to the kinds of hands-on presentations that work well for this course and would complement topics we will be covering as a group.

1. Introduction to Bayesian and ABC methods of model-fitting
2. Phylogenetic path analysis (von Hardenberg)
3. Phylogenetic eigenvector methods
   1. Diniz-filho JAF, Bini LM, Sant’Ana CER (1998) An Eigenvector method for estimating phylogenetic inertia. Evolution 52: 1247–1262.
   2. Diniz-Filho JAF, Bini LM, Rangel TF, Morales-Castilla I, Olalla-Ta´rraga MA´, et al. (2012) On the selection of phylogenetic eigenvectors for ecological analyses. Ecography 35: 239–249.
   3. Diniz Filho JAF, Rangel TF, Santos T, Bini LM (2012) Exploring patterns of interspecific variation in quantitative traits using sequential phylogenetic eigenvector regressions. Evolution 66: 1079–1090.
4. Detecting transitions in diversification rates on trees (start with Rabosky)
5. Phylogenetic mixed models (Hadfield, Lynch etc.)
   1. Hadfield JD, Nakagawa S. 2010. General quantitative genetic methods for comparative biology: phylogenies, taxonomies and multi-trait models for continuous and categorical characters. Journal of Evolutionary Biology 23: 494–508.
   2. Housworth EA, Martins EP, Lynch M. 2004. The phylogenetic mixed model. Am Nat 163(1): 84-96.
   3. Lynch M. 1991. Methods for the analysis of comparative data in evolutionary biology. Evolution 45(5): 1065-1080.
6. Applying comparative methods below the species level
7. Using fossil data in phylogenetic comparative analyses (Graham Slater’s work)
8. Tutorial: simulating data and using simulations to evaluate hypotheses and model fit
9. Testing for convergence (Ané approaches, Mahler)
10. Disparity-through-time (start with Harmon)
11. ML estimates of ancestral states, discrete data (Pagel et al.)
12. Biogeography (DEC, Bayesian diffusion methods, GeoSSE, DIVA)
13. Parsimony vs likelihood reconstructions for discrete traits
14. Stochastic mapping