

EEB 2245 & EEB 2245W
Preliminary 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

- What is biogeography? What are its 2 major components? (description of distributions vs. explanations for distributions)
- 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)
- 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; barriers bounding each biogeographic realm; Wallace's line- What is it? Where is it? Variation in imperviousness of barriers depending on type and vagility of Organisms.
- Terminology for types of distributions- endemism, cosmopolitan, disjunct: what do they mean, provide and/or recognize examples
- Differences between vicariance vs dispersal explanations for geographic distributions of organisms
- Barriers change over time, example?
- Continental Drift- what is it? know basic sequence and time of continental configurations of Pangaea, Laurasia, Gondwana, modern positions; plate tectonics as a mechanism (why not Rodinia?)
- Examples of vicariant events explained by continental drift (e.g., *Glossopteris* flora, *Lystrosaurus*)
- Historical biogeography: importance of establishing age of a taxon and its phylogenetic relationships prior to developing explanations for its distribution.
- Example of major Dispersal event (Great American Interchange)

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.