

Exam 3 Study Guide

The third quiz will cover material from weeks 7-10, as well as the review of phylogenetic inference in the first part of lecture on April 10, (i.e. all of the material on speciation and phylogenetics). It will not specifically cover material from earlier in the course, but you may need to use material from those weeks in answering questions about the covered topics.

Definitions and concepts (Be able to define these terms, and tell whether/how they apply in particular examples)

species, speciation, epistasis, phylogeny, tree, sister group, common ancestor (including most recent common ancestor), monophyletic group, paraphyletic group, polyphyletic group, clade, homology, homoplasy, convergence, reversal, principle of parsimony, root, polytomy, trichotomy, ancestral, derived, synapomorphy, outgroup

Speciation

genetic models of speciation
 fitness landscapes associated with genetic models of speciation
 role of the following in models of speciation: natural selection, epistasis, gene flow, assortative mating, prezygotic reproductive isolation, postzygotic reproductive isolation, geographic isolation
Ensatina example, Lake Apoyo cichlid example

Interpreting and using trees

What is the general structure of phylogenetic trees?
 Given a tree with a polytomy, draw or identify trees that are compatible with it (i.e. that are resolutions of the polytomy)
 Given a tree and the character states in the terminal taxa, be able to do the following:
 reconstruct the most parsimonious evolutionary history of the trait
 identify which state is ancestral and which state is derived
 distinguish homologous and homoplastic similarity
 determine whether homoplasy results from convergence or reversal
 Given information on relationships or characters, be able to draw an appropriate tree
 Given a hypothesis and a tree, say whether the tree supports the hypothesis
 Given a hypothesis, say how it could be tested using a tree
 Test hypotheses of coevolution of traits (using independent contrasts) and taxa (using sister group comparisons)

Reconstructing trees

Why do shared derived characters indicate relationships among organisms?
 What complicates use of shared derived characters in the real world? How do we deal with these complications?
 What general method did we use to reconstruct/infer the phylogenetic relationships of a group of taxa?
 What is the importance of homology assessment in phylogenetic inference? How can hypotheses of homology be tested without a tree? What supports the hypotheses of homology in the case of tetrapod limbs and fish fins? What about mammalian ears and reptile jaws?
 What assumptions are made in phylogenetic inference?
 What is the role of the outgroup? What is the importance of the root?
 How can support for a phylogenetic hypothesis be tested?
 Use a small data set to infer a phylogeny

I hope to have Problem Set 10 graded by Friday. I will leave them outside my office once they are done, and post an announcement on the website.

Don't forget about office hours, Monday 4-5 in BioPharm 305B, if you have questions.