

Study Guide
Introduction to Evolution
Lecture 4: Phylogeny Reconstruction

Important Terms and Concepts

Advanced Character
Analogy
Apomorphy
Bayesian Analysis
Binomial Nomenclature
Bootstrapping
Branch Swapping
Chronogram
Clade
Cladistics
Classification
Code of Nomenclature
Consensus Tree
Consistency Index
Convergent Evolution
Data Matrix
Distance Matrix
Dendrogram
Distance Measure
Evolutionary Systematics
Heuristic Search
Homology
Homoplasy
Ingroup
Internode
Linnaean Hierarchy
Maximum Likelihood
Modern Synthesis
Monophyletic
Node
Nomenclature
Numerical Taxonomy
Ocham's Razor
Outgroup
Parallel Evolution
Paraphyletic
Parsimony
Phenetics
Phenogram
Phylogenetics
Phylogenetic Classification (Systematics)
Phylogeny
Phylogram
Plesiomorphy

Polyphyletic
Polytomy
Primitive Character
Priority of Names in Nomenclature
Reversal
Rooted Tree
Scaled Tree
Similarity
Sister Group
Splitter
Synapomorphy
Synonym
Systematics
Taxon
Taxonomy
Topology
Tree of Life
Type Concept
Tree Root
UPGMA
Willi Hennig

Study Questions

1. What is systematics? What sort of things do systematists do?
2. What is the importance of classification and stable nomenclature?
3. What are some differences between artificial, natural, and phylogenetic systems of classification?
4. What are some rules that are applied to scientific names? Who makes these rules? Why are they important?
5. Compare and contrast the basic goals and methods of phenetics (numerical taxonomy) and cladistics.
6. What are homologous characters? Why is their importance in reconstructing phylogenies?
7. What is cladistics? What kinds of problems does cladistics help us to solve? In what way does cladistics differ from older methods?
8. What is a phylogeny? What is a phylogenetic tree? From what general kinds of data can phylogenies be inferred, and what general issues must researchers address when estimating phylogenies?
9. What is a synapomorphy, and why are these characters uniquely valuable for phylogeny inference? What is the name of the methods that use these principles for phylogeny inference?
10. What is homoplasy? What processes give rise to it, and what specific, problematic pattern does each produce? What qualities do researchers look for in characters in hopes of reducing homoplasy?

11. What is the general logical criterion of parsimony? What is the rationale for invoking parsimony in phylogeny inference (i.e., what underlying evolutionary principles justify its use)?
12. Define the term systematics and compare and contrast phenetic with cladistic approaches to classification.
13. What is the principle of parsimony? What is a clade?
14. What is an outgroup? Why is the outgroup crucial in interpreting evolution in a clade? How can we use the concept of an outgroup to reconstruct the pattern of evolution?
15. What does Ockam's Razor refer to? Which cladogram version is considered the "best" (out of several which could be made for a particular group of organisms)?
16. Why are we interested in shared derived characters and shared ancestral characters? Give some examples from the vertebrates.
17. What is the difference between monophyletic and paraphyletic groups? Illustrate these concepts on a tree. Give several examples of paraphyletic groups.
18. What techniques does a cladist use to describe the support for clades on a tree? How do these techniques work? How does a cladist deal with multiple most-parsimonious trees in the analysis?