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

2. If an organism gets its energy from light and carbon by fixing CO₂, it is a/an ___________. (1 point)
   A. Chemoheterotroph
   B. Chemoautotroph
   C. Phototroph
   D. Photoautotroph
   E. none of the above

3. How do we know that all known life on Earth has a common ancestry? (1 point)
   A. because it’s all on the same planet
   B. because all of fundamental biochemistry in the same
   C. because all life is exactly the same
   D. because all life on Earth came from Mars
   E. known life on Earth does NOT have a common ancestry

4. Species evolve _________________(1 point)
   A. diversification from common ancestors
   B. moving up the evolutionary ladder
   C. progressing to superior forms
   D. inheriting acquired traits
   E. Trick question! Species do NOT evolve!

5. Molecular phylogenetic trees are ______ & ______ (1 point)
   A. taxonomic and phylogenetic
   B. subjective and qualitative
   C. objective and quantitative
   D. linear and progressive
   E. dumb and meaningless

6. Which of the following is NOT a component of a taxonomy? (1 point)
   A. Grouping and organizing organisms based on similarity
   B. Naming organisms and groups of organisms
   C. Identifying previously unknown organisms
   D. estimating evolutionary relationships between organisms
   E. All of the above are components of a taxonomy

7. The term “prokaryote” means _______________ (1 point)
   A. microscopic
   B. not a eukaryote
   C. Gram-positive or Gram-negative
D. bacterial  
E. simple and barely qualifying as alive

8. ES-2 (later named *Eubacterium thermomarinus*) turned out to be ________________ (1 point)
   A. a Gram-positive organism related to *Clostridium*  
   B. a Euryarchaeon related to *Methanocaldococcus*  
   C. a novel organism not at all related to anything else known at the time  
   D. A deep-sea vent eukaryote  
   E. none of the above

9. Which if the following is NOT a reasonable alternative to ssu-rRNA for distinguishing close relatives? (1 point)
   A. RNase P RNA  
   B. the ssu-lsu rRNA spacer sequence  
   C. protein sequences  
   D. alignments made by joining several RNA or several protein sequences together  
   E. all of the above

10. Which if the following is NOT true of “horizontal transfer”? (1 point)
    A. was more common before the last common ancestor  
    B. occurs between organisms of all phylogenetic distances  
    C. is most frequent between close relatives  
    D. probably is not a major factor in microbial evolution  
    E. All of the above are true

11. What is the purpose of bootstrapping? (1 point)
    A. to determine the reliability of branches in a tree  
    B. to convert a similarity matrix into a distance matrix  
    C. an algorithm used to generate phylogenetic trees  
    D. a method of calculate ancestral sequences  
    E. none of the above

12. Which of the following is and important feature of a useful molecular clock? (1 point)
    A. Functional constancy  
    B. Comprised of a large number of independently-evolving units  
    C. Large database of sequences and resources  
    D. Not (often) transferred horizontally  
    E. all of the above

13. Which of the following is NOT a major lesson drawn from the “Big tree” of life? (1 point)
    A. Big eukaryotes represent a small portion of diversity  
    B. Chloroplasts bacterial symbionts are  
    C. Gram-positive/negative are not the major divisions of Bacteria  
    D. Mitochondria are bacterial endosymbionts  
    E. protists (unicellular eukaryotes) evolved from Bacteria

14. The “universal tree” was rooted using _________ (1 point)
    A. the fossil record  
    B. small-subunit ribosomal RNA  
    C. ancient duplicated genes  
    D. Archaea as the outgroup  
    E. none of the above

15. Archaea are most closely-related by ancestry to (i.e. have a common ancestor with) _________________ (1 point)
    A. Viruses  
    B. Bacteria  
    C. Eukarya  
    D. mitochondria  
    E. none of the above

16. What is an outgroup, and how is one used in a phylogenetic tree? (5 points)
17. Answer the following questions from this tree (1 point each)

![Evolutionary Distance Tree](image)

- a. Which sequence is most similar to that of *Pectinatus sottaceto*? 

- b. What is the outgroup? 

- c. Which is the most primitive sequence (excluding, perhaps, the outgroup)? 

- d. Circle the least-reliable branch on the tree and label it “D”. 

- e. What is the approximate evolutionary distance between *M. hypermegale* and *S. ruminantium*? 

- f. Circle the last common ancestor of the genus *Pectinatus* and label it “G”. 

18. On this 3-Domain molecular phylogenetic tree, circle and label each of the 5 “Kingdoms” in the old-fashioned Whitaker tree (5 points)
19. Describe one method OTHER than molecular phylogenetic analysis used to identify microbes. (5 points)

20. What features of the ssu-rRNA make it such a good molecular clock of molecular phylogenetic analysis? (5 points)
21. The Europa Explorer, in the year 2035, returns to Earth with a sample of sediment drilled from beneath the icy crust of this moon of Jupiter. Attempts to cultivate anything from the sample fail, but you successfully use small-subunit ribosomal RNA-targeted primers and PCR to obtain 4 reasonable-looking ribosomal RNA sequences (called Europa-1, Europa-2, Europa-3, and Europa-4) from the sample. Below is a tree of these sequences relative to some representative Earth sequences. What can you tell me about how life on Europa and Earth are related, assuming you’re able to show that the sequences are not contamination from Earth, are clean sequences (no sequencing errors) and are properly aligned? (5 points)
Midterm Exam #1 : Take-home questions

MB 451 : Microbial Diversity : Spr 2012

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

The rules: You are free to use any notes, books, or online material while taking this take-home exam. You are also free to use a calculator and ruler or other drawing material. You are NOT allowed to get (or give) help of any kind from (or to) anybody. If you have questions about the exam, send an email to Dr. Brown at james_brown@ncsu.edu. You MUST turn this completed take-home portion of the exam in with the rest of the exam when you take it, unless you take the exam in the DELTA offices or via remote proctor.

Signed : ____________________________ Date : __________________________

Name : ____________________________

1. Align the following sequences: (4 points)

   Oak  U A C G A G C C U G G C A
   Elm  U A G G A G C C C U G G U
   Maple A U G A G C C A U G G C A
   Pine U A A G A G C C U G A U A

2. Align the following RNAs: (5 points)

   A A
   G A
   A U
   U G
   U U
   A U
   U A
   G U
   C G
   A G
   C U A U
   G C A U
   A G C A A U
   Bob
   Mike
   John

3. Draw the secondary structures of the Jill and Mary RNAs in this alignment: (5 points)

   Jill  - - G G G G G U A A G C C U - - C C - U A U
   Mary  U C G G C G - - A U A - C G U A C C G - A U
   Steph - C G G A G A - U U U U C U - - C C G - - -

   U
   U U
   A U
   G - C
   A U
   G - C
   G - C
   C - G

   Steph RNA
4. Create a similarity matrix from the following alignment, using a 2-parameter model in which transversions count as a full difference (-1.0), and transitions count as half a difference (-0.5): (5 points)

Bob  G G G G G G G G G G
Jim  G G G G G G G G G A
Sue  G G A G G G G G G U
Spot G G C G G G U A G C
Bubbles G A U G G A A G -

5. Convert this dendrogram into a phenogram. Notice the bootstrap values! The yeast L30 sequence is the outgroup: (5 points)
6. Use the following distance matrix to generate a tree (with branch lengths) using the neighbor-joining method. SHOW ALL OF YOUR WORK! (26 points)

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