

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

Signed : _____

Date : _____

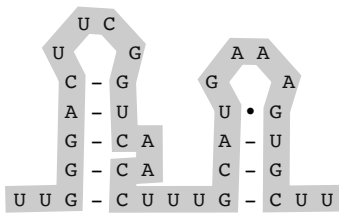
Name : _____

TOTAL = 60 out of 100 points

1. Below is an alignment of the regulatory RNA "fauX RNA" from a variety of organisms. These RNAs have been aligned on the basis of their structure. An example structure, that of *Examplobacillus testii*, is shown:

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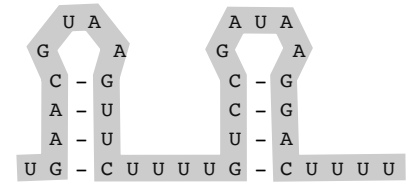
-- ( ( ( ( - - - - ) ) - - ) - - - - ( ( ( - - - - ) ) ) - - - -
E. testii          - U G G G A C U U C G G U C A A C C U U U - G C A U G A A A G U G C U U - -
C. testosteroni   - U G G A A C C U U G G U U - - C C U U U - G A U U G A G A A A U C U U U U
S. bikiniensis    U U G G U U - U U U - - A A A A C C U U U A G U U C G U A A G A A C U A U U
B. thetaiotaomicron - U G C U C - G C A A - G A - - G C U U U G G G G U U U C G A C C C U U - -
R. strabismus WTF
    
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fauX RNA from *E. testii*



fauX RNA from *S. bikiniensis*



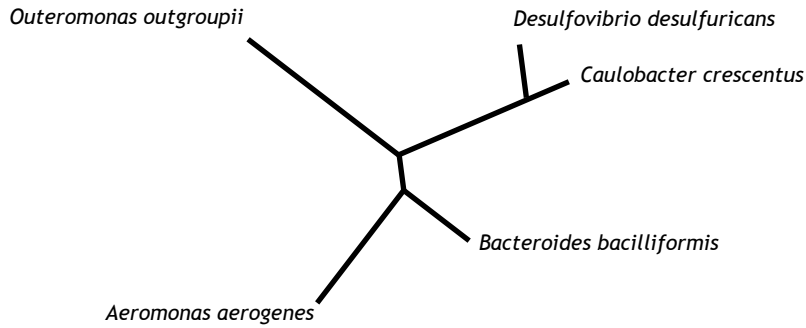
fauX RNA from *R. strabismus* str. WTF

- Draw the secondary structure of the *Streptomyces bikiniensis* fauX RNA. (8 points)
- Add the fauX RNA from *Ribonucleon strabismus* strain WTF to the alignment. (8 points)

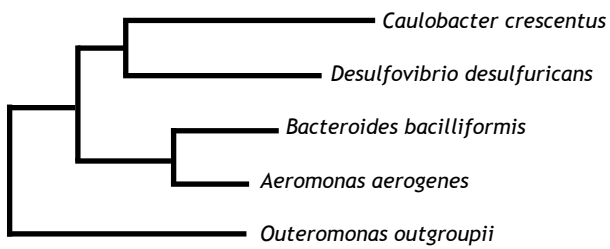
2. Create a similarity matrix from the following alignment using a 2-parameter model in which transversions count for a full difference, but transitions count as only 0.33 (1/3rd) of a difference. (6 points)

	Jane	Fred	Susan	Spot
Jane	A G U C G G C A U U	<u> X </u>	<u> X </u>	<u> X </u>
Fred	A G C C G A C A U U	<u> </u>	<u> X </u>	<u> X </u>
Susan	A G A C G A C G U C	<u> </u>	<u> </u>	<u> X </u>
Spot	A A A C G C C U U A	<u> </u>	<u> </u>	<u> X </u>

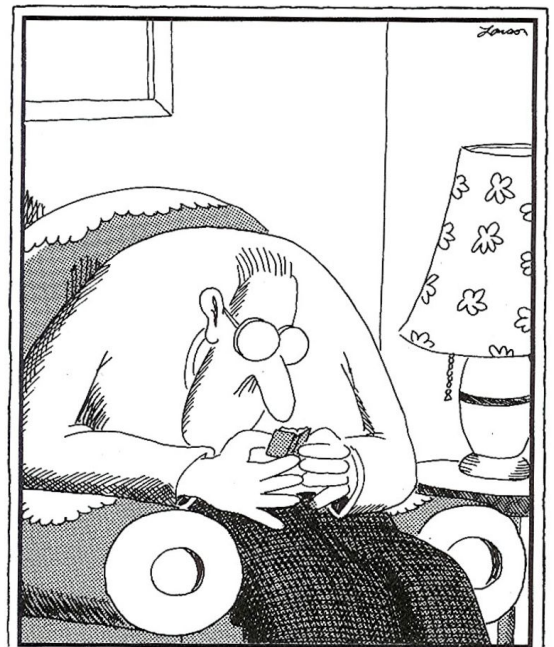
4. Convert this dendrogram into a phenogram. Please keep the tree to the same scale. Notice the bootstrap values, and assume that *O. outgroupii* is the outgroup. (10 points)



5. Rearrange (and redraw) the following dendrogram to put the organisms in alphabetical order on the tree. Please keep the tree to the same scale. (10 points)

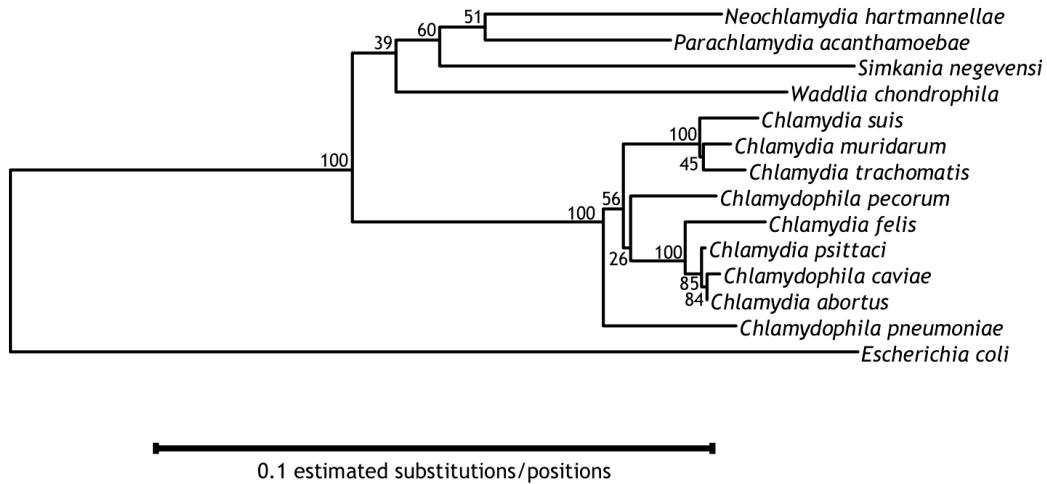


Gary Larson

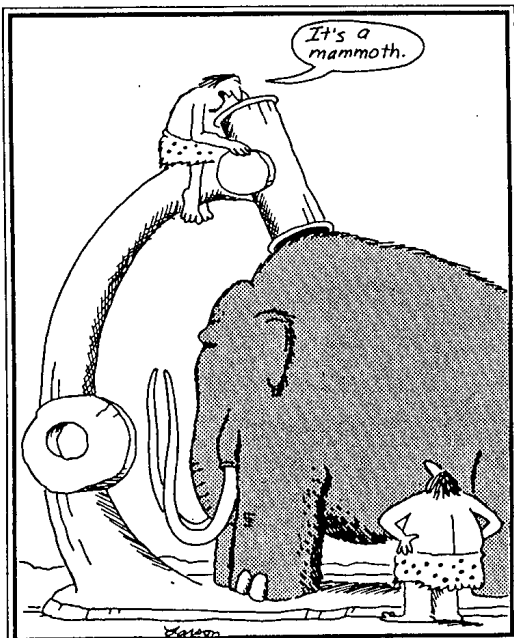


Roger crams for his microbiology midterm.

6. Answer the following questions from the tree below (1 point each except where indicated):



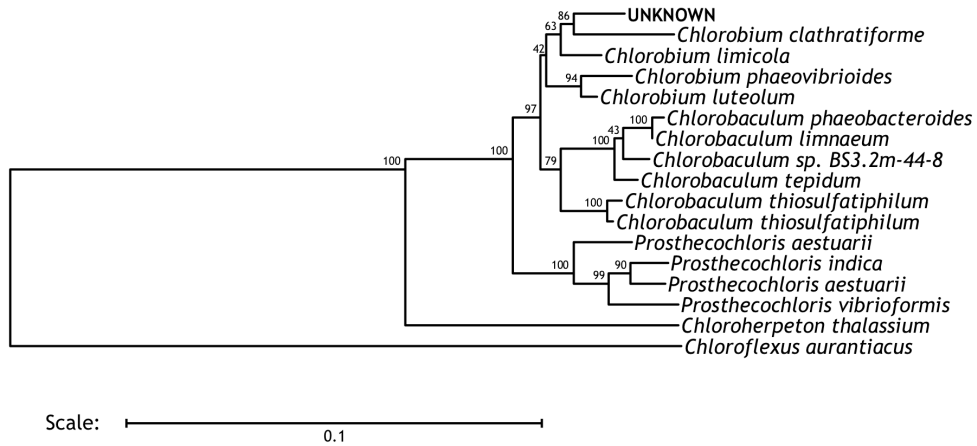
- Which of these sequences (other than perhaps the outgroup) is the most highly-derived? _____
- Which organism is most closely-related to *Parachlamydia acanthamoebae*? _____
- Which sequence is most similar to that of *Chlamydiae psittaci*? _____
- Which node is the least reliable in this tree? (circle and label "D")
- What is the approximate evolutionary distance between *C. suis* and *C. felis*? _____ (in estimated substitutions/position)
- What problem do you see with the genera *Chlamydia* and *Chlamydophila* in this tree? (2 points)



Early microscope

Gary Larson

6. You have cultivated an unknown organism from a pond sediment sample 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:



A. How specifically can you name this organism based on this tree? (1 point) _____

B. Make 5 *independent, specific, testable* predictions about the *properties* of your organism. (2 points each)

B1.

B2.

B3.

B4.

B5.

USE THIS PAGE FOR ANY ANSWERS YOU MAY HAVE BEEN LONG-WINDED ON:

