

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

Signed : \_\_\_\_\_

Date : \_\_\_\_\_

Name : \_\_\_\_\_

TOTAL = 45 points

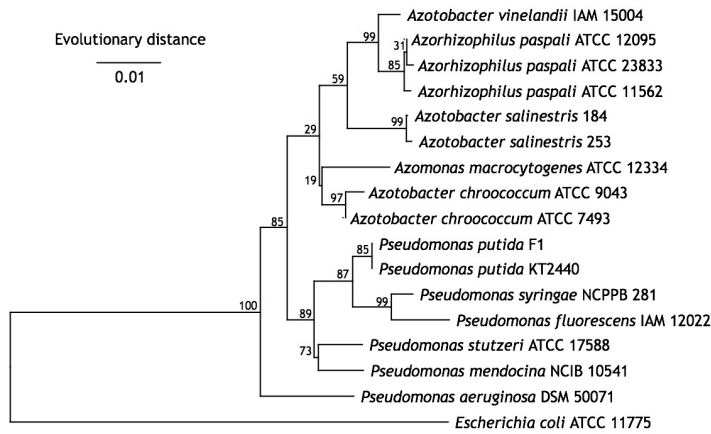
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1. What are the 3 primary evolutionary branches of life? (5 points)

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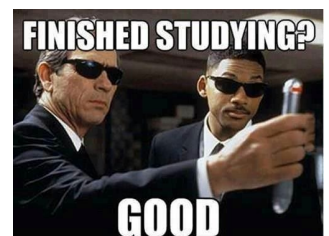
2. \_\_\_\_ An organism that gets its energy from light but needs organic compounds for growth (carbon) is a ... (1 point)
- A. Photoautotroph
  - B. Photoheterotroph
  - C. Chemoautotroph
  - D. Chemoheterotroph
  - E. All of the above
3. \_\_\_\_ Organisms evolve by ... (1 point)
- A. advancement
  - B. progression
  - C. diversification
  - D. regression
  - E. force of will
4. \_\_\_\_ Evolutionary relationships are usually best represented in the form of ... (1 point)
- A. Taxonomies
  - B. Field guides
  - C. Binomial nomenclature
  - D. Phylogenetic trees
  - E. Evolutionary ladders
5. \_\_\_\_ Which of the following is **NOT** required for a sequence to be a good molecular clock? (1 point)
- A. Member of a large gene family
  - B. Absence of horizontal transfer
  - C. Comprised of many independently-evolving bits
  - D. Conserved biological function
  - E. Appropriate amount of evolutionary variation
6. \_\_\_\_ Which of the following is **NOT** a treeing algorithm?. (1 point)
- A. Parsimony
  - B. Neighbor-joining
  - C. Maximum-likelihood
  - D. Phylogenetic covariation
  - E. Fitch-Margoliash
7. \_\_\_\_ Sometimes methods other than ssu-rRNA analysis is used because ... (1 point)
- A. ssu-rRNA can't reliably differentiate close relatives
  - B. other genes behave in a more clock-like fashion
  - C. protein sequences contain more phylogenetic info
  - D. ssu-rRNA sequences are so difficult to obtain and align
  - E. you can better identify organisms by direct examination
8. \_\_\_\_ The universal tree was rooted by phylogenetic analysis of ... (1 point)
- A. small subunit ribosomal RNA
  - B. precambrian fossils
  - C. entire genomes
  - D. morphological and phenotypic traits
  - E. pairs of anciently-duplicated genes
9. \_\_\_\_ Which of the following organelles originated by endosymbiosis of an early Eukarya and an alpha-proteobacterium? (1 point)
- A. Nucleolus
  - B. Chloroplasts
  - C. Golgi
  - D. Mitochondria
  - E. Centrioles
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10. Answer the following questions from this ssu-rRNA-based tree (1 point each)

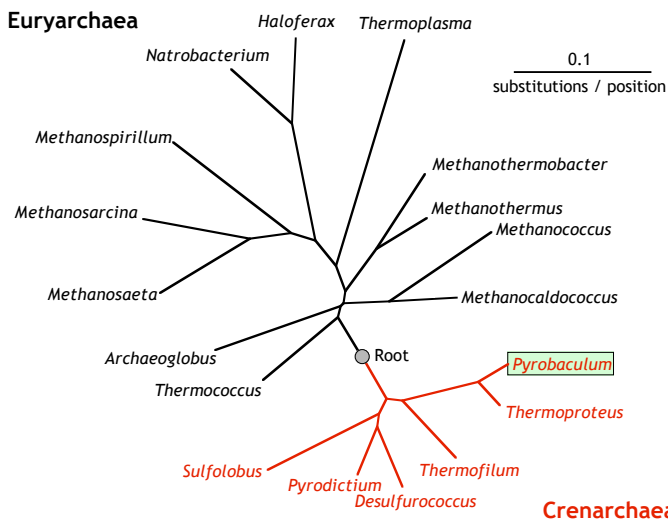


- Which sequence is most similar to that of *A. paspali* ATCC 11562? \_\_\_\_\_
- What is the outgroup in this tree? \_\_\_\_\_
- What is the approximate evolutionary distance between *P. putida* KT2440 and *P. aeruginosa* DSM 50071 ? \_\_\_\_\_
- What is the approximate evolutionary distance between *Pseudomonas putida* strains F1 and KT2440? \_\_\_\_\_
- Circle the last common ancestor of the species *Azorhizophilus paspali* and label it "E".
- Circle the last common ancestor of the genus *Pseudomonas* and label it "F".
- Circle the least reliable branch on the tree and label it "G".
- Which is the *most* primitive sequence (not considering the outgroup)? \_\_\_\_\_
- Which is the *least* primitive sequence (not considering the outgroup)? \_\_\_\_\_

11. On the tree in question above, what does the number "97" mean on the branch leading to the two strains of *Azotobacter chroococcum*? How was this number determined? (5 points)



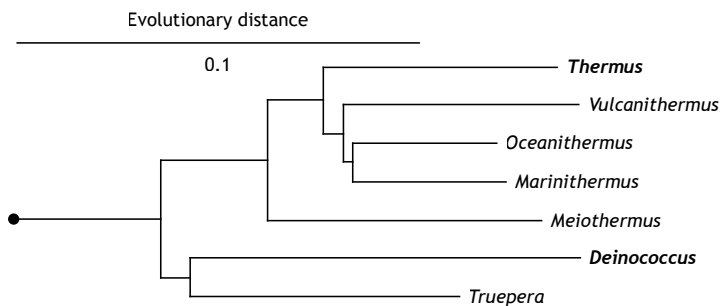
12. Answer the following questions from this ssu-rRNA-based tree (1 point each)



- Which sequence is most closely related to *Pyrobaculum*? \_\_\_\_\_
- All of these are Archaea. What might have been used to place the root? \_\_\_\_\_
- Which is the most primitive of the crenarchaeal sequences? \_\_\_\_\_
- Circle the last common ancestor of the methanogens (their names all start with “Methano-” and label it “D”).
- Circle the two major phylogenetic groups of Crenarchaea (1 point per circle).
- What is the approximate evolutionary distance between *Methanosaeta* and *Archaeoglobus*? \_\_\_\_\_
- Thermoplasma* in this tree is represented by the species *Thermoplasma acidophilum*. Draw on the tree what it might look like if a second species, *Thermoplasma volcanium*, was also included.

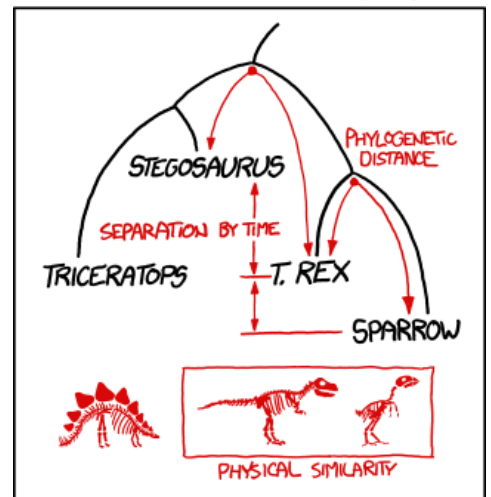
THOUGHT QUESTIONS

13. Below is a phylogenetic tree of Deinococci (based on ssu-rRNAs). How would this tree be different if, for some reason, the sequence data from *Thermus* was not very high quality and contained a lot of errors? (Describe or just draw it in.) (5 points)



14. Describe a *specific* example in which ssu-rRNA analysis might not be the best way to identify or distinguish organisms, and suggest a better approach. (5 points)

BY ANY REASONABLE DEFINITION, T. REX IS MORE CLOSELY RELATED TO SPARROWS THAN TO STEGOSAURUS.



BIRDS AREN'T DESCENDED FROM DINOSAURS,  
THEY ARE DINOSAURS.

WHICH MEANS THE FASTEST ANIMAL ALIVE TODAY IS  
A SMALL CARNIVOROUS DINOSAUR, *FALCO PEREGRINUS*.



IT PREYS MAINLY ON OTHER DINOSAURS, WHICH  
IT STRIKES AND KILLS IN MIDAIR WITH ITS CLAWS.

THIS IS A GOOD WORLD.

[xkcd.com/1211/](http://xkcd.com/1211/)

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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](mailto: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 : \_\_\_\_\_

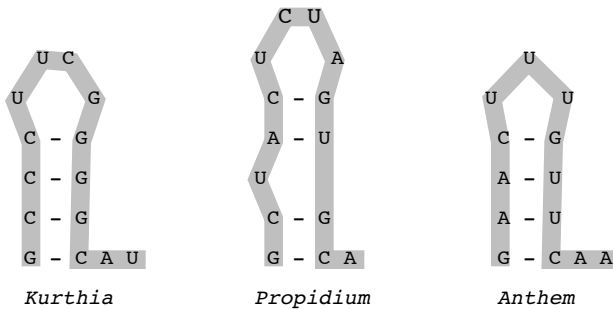
TOTAL = 55 points

1. Align the following sequences: (5 points)

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Erwinia      G A A U C C G U U C
Proteus      A A A U U C G U U U
Vibrio       A A U C C G U U
Klebsiella   C A A U A U C G U U A
    
```

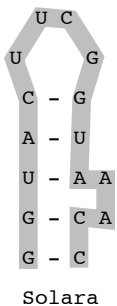
2. Align the following RNAs: (4 points)



3. Draw the secondary structures of the *Aster* and *Stella* RNAs in this alignment: (4 points)

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                ( ( ( ( ( - - - - ) ) ) - - ) )
Solara      G G U A C U - U C G G U A A A C C
Aster      G A C G U U A U U G A C G - - U C
Stella     G G C - - G U A G A - - G A A C C
    
```

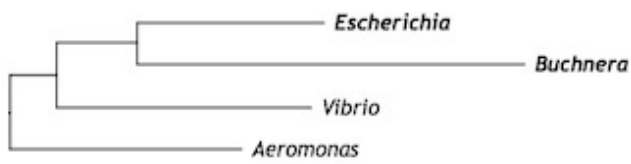


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4. Create a similarity matrix from the following alignment, using a 2-parameter model in which transversions count as a full difference (-1.0), and transitions count as half a difference (-0.5). (5 points)

Anaplasma G A U C G A U C G A  
Ehrlichia G A C C G A U C G A  
Wolbachia G G U C A A U C G A  
Holospora G U U C U A U C G A  
Geobacter G C A C C A U C G A

5. Convert this phenogram into a dendrogram. Please keep the tree to the same scale. (5 points)



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6. Use the following distance matrix to generate a tree (with branch lengths) using the neighbor-joining method. SHOW ALL OF YOUR WORK! (32 points)

	A	B	C	D	E	F
A	---	---	---	---	---	---
B	0.9	---	---	---	---	---
C	1.1	0.6	---	---	---	---
D	1.2	1.1	1.3	---	---	---
E	1.6	1.5	1.7	1.6	---	---
F	1.5	1.4	1.6	1.5	0.5	---

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(CONTINUE YOUR WORK HERE)