EEB 2245 & EEB 2245W
Final STUDY GUIDE for EXAM 2
SPRING 2019

Evolution of Biodiversity and Extinction

-total number of taxa at any time is difference between diversification and extinction rates
-relationship between # fossils found and sediment volume (& explanation for this relationship)
-Pull of the recent: what is it? Example?
-Evidence of qualitative changes in diversity over time? Examples?
-Evidence of quantitative changes in diversity over time? Category of taxonomic classification most appropriate for addressing this question & why this category is most appropriate (i.e., families vs. species or phyla, etc.)
-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 end of the Cretaceous and evidence that supports that explanation; explanations for other 4 mass extinctions; same or different causes? (asteroid impact?; other cause of each)
-Is there evidence that plants experienced mass extinctions? If not, why not?
-What is a diversity profile? Be able to interpret diversity profiles for different taxa
-Sepkoski's 3 marine animal faunas (focused on families), what are they (Cambrian, Paleozoic, Modern); what major groups characterize each?
-# marine animal families now vs. in the past?
-3 types of conditions that may foster increases in diversity within an individual taxon: Ecological displacement and Ecological Replacement: What are they? How do they differ? Recognize/provide an example of each; key innovations/adaptive radiation: what is this? Recognize/provide an 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?
-Types of characters (e.g. morphology, molecular, etc.); what is a character-state? Be able to distinguish between characters and character-states 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? Recognize a reversal on a phylogenetic tree or from a verbal description in which necessary taxonomic context is provided. Be able to recognize 3 different types of homoplasy with different character types (i.e., morphological, chemical, molecular, etc.) and on a phylogenetic tree.

Reconstructing Evolutionary History from Indirect Evidence

-BE CERTAIN TO COMPLETE THE PROBLEM SET DISTRIBUTED IN CLASS 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, apomorphy, synapomorphy
-Distinction between ingroup and 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).

-Understand that there are other methods for generating phylogenetic trees (i.e., Likelihood, Bayesian methods); you don't need to know these methods, but you should know they exist.

-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 for both binary and multistate characters; be able to map characters on a tree from a data matrix with either type of characters.

-Be able to determine which tree topology is most parsimonious and generate the most parsimonious tree topology based on a 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, etc.) and disadvantages (multiple hits, etc.); understand that all 3 types of homoplasy exist with molecular character data; recognize examples of each.

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 8 Biogeographic realms: Palearctic, Nearctic, Neotropical, Ethiopian, Oriental, Australian, Oceania & Antarctic) What are they? Where are they? 3 main types of barriers (climate, mountains, etc.); barriers bounding each biogeographic realm; Wallace's line-What is it? Where is it? Understand that barriers differ in imperviousness depending on type of organisms (e.g. Panama isthmus); barriers also change over time, example?

-What is vagility? Variation in imperviousness of barriers depending on type and vagility of organisms.

-Terminology for types of distributions (i.e., endemic, cosmopolitan, etc.); what do they mean? Illustrate and/or recognize examples of each.

-Physical features of the earth worth considering in developing explanations for distributions: continental shelf—what is it? Where is it? Distinguish between continental vs. oceanic islands; recognize islands of each type from a map illustrating continental shelf; provide an example of each type of island; differences in effects of changes in sea level on each type of island and implications for dispersal and thus distributions of organisms; continental drift—what is it? Know basic sequence and time of continental configurations of Pangaea, Laurasia, Gondwana, modern positions; why theory of continental drift was initially poorly received by scientific community; discovery that changed this situation? Alfred Wegener's biological evidence for continental drift

-Explanations for disjunct distributions: understand situation with repeated patterns in the *Glossopteris* flora and *Lystrosaurus* and evidence for vicariance in both cases. Differences between dispersal and vicariance explanations of disjunct distributions (active vs. passive, abiotic vs. biotic). Historical biogeography: Vicariance explanations: Methods for assessing vicariance—phylogenetic relationships of group of interest, assessing current distributions, constructing area cladograms, looking for commonalities across unrelated taxa, importance of considering age of focus lineage relative to age of barrier; details of various examples (chelid turtles, hylid frogs, galliform birds, cypress). What is the molecular clock? How is it used in historical biogeography? How is it calibrated? Dispersal explanations: Can common patterns emerge from dispersal scenarios? Consider the Hawaiian Islands—geological formation of islands over 5+ million years; *Psychotria* distributions and phylogeny, Hawaiian cricket distributions and phylogeny. Pleistocene glaciation and example of disjunct distributions resulting from a *combination* of dispersal and vicariant events (e.g., in saxifrages). Why disjunct distributions are so important to evolution (i.e., effect on gene flow, speciation). Example of Madagascar (oceanic island, age of separation from continental Africa, highly endemic fauna).

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.