

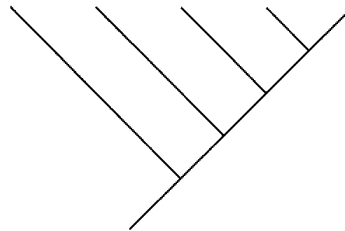
**Part I**

1. What types of organisms are most likely to appear in the fossil record?
2. What two complications may make it difficult to determine phylogenetic relationships based on morphological similarities between species?
3. Base deletions have changed the lengths and alignments of these two homologous regions of DNA. Determine the best possible fit between these two DNA sequences. How many deletions and base changes have occurred in these DNA segments?

A C G T G C A C G  
A G T G A G G

4. Place the taxa (outgroup, A, B, C, and D) on the cladogram based on the presence or absence of the characters 1-4 as shown in this table. Indicate before each branch point the number for the shared derived character that evolved in the ancestor of the clade.

Characters	Outgroup	Taxa			
	O	A	B	C	D
1	0	1	1	1	1
2	0	0	1	0	1
3	0	1	1	0	1
4	0	0	1	0	0



5. According to the principle of parsimony, the evolution of the four-chambered heart should place birds and mammals in the same clade. Why does the most accepted evolutionary tree show them as separate branches from the reptilian line?
6.
  - a. Give an example of genes that would be compared to uncover phylogenetic relationships among the earliest branches on the tree of life.
  - b. Give an example of genes that evolve very rapidly and are used to discriminate among closely related species.
  - c. Give an example of paralogous genes.
7. Using the neutral theory of molecular evolution, explain why different genes might have a different molecular clock rate.

**Part II.**

Note: Phylogenies are Based on Common Ancestries

1. Distinguish between phylogeny and systematics.
2. Describe the process of sedimentation and the formation of fossils. Explain which portions of organisms are most likely to fossilize.
3. Explain why it is crucial to distinguish between homology and analogy before selecting characters to use in the reconstruction of phylogeny.
4. Explain why bird and bat wings are homologous as vertebrate forelimbs but analogous as wings.
5. Define molecular systematics. Explain some of the problems that systematists may face in carrying out molecular comparisons of nucleic acids.
6. Explain the following characteristics of the Linnaean system of classification:
  - a. binomial nomenclature
  - b. hierarchical classification
7. List the major taxonomic categories from most to least inclusive.
8. Define a clade. Distinguish between a monophyletic clade and paraphyletic and polyphyletic groupings of species.
9. Distinguish between shared primitive characters and shared derived characters.
10. Explain how shared derived characters can be used to construct a phylogenetic diagram.
11. Explain how outgroup comparison can be used to distinguish between shared primitive characters and shared derived characters.
12. Define an ingroup.
13. Distinguish between a phylogram and an ultrametric tree.
14. Discuss how systematists use the principles of maximum parsimony and maximum

likelihood in reconstructing phylogenies.

15. Explain why any phylogenetic diagram represents a hypothesis about evolutionary relationships among organisms.
16. Distinguish between orthologous and paralogous genes. Explain how gene duplication has led to families of paralogous genes.
17. Explain how molecular clocks are used to determine the approximate time of key evolutionary events. Explain how molecular clocks are calibrated in actual time.
18. Describe some of the limitations of molecular clocks.
19. Explain the neutral theory of evolutionary change.
20. Explain how scientists determined the approximate time when HIV-1 M first infected humans.
21. Describe the evidence that suggests there is a universal tree of life .