

Honor pledge: "I have neither given nor received unauthorized aid on this test."

Signed : _____

Date : _____

Name : _____

TOTAL = 45/100 points

1. What are the 3 primary evolutionary branches of life? (5 points)

2. _____ All living cells are fundamentally the same in the following ways *except* (2 points)

- A. DNA structure
- B. types of RNAs they have
- C. what metabolic processes they carry out
- D. how big they are
- E. what amino acids they use to make proteins

3. _____ Taxonomies are *what?*(2 points)

- A. evolutionary trees
- B. ways of grouping, naming and identifying things
- C. quantitative and objective
- D. the same as phylogeny
- E. due on April 18th this year

4. _____ The term "prokaryote" is often used (badly) to describe what kinds of organisms? (2 points)

- A. plants, animals, and fungi
- B. bacteria
- C. unicellular creatures
- D. bacteria and archaea
- E. germs

5. _____ Which of the following will prevent a molecular sequence from behaving in a clock-like fashion? (2 points)

- A. if it has functional constancy
- B. if it is made of many independently-evolving units
- C. if it is horizontally transferred
- D. if it is found in all organisms
- E. none of the above

6. _____ What molecular sequence is most commonly used for phylogenetic analysis? (2 points)

- A. signal recognition particle RNA
- B. beta-lactamase messenger RNA
- C. ribonuclease P RNA
- D. large subunit ribosomal RNA
- E. small subunit ribosomal RNA

7. _____ G+C bias can create artifacts in a tree, but this can be avoided by ... (2 points)

- A. avoiding sequences with uneven G+C contents
- B. transversion analysis
- C. correcting for long-branch attraction
- D. using a 2- or 6-parameter model
- E. you cannot correct for G+C bias

8. _____ Sequence alignment is the process of ... (2 points)

- A. correcting for undercounting in a similarity matrix
- B. collecting the sequences you wish to use
- C. maximizing sequence similarity
- D. identifying homologous residues
- E. determining the reliability of a tree

9. _____ Which of the following is *not* a tree construction algorithm? (2 points)

- A. Maximum-likelihood
- B. Neighbor-joining
- C. Fitch-Margoliash
- D. FAME
- E. Parsimony

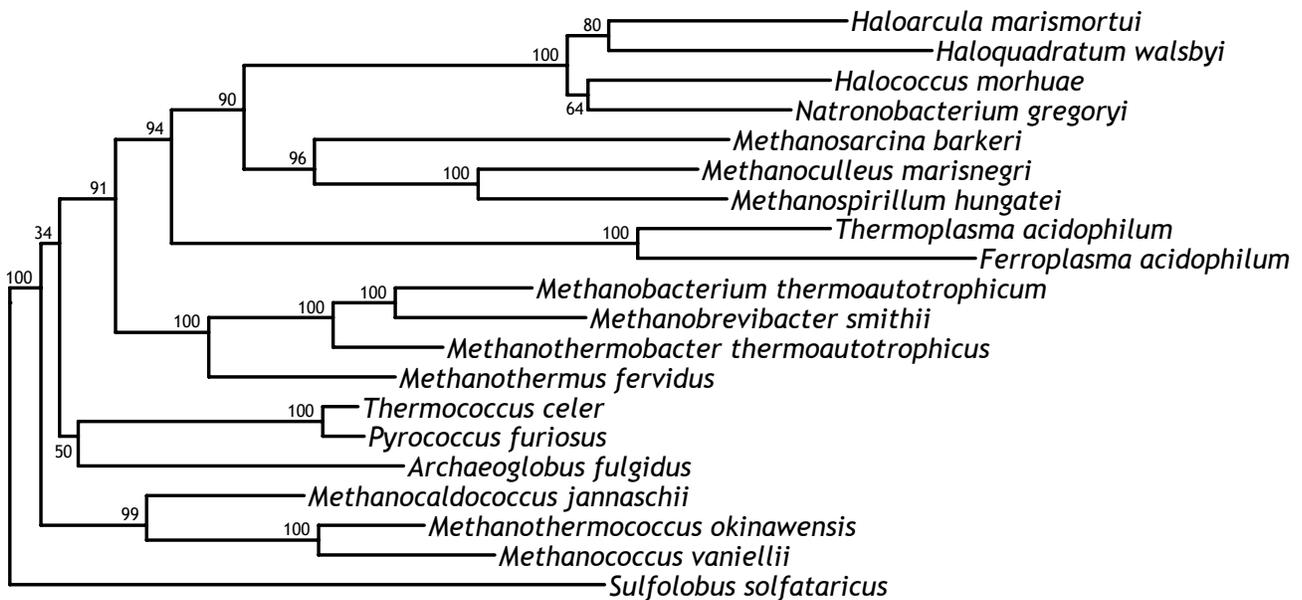
10. ____ Molecular phylogenetic analysis using the molecule in question 6 is usually unable to do what? (2 points)

- A. distinguish what genus an organism is a member of
- B. distinguish closely-related species or strains
- C. distinguish Gram-positive from Gram-negative
- D. distinguish Bacteria, Archaea and Eukarya
- E. create reliable trees

11. ____ Which of the following is **not** an alternative to molecular phylogenetic analysis for identifying organisms? (2 points)

- A. phenotypic analysis
- B. lipid (FAME) profiling
- C. serotyping
- D. RFLP analysis
- E. protein sequence analysis

17. Answer the following questions from this phylogenetic tree, (2 points each)



Scale: 0.1 (evolutionary distance)

- a. Which sequence is most similar to that of *Methanothermus*? _____
- b. Which is the *most* primitive sequence (excluding, perhaps, the outgroup)? _____
- c. What is the approximate evolutionary distance between *Methanosarcina* and *Methanospirillum*? _____
- d. Circle and label "G" the last common ancestor of the Class "Methanococci" (any genus that starts with "Methano-" and ends with "-coccus").
- e. If another specie of *Haloarcula* were to be added to this tree, draw what it might look like (on the tree above).

18. On the tree in question above, what does the number “80” mean above the branch leading to *Haloarcula* and *Haloquadratum* mean? How was this number determined? Be sure to both name the process and describe the how it’s done. (5 points)

19. Given that you must have an outgroup to root a tree, how was the “universal” phylogenetic tree rooted? (5 points)

