

# MB 451 : Microbial Diversity : Midterm Exam #1

Honor Pledge:

*I have neither given nor received unauthorized aid on this test.*

Sign \_\_\_\_\_ *KEY* \_\_\_\_\_

Date *2/7/06* \_\_\_\_\_

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

1. *Bacteria*
2. *Archaea*
3. *Eukarya*

2) (5 points) What is a *substitution model*?

*A substitution model is a mechanism (equation or algorithm) used to estimate evolutionary distance from a similarity matrix (or directly from aligned sequences).*

3) (5 points) What does the fact that all living organisms are much alike biochemically mean?

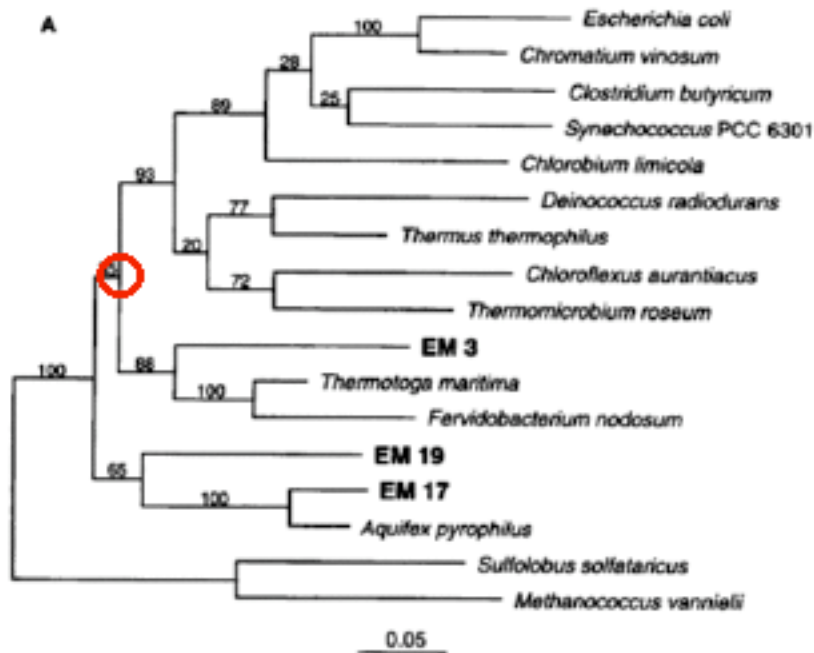
*It means that all living things have a common ancestry, and that the last common ancestor was a biochemically complex entity.*

4) (10 points) *Briefly describe* a method *other* than rRNA molecular phylogenetic analysis for determining phylogenetic relationships.

*e.g. Lipid profiling :*

*A culture growth under highly controlled conditions is extracted with organic solvents to collect the lipids, and these are analyzed by gas chromatography. The profile of resulting peaks is compared to a bank of known species.*

5) (2 points each, 10 points total) Answer the questions below about this tree:



a) What is the closest relative of *Thermus thermophilus*?

*Deinococcus radiodurans*

b) Which organism(s) is/are probably the outgroup?

*Sulfolobus solfataricus* & *Methanococcus vannielii*

c) What is the approximate evolutionary distance between *Deinococcus radiodurans* and *Thermomicrobium roseum*?

0.29 (anything in the vicinity of 0.3 or a little below is fine)

d) Circle the last common ancestor of *Thermotoga maritima* and *Chromatium vinosum*.

e) What are the numbers on the branches?

These are bootstrap values

7) (10 points) Why is the small subunit ribosomal RNA a good choice for molecular phylogenetic analysis?

*In most cases, the gene encoding the RNA in the small subunit of the ribosome (ssu rRNA) is the best choice because:*

- \* It is present in all cells*
- \* It has exactly the same function in all cells*
- \* It is comprized of 1500-2000 residues, large enough but not too large to be time-consuming to sequence.*
- \* It is made up of ca. 50 independently-evolving helices and ca. 500 base-pairs.*
- \* It is conserved enough in sequence & structure of be readily & accurately aligned.*
- \* It contains both rapidly & slowly evolving regions - the fast regions are useful for determining closely-related species, whereas the slow regions are useful for determining distant relationships*
- \* Horizontal transfer of rRNA genes apparently does not occur (also true for other genes in the central information processing pathways of the cell).*
- \* There is a large database (about 10,000) of aligned sequences available*

8) (10 points) Align the sequences below.

Sequence A      UGGGAUCCGGAUGUUA

Sequence B      GGAUCCAUGCUA

Sequence C      CGGGACCCAUACUA

*Sequence A      U G G G A U C C G G A U G U U A*

*Sequence B      - G G G A U C C - - A U G C U A*

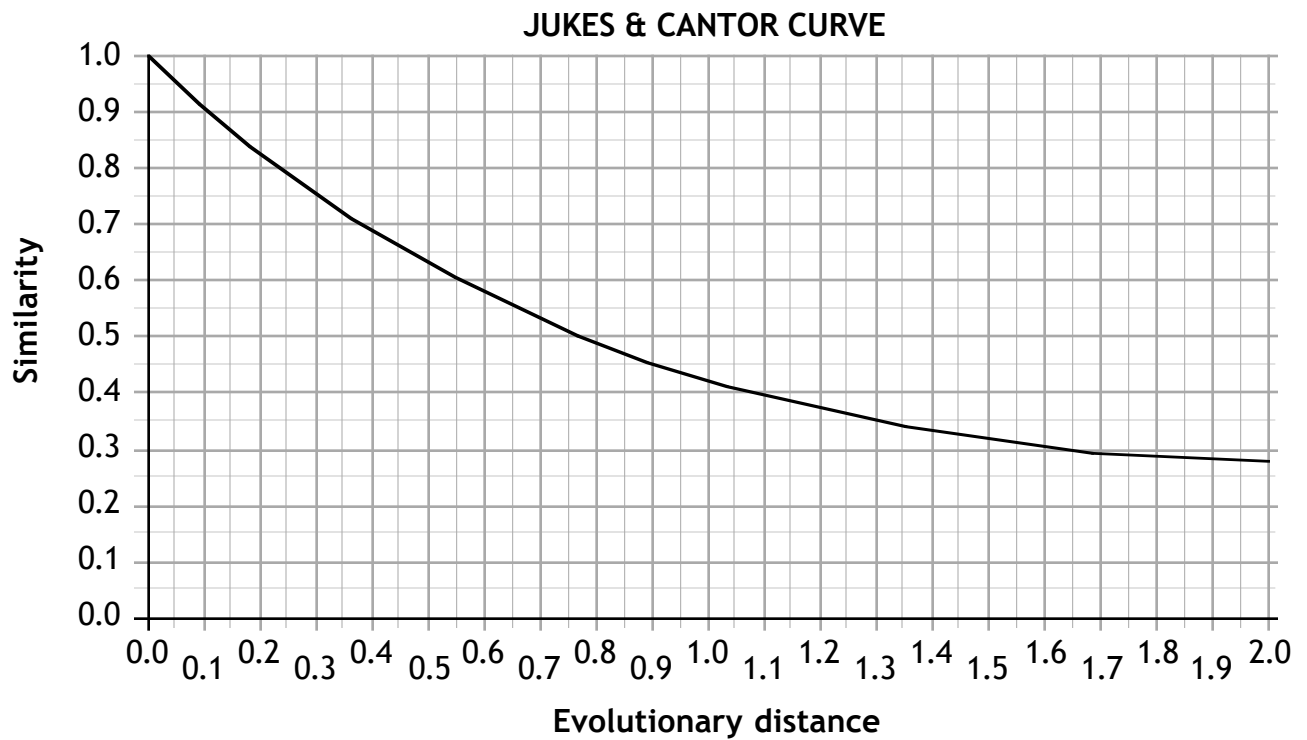
*Sequence C      C G G G A C C C - - A U A C U A*

9) (10 points) Create a similarity matrix for the alignment below.

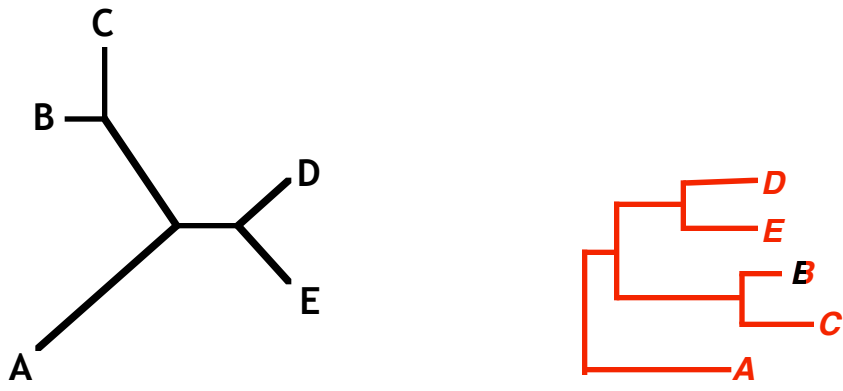
			A	B	C	D	E
Sequence A	GAUCGAUCGA	A	X	X	X	X	X
Sequence B	GAUGGAUCGA	B	0.9	X	X	X	X
Sequence C	GGUCGGUCGA	C	0.8	0.7	X	X	X
Sequence D	GGUCGGUCGA	D	0.8	0.7	1.0	X	X
Sequence E	GACCGAUCGA	E	0.9	0.8	0.7	0.7	X

10) (10 points) Convert the similarity matrix to a distance matrix using the Jukes & Cantor curve.

Similarity matrix					Distance matrix				
	A	B	C	D		A	B	C	D
A	X	X	X	X	A	X	X	X	X
B	0.95	X	X	X	B	<b>0.05</b>	X	X	X
C	0.75	0.80	X	X	C	<b>0.30</b>	<b>0.25</b>	X	X
D	0.50	0.60	0.45	X	D	<b>0.75</b>	<b>0.55</b>	<b>0.90</b>	X

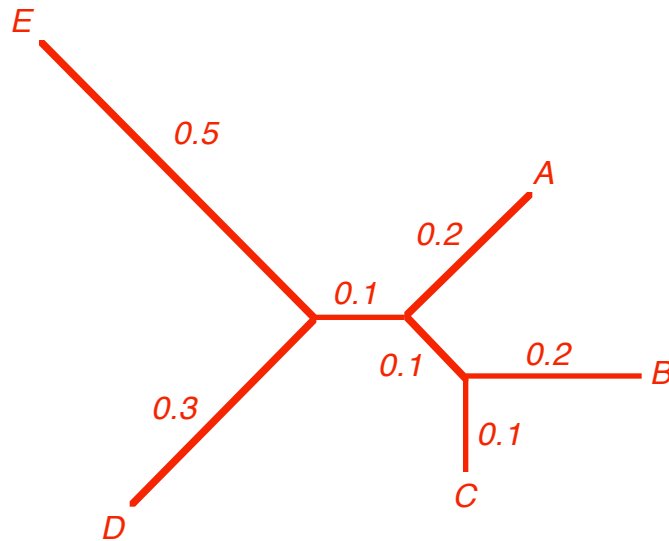
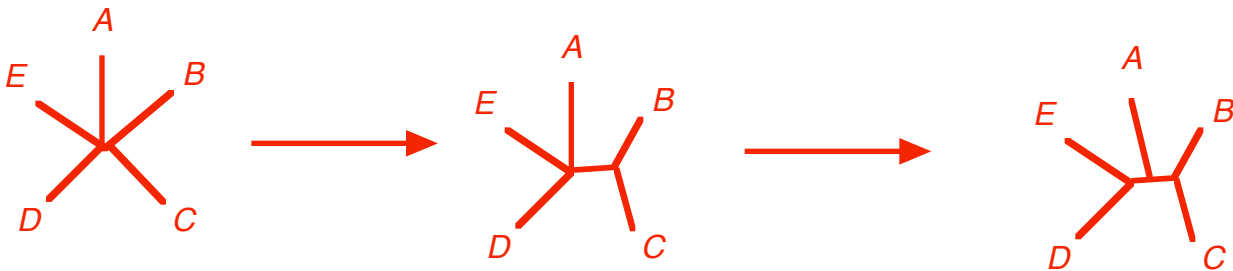


11) (10 points) Redraw the dendrogram below, to the same approximate scale, as a phylogram.



11) (10 points) Use the distance matrix below to create a phylogenetic tree (the structure of the tree only, you are not required to sort out the lengths of the branches) using the Neighbor-joining method. Show your work.

	A	B	C	D	E		A	B/C	D	E
A	X	X	X	X	X	A	x	x	x	x
B	0.5	X	X	X	X	B/C	0.45	x	x	x
C	0.4	0.3	X	X	X	D	0.6	0.65	x	x
D	0.6	0.7	0.6	X	X	E	0.8	0.85	0.8	x
E	0.8	0.9	0.8	0.8	X					



12. (5 points) Now fill in the length of each branch in the tree above.