AP Biology   Name _____

Cladistics and Bioinformatics Questions 2013

1. The following table shows the percentage similarity in sequences of nucleotides from a homologous gene derived from five different species of mammals compared to that of a homologous human gene. In simpler terms, the percentage similarity between the human gene and the Chimpanzee gene is 99.7%

Species	Percentage Similarity
Chimpanzee	99.7
Baboon	97.2
Rabbit	93.7
Rhesus Monkey	96.9
Orangutan	98.6

Draw a cladogram depicting the evolutionary relationships among all six species (including humans) according to their percentage similarity in the gene shown in the table.

An **outgroup** is a species of organism that acts as a reference group when determining the evolutionary relationships between three or more other species of organisms. It is hypothesized to be related to the species in question but less closely than any of the other species are to each other. Outgroup species therefore share more *primitive* characteristics with the group in question. In a phylogenetic tree, the line for the outgroup should branch from the ancestral lineage *before* any of the other groups. It gives you an overall comparison between a distantly related species and those that are more closely related.

2. What probably explains the inclusion of rabbits in this research from Question 1?
   A. Their short generation time provides a ready source of DNA.
   B. They possess all of the shared derived characters as do the other species.
   C. They are the closest known relatives of the rhesus monkeys.
   D. They are the outgroup.
   E. They are mammals.

3. What conclusions can be drawn from the data shown in Question 1?
   A. Humans and other primates evolved from rabbits within the past 10 million years.
   B. Most of the genes of other organisms are similar to human genes.
   C. Among the species listed, humans shared a common ancestor most recently with chimpanzees.
   D. Humans evolved from chimpanzees somewhere in Africa within the last 6 million years.
   E. Both B and C are correct.

4. Use the following data table to construct a cladogram of the major plant groups. From this data table, you should first construct a table similar to the one in Question 5 below. This will make it easier to construct the cladogram.

Organism	Vascular Tissue	Flowers	Seeds
Mosses	0	0	0
Pine Trees	1	0	1
Flowering Plants	1	1	1
Ferns	1	0	0
Total	3	1	2

5. Draw a cladogram based on the first **five** characters (**not** 'dorsal fin') in the table below. Place hatch marks on the tree to indicate the origin(s) of each of the five characters.

Character	Lancelet (outgroup)	Lamprey	Tuna	Salamander	Turtle	Leopard	Dolphin
Backbone	0	1	1	1	1	1	1
Hinged jaw	0	0	1	1	1	1	1
Four limbs	0	0	0	1	1	1	1*
Amnion	0	0	0	0	1	1	1
Milk	0	0	0	0	0	1	1
Dorsal fin	0	0	1	0	0	0	1

*Although adult dolphins have only two obvious limbs (their flippers), as embryos they have two hind-limb buds, for a total of four limbs.

6. Notice that the character "dorsal fin" is included in the table, a character possessed by both the Tuna and the Dolphin. Why was the character of "dorsal fin" not used to construct the cladogram, even though it is a character shared by both the Tuna and the Dolphin?

Use the phylogenetic tree to the right to answer the following questions.
Note: This phylogenetic tree is not a true cladogram, because it is based on the time that these organisms diverged from a common ancestor, not shared derived characters.
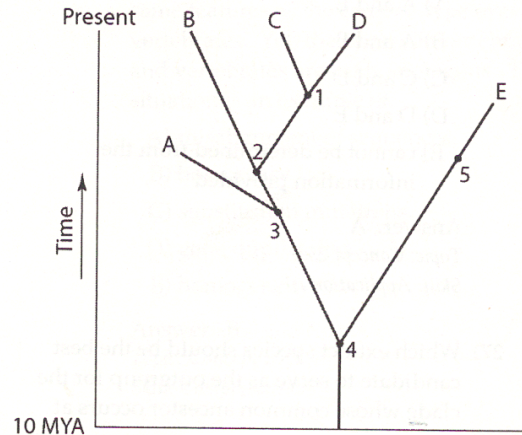
7. A common ancestor of species E and C would be
    at position number:
    A. 1   B. 2   C. 3   D. 4   E. 5

8. The two species in the tree that are most closely
    related to each other are:
    A.   A and B   C. C and D
    B.   B and C   D.   D and E
                         E. E and A

9.   If this tree was derived from common homologies, a
     clade within the tree would include (choose all that
     apply)
     A. A, B, C and E   C. A, B, C and D
     B. A, C and E   D. B, C, and D
               E. A, B, C, D and E



10. If you were using cladistic analysis to build a phylogenetic tree of cats, which of the following would make
    the best outgroup?
    A. lion   B. wolf   C. tiger   D. leopard   E. domestic cat

11. All of the following describe a way in which Bioinformatics can be used. Which of the following describes
    best what you were doing in the bioinformatics assignment?
    A. Using gene sequences to determine the amino acid sequence of a protein
    B. Comparing nucleotide sequences from an organism in question to known sequences in order to
        make inferences about the relatedness of that organism to others (Comparative Biochemistry).
    C. Using gene sequences to determine the three dimensional structure of a protein.
    D. Analyzing gene sequences to determine which mutations cause disease.
    E. Use known gene sequences to produce genes for genetic engineering research.

Five new species of bacteria were discovered in Antarctic ice core samples. The nucleotide (base) sequences of rRNA subunits were determined for the new species. The table below shows the number of nucleotide differences between the species.

NUCLEOTIDE DIFFERENCES

Species	1	2	3	4	5
1	--	3	19	18	27
2		--	19	18	26
3			--	1	27
4				--	27
5					--

12. Which of the following phylogenetic trees is most consistent with the data?

(A)

(B)

(C)

(D)
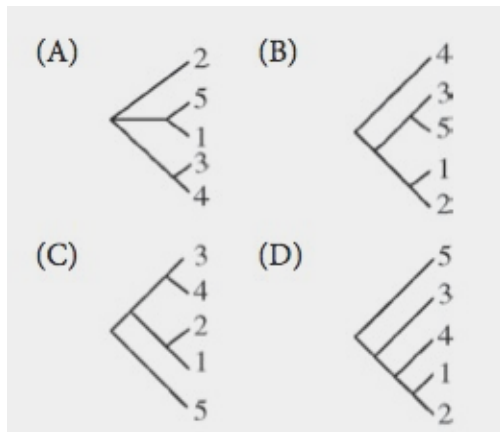
13. Data regarding the presence (+) or absence (-) of five derived traits in several different species are shown in the table below.

Species	Trait				
	1	2	3	4	5
V	+	+	+	−	−
W	+	+	−	−	−
X	+	−	−	+	+
Y	−	−	−	−	−
Z	+	−	−	−	+

Which of the following cladograms provides the simplest and most accurate representation of the data in the table?

(A) Y   W   V Z   X

(B) X   Y Z   W   V

(C) Y   V   X W   Z

(D) Z   W X   V   Y