

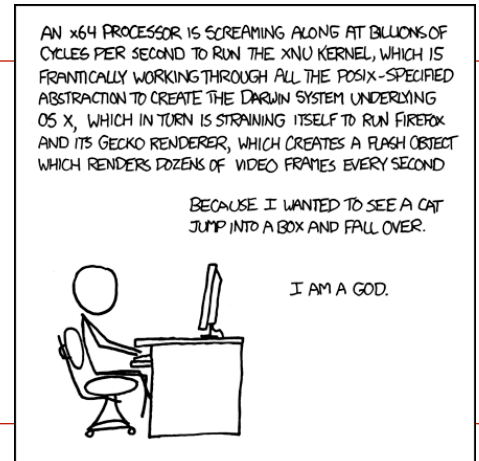
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Signed : _____

Date : _____

Name : _____

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



Multiple choice questions (1 point each)

2. ____ An organism that gets its energy from light and its carbon from organic compounds (it can't fix CO₂) is a:
 - A. Photoautotroph
 - B. Chemoautotroph
 - C. Photoheterotroph
 - D. Chemheterotroph
 - E. no such organisms exist
3. ____ Which of the following is a reasonable representation of phylogenetic diversity?
 - A. The Chain of Being
 - B. The Ladder of Life
 - C. The 5-Kingdom Tree
 - D. The 3-Domain Tree
 - E. The Circle of Life
4. ____ Which of these terms is scientifically meaningful?
 - A. Superior
 - B. Higher eukaryote
 - C. Prokaryotes
 - D. Bacteria
 - E. Phlogiston
5. ____ What does "ssu-rRNA" stand for?
 - A. small structured uncoding regulatory RNA
 - B. small subunit ribosomal RNA
 - C. *Staphylococcus subcutaneous* ribosomal RNA
 - D. Siderophore-secretion universal suppressor RNA
 - E. Sonoma State University Reptile Reserve National Archive
6. ____ Which of the following is *not* a feature of a good molecular clock?
 - A. Readily transferred horizontally
 - B. Wide phylogenetic range
 - C. Functional constancy
 - D. Comprized of a large number of independent units
 - E. Lots of available sequences and resources
7. ____ Which of the following is likely to count as the smallest change in a 2-parameter "Kimura" substitution model?
 - A. A to C
 - B. G to C
 - C. A to G
 - D. G to U
 - E. all of the above will be counted equivalently

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8. ____ Which of the following is *not* an algorithm for generating phylogenetic trees?
- A. Parsimony
 - B. Bayesian inference
 - C. Neighbor-joining
 - D. Fitch
 - E. Jukes & Cantor
9. ____ Phylogenetic analysis of ES-2 showed that it is . . .
- A. a deep-sea hydrothermal vent organism
 - B. a novel organism worth a great deal of effort to study
 - C. in the *Clostridium/Eubacterium* family of Firmicutes
 - D. *Bacillus mycoides*
 - E. most closely related to *Eubacterium thermomarinus*
10. ____ Which is *not* a component of any Taxonomy of living things?
- A. The identification of organisms
 - B. The organization of similar organisms into groups
 - C. Labeling organisms and groups with names
 - D. The evolutionary pathway of related organisms
 - E. All of the above are components of any such taxonomy
11. ____ The root of the universal 3-Domain tree separates...
- A. prokaryotes from eukaryotes
 - B. Eukarya from (Bacteria and Archaea)
 - C. Bacteria from (Archaea and Eukarya)
 - D. Archaea from (Bacteria and Eukarya)
 - E. the root lies exactly at the node between all 3 groups
-

Short answers (points as indicated)

12. All living things are much alike in most ways. What does this imply about our ancestry? (2 points each)

(1)

(2)

13. List 5 features of ssu-rRNA that make it a good molecular clock for phylogenetic analysis. (1 point each)

(1)

(2)

(3)

(4)

(5)

14. **How** was the “Universal 3-Domain Tree” rooted? (5 points)

15. **Describe** an example of an alternative to ssu-rRNA analysis for phylogenetic analysis. (5 points)

16. What is *Bootstrapping*, and how does it work? (5 points)

Answer the following questions about this phenogram (10 points)

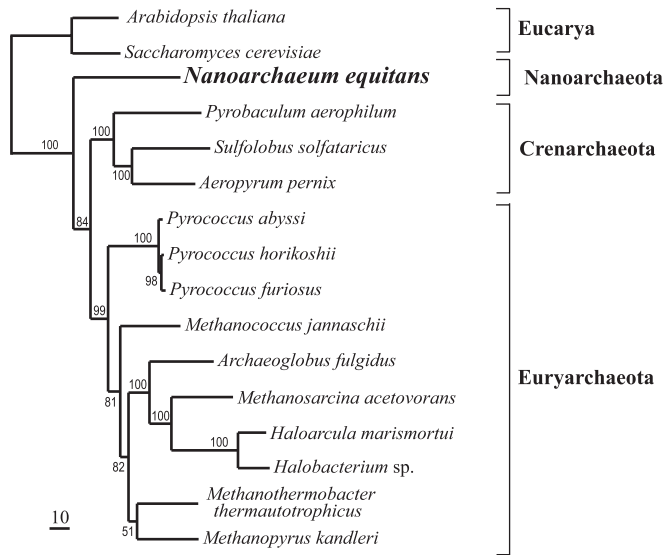
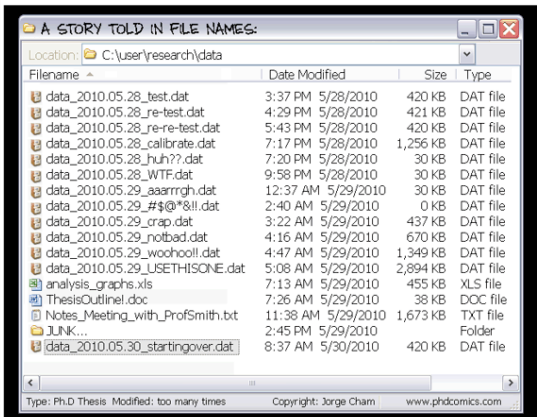


Fig. 3. Phylogenetic position of *N. equitans* within the Archaea. The tree was determined by the maximum likelihood method, based on 35 concatenated ribosomal protein sequences. Numbers indicate percentage of bootstrap resamplings. The scale bar corresponds to 10 estimated substitutions per 100 amino acid positions.

18. Which sequence(s) are likely to be the outgroup? _____
19. Assuming you're correct about the outgroup, circle the root defined by this outgroup and label it "19".
20. Which two sequence are most closely-related? _____ and _____
21. Which genus is the most primitive (in terms of the sequences used in this tree)(Ignore the outgroup) _____
22. Circle the least reliable branch on the tree and label it "22".
23. What is the approximate evolutionary distance separating *Haloarcula* and *Halobacterium* (in substitutions per 100 aa) _____
24. Circle the last common ancestor of *Halobacterium sp.* and *Methanothermobacter thermoautotrophicus* and label it "24".
25. What is/are the closest relative(s) of *Aeropyrum pernix*? _____



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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 with the rest of the exam when you take it, unless you take the exam in the DELTA offices, in which case you need to turn it in at my office or mailbox.

Signed : _____

Date : _____

Name : _____

1. Align the following sequences: (5 points)

Herring	G A G C U G G A U A
Tuna	C G A G C U G A A
Skipjack	A G A G C U U G A A
Grouper	G A G C U C G A U A

2. Draw the secondary structures of the RNAs in this alignment: (5 points)

Structure	. . ((. . . .)) . . ((. . .)) .
Toadfish	U U G G G U U C G C C C U U G G U U U C C A
Flounder	- A U A C U U U - G U G - U C - C U G - G U

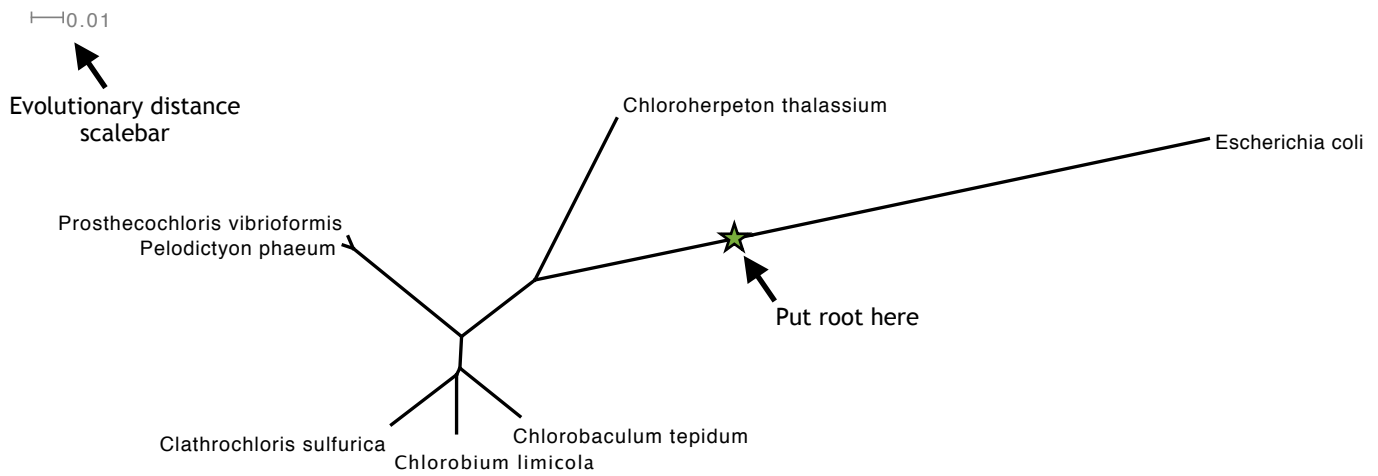
3. Align the following RNAs: (5 points)

U A	A	
U G	U A	A G
C - G	C - G	G A
A - U	G • U	C - G
U G - C A U A	U • G A A	A U - A A C A
Bluehead	Tomtate	Sheepshead

4. Create a similarity matrix from the following alignment. Assume that any difference is counted equivalently (a 1-parameter model). (5 points)

Coney	G G C U A U - G C C
Scamp	G G C U G U U G C C
Bigeye	G G C U U C G G C C
Highhat	G C U G A A A G G C
Mako	G A G C U U G U U C

5. Convert this dendrogram into a phenogram: (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)

	A	B	C	D	E	F
A	---	---	---	---	---	---
B	0.2	---	---	---	---	---
C	0.4	0.4	---	---	---	---
D	0.5	0.5	0.5	---	---	---
E	0.6	0.6	0.6	0.3	---	---
F	0.8	0.8	0.8	0.7	0.8	---

