

ECOL-346 Bioinformatics HW 07

After reading the Harrison and Langdale (2006) paper, provide a brief description of how you would construct a phylogeny for a gene family. What are the steps involved and what sorts of data do you need for each step? What are the tradeoffs of building phylogenetic trees with protein vs nucleic acid data? What are the differences between parsimony and likelihood optimized trees?