EEB 2245 & EEB 2245W
Final STUDY GUIDE for EXAM 2
SPRING 2017

Evolution of Biodiversity and Extinction

-Description of, and differences between, Background and Mass extinctions (global vs local causes; are causes for both events the same? etc.); proposed cause of the Mass extinction at the end of the Cretaceous and evidence that supports that explanation.
-Pull of the recent: what is it? Example?
-Anthropocene: What is it? When is/was it? What is its cause? Criteria for a new interval to be added to the Geological Time Scale? Options of such criteria for the Anthropocene?

Characters, Homology and Homoplasy

-Distinction between direct and indirect evidence for elucidating patterns of evolutionary change.
-distinction between macro- and microevolution?; level at which systematic methods apply
-what is a character (e.g. morphology, molecular, etc.)? What is a character-state? Be able to distinguish between them and recognize/provide examples of each
-mosaic evolution: what is it? How does it relate to the concept of entire species being "primitive" or "derived"? example?
-in reconstructing evolutionary relationships, seek homologies, rather than homoplasies (i.e., rather than features that are merely analogous in two taxa)
-understand and be able to define the concept of homology; basic criteria used to determine homology (e.g., position, structure, etc.); must always identify the taxonomic context
-problems with organisms that look similar, but are not closely related (i.e. homoplasy)
-be able to explain the difference between homoplasy and homology
-why strive to use homologies over homoplasies for the generation of phylogenetic trees?
-definition of homoplasy; describe/distinguish among the 3 different types of homoplasy: Convergence- what is it? Describe an example of convergence; recognize convergence on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided. Parallelism- what is it? Describe an example of parallelism; recognize parallelism on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided. How would you distinguish parallelism from convergence? Reversal- what is it? Describe an example of a reversal; recognize a reversal on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided; describe an example of a chemical reversal. Be able to recognize three different types of homoplasy with different character types (i.e., morphological, chemical, molecular, etc.)

Reconstructing Evolutionary History from Indirect Evidence

-BE CERTAIN TO COMPLETE THE PROBLEM SET DISTRIBUTED IN CLASS ON TUESDAY AND POSTED ON THE COURSE WEBSITE.
-What is systematics? What is a phylogenetic tree?
-How do we infer branching patterns among taxa? Initial methods were subjective (e.g., Haeckel, Romer)
-Hennig's contributions: developed a formalized, objective, character-based method, use of outgroups
-understand and be able to define, and/or recognize in a data matrix and/or on a phylogenetic tree as appropriate the following terms: terminal taxon, node, branch, dichotomy, polytomy, sister taxon (taxa), most recent common ancestor, distant common ancestor, root, clade/monophyletic group, paraphyletic group, character, character-state, plesiomorphy, symplesiomorphy, apomorphy, synapomorphy
-ingroup vs outgroup- how do they differ? Criteria for selection of each; importance of monophyly of ingroup relative to outgroup
-understand the distinction between an ancestral homology and a derived homology; importance of including taxonomic context (i.e., group under consideration) in statements of homology
-role outgroup plays in systematics (allows polarization of character states- i.e., determination of ancestral/plesiomorphic state of characters; state in outgroup is plesiomorphic); be able to polarize characters using an outgroup
-What is parsimony? What role does the principle of parsimony play in systematics? Steps in conducting a phylogenetic analysis using parsimony as the optimality criterion; be able to map characters on tree topologies from a data matrix optimally (i.e., so as to minimize the total number of changes for each character on a particular tree topology).
-Other methods for generating phylogenetic trees (i.e., Likelihood, Bayesian methods)
-Be able to identify all possible sets of (dichotomous) relationships (tree topologies) for a SMALL set

of taxa, identify plesiomorphic vs. apomorphic states of characters using an outgroup, map characters onto the possible tree topologies, determine the most parsimonious topology, etc.; from morphological and molecular data matrices; be able to use outgroup data to polarize both binary and multistate characters; limitations of outgroup for polarization of multistate characters.

-Be able to summarize character data in a data matrix; be able to interpret character data from a data matrix for both morphological and molecular data

-Be able to determine which tree topology is most parsimonious and generate the most parsimonious tree topology based on a *simple* data matrix for a SMALL set of taxa.

-Why are computer programs required to determine the most parsimonious tree topology/set of relationships when dealing with greater than 4 or so taxa?

-Molecular data: advantages (large number of characters, broadly comparable) and disadvantages (multiple hits, alignment, etc.); understand that all 3 types of homoplasy exist with molecular character data; recognize examples of each. Sources of sequence data: nuclear, organelle (mitochondria, chloroplasts, etc.); sources of differences between nuclear and organelle gene trees (endosymbiotic origin of organelles, maternal inheritance of mitochondria)

-Haeckel's Biogenetic Law? Does ontogeny actually recapitulate phylogeny? Can development be used to polarize characters?

Biogeography and Continental Drift

-Importance of knowing the actual distribution of a taxon before attempting to explain it

-Importance of understanding phylogenetic relationships of taxon before attempting to explain its distribution (group under consideration should be monophyletic)

-What is biogeography? What are its 2 major components? (description of distributions vs. explanations for distributions)

-Formal descriptions of distributions of organisms: common recurring distributional patterns and the Biogeographic realms: Palearctic, Nearctic, Neotropical, Ethiopian, Oriental, Australian, Oceania & Antarctic) What are they? Where are they? 3 major categories of barriers (climate, mountains, etc.; barriers bounding each biogeographic realm; Wallace's line-What is it? Where is it? What is vagility? Variation in imperviousness of barriers depending on type and vagility of organisms. Barriers change over time, example? Terminology for types of distributions- endemic, cosmopolitan, disjunct: what do they mean? Illustrate and/or recognize examples of each.

-Explanations for distributions: Differences between dispersal and vicariance explanations for geographic distributions of organisms

-Continental Drift- what is it? know basic sequence and time of continental configurations of Pangaea, Laurasia, Gondwana, modern positions. Examples of vicariant events explained by continental drift (e.g., *Glossopteris* flora, *Lystrosaurus*)

-Historical biogeography: importance of establishing age of a taxon and age of land masses on which it is distributed prior to developing explanations for its distribution.

-Continental shelf: What is it? Where is it? Continental vs. Oceanic islands: distinguish between the 2; recognize islands of each type from a map illustrating continental shelf; provide an example of each type of island; distinction between continental islands and oceanic islands when sea levels fall and implications for dispersal and thus distributions of organisms. Expectations of similarity between faunas and floras of continental vs. oceanic islands relative to the closest mainland.

NOTE: you are not responsible for the information presented by our Prominent Evolutionary Biologists who visited the class…but a bonus question is not beyond possibility.