

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

Signed : _____

Date : _____

Name : _____

TOTAL = 55 points

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 _____. (2 points)

- A. Chemoheterotroph
- B. Chemoautotroph
- C. Photoheterotroph
- D. Photoautotroph
- E. none of the above

3. ____ How do we know that all known life on Earth has a common ancestry? (2 points)

- A. because it's all on the same planet
- B. because all of its fundamental biochemistry is 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 by _____. (2 points)

- 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 ____ & ____ (2 points)

- A. taxonomic and phylogenetic
- B. subjective and qualitative
- C. objective and quantitative
- D. linear and progressive
- E. dumb and meaningless

6. ____ Which if the following is NOT a component of a taxonomy? (2 points)

- A. Grouping and organizing organisms based on similarity
- B. Naming organisms and groups of organisms
- C. Identifying previously unknown organisms
- D. determining evolutionary relationships
- E. All of the above are components of a taxonomy

7. ____ The term *prokaryote* means _____. (2 points)

- 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 _____. (2 points)

- 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? (2 points)

- A. RNase P RNA
- B. the ssu-lsu rRNA spacer sequences
- C. protein sequences
- D. alignments made by joining several RNA or several protein sequences together
- E. all of the above can be useful for this purpose

10. ____ Which of the following is NOT true of “horizontal transfer”? (2 points)

- 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*? (2 points)

- 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 an important feature of a useful molecular clock? (2 points)

- 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? (2 points)

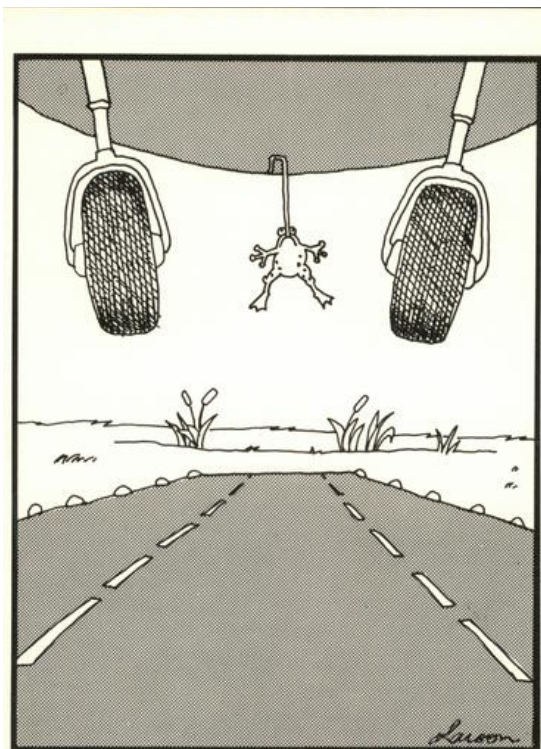
- A. Big eukaryotes represent a small portion of diversity
- B. Chloroplasts are bacterial endosymbionts
- C. Gram-positive/negative are not the major divisions of Bacteria
- D. Mitochondria are bacterial endosymbionts
- E. protists (unicellular eukaryotes) evolved from Bacteria

14. ____ The “universal tree” was rooted using _____ (2 points)

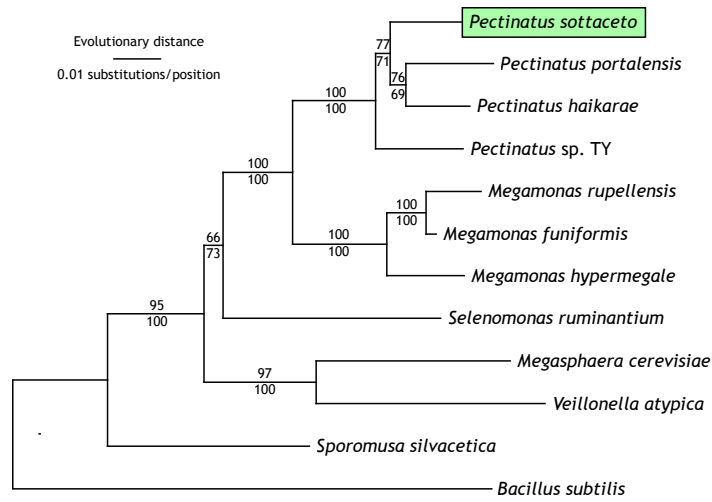
- A. the fossil record
- B. small-subunit ribosomal RNA
- C. ancient duplicated genes
- D. Archaea as the outgroup
- E. none of the above

15. ____ Archaea are most closely-related by ancestry (i.e. have a common ancestor with) to _____ (2 points)

- A. Viruses
- B. Bacteria
- C. Eukarya
- D. mitochondria
- E. none of the above



16. Answer the following questions from this ssu-rRNA-based tree (2 points each)



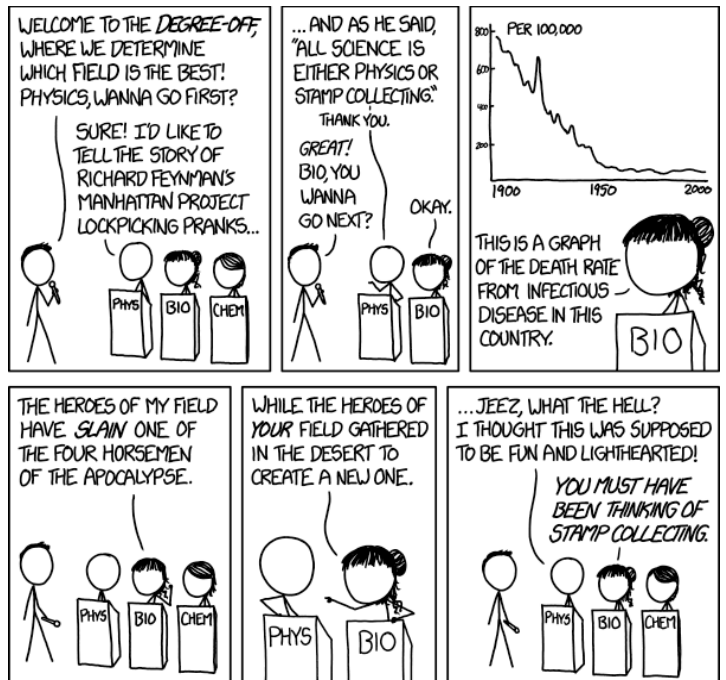
Upper numbers : Maximum Likelihood bootstrap values (% of 1000 trees, rounded to nearest %)
Lower numbers : Weighted neighbor-joining bootstrap values (RDP, % of 100 trees)

- Which sequence is most similar to that of *Megamonas hypermegale*? _____
- What is the outgroup? _____
- Which is the *least* primitive sequence (excluding, perhaps, the outgroup)? _____
- Circle the least-reliable branch on the tree and label it "D".
- What is the approximate evolutionary distance between *Pectinatus* sp TY and *M. rupellensis*? _____
- Circle the last common ancestor of the genus *Megamonas* and label it "G".
- If another specie of *Selenomonas* were added to this tree, draw what it might look like (on the tree above).



17. On the tree in question above, what does the number “76” mean above the branch leading to *P. portalensis* and *P. haikarae* mean? How was this number determined? Be sure to both give it’s name and describe the process. (5 points)

18. Given that you must have an outgroup to root a tree, how was the “universal” phylogenetic tree rooted? (3 points)



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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 no later than when the start of the rest of the exam.

Signed : _____

Date : _____

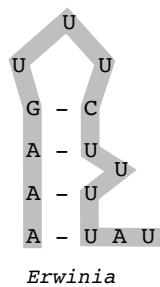
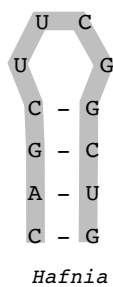
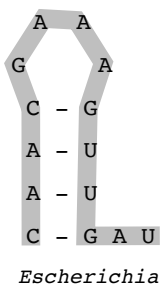
Name : _____

TOTAL = 55 points

1. Align the following sequences: (5 points)

B. anthracis A U G A G A C U U G C A A U
B. brevis A C G A G A C C A U G C A A
B. cereus A C G A G A U C U G C A A U
B. diminuta A G A G A C U U G U A A U

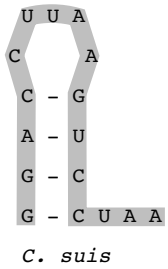
2. Align the following RNAs: (5 points)



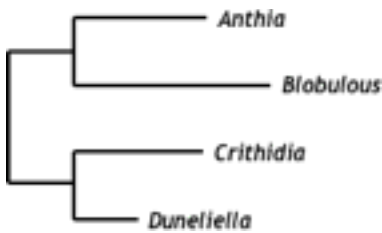
3. Draw the secondary structure of the *C. rattus* RNA in this alignment: (5 points)

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C. suis      G G A C - C U U A A - G U - - C C U A A
C. rattus    C C G C C U U C - G G G U A A G G U U -
    
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4. Convert this phenogram into a dendrogram. Please keep the tree to the same scale. (5 points)

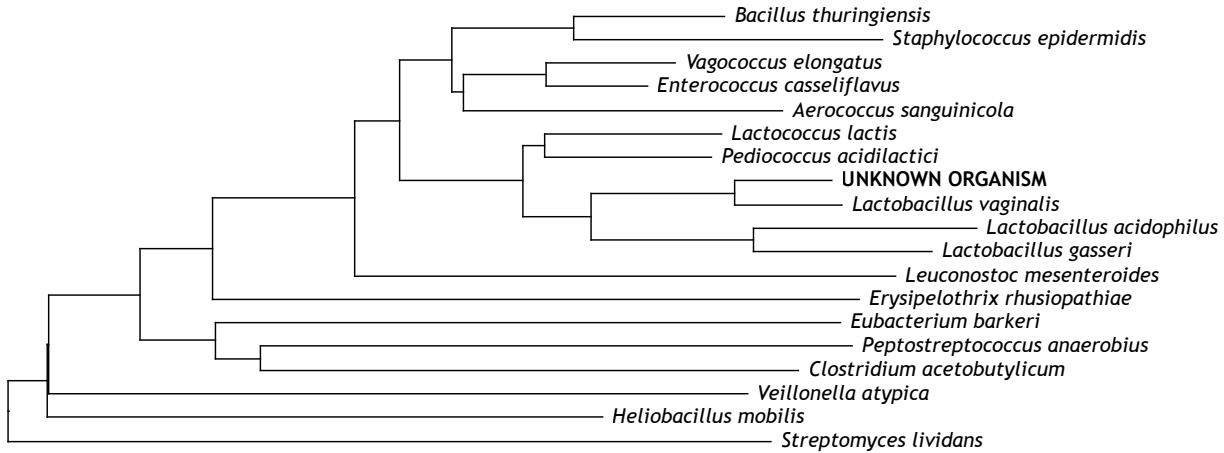


5. Use the following distance matrix to generate a tree (with branch lengths) using the neighbor-joining method. SHOW ALL OF YOUR WORK! (15 points)

	A	B	C	D	E
A	-	-	-	-	-
B	0.3	-	-	-	-
C	0.8	0.9	-	-	-
D	0.6	0.7	0.8	-	-
E	0.4	0.5	0.8	0.6	-



6. You have cultivated an unknown organism from your skin and have obtained its ssu-rRNA sequence. After running a couple of preliminary trees, you've zoomed it down to the following tree of relatives:



Based on this tree, make 5 *independent, specific, testable* predictions about the properties of your organism. (2 points each)

6a.

6b.

6c.

6d.

6e.

EXTRA CREDIT!

7. For up to 2 extra-credit points, list a couple of specific properties of your unknown that your tree does *not* allow you to predict with any confidence: (1 point each)

7a.

7b.

