

Midterm Exam VTMB 421
Winter/Spring 2000
120 Total points

1. To determine the number of chromosomes of a newly discovered microorganism you are guided by information on the genome size and the number of chromosomes present in a closely related microbe whose genome of 11 MB is distributed among 7 chromosomes. What range of switch frequencies will you use in an attempt to resolve, and thereby identify, the chromosomes contained in this new microorganism by pulse-field electrophoresis. (10 points).
2. The 34 MB malaria genome is divided among 11 chromosomes. Provide an estimate of the number of 150 mm plates containing 40,000 genomic clones each that will be needed to fully screen a genomic library made from the 3.5 MB chromosome of malaria where the average insert size of the library is 2,345 nt (10 points).
3. In the differential display method of Liang and Pardee cellular mRNAs are divided into pools based on what principle. (5 points)
4. Describe the key steps in chromosome walking. (10 points).
5. What is the frequency of cutting for restriction endonuclease Not-1 which recognizes the DNA sequence GCGGCCGC. (5 points)
6. List the common enzyme(s) used in molecular biology that have the following activities. (5 points each)
 - a. nucleotide kinase
 - b. DNA ligase
 - c. DNA exonuclease
 - d. DNA-dependent DNA polymerase
7. Define the essential features of telomeres. (5 points).
8. Describe what is meant by dynamic programming. (5 points)

9. Describe the purpose of a distance matrix in sequence comparisons. Give an example of a distance matrix (10 points)
9. What important enzyme was introduced into the construction of cDNA libraries by Okayama and Berg in 1982? Define the activity of this enzyme. (5 points)
10. Describe what is involved in the annotation of genomic sequence. (5 points)
11. Compare an organism's genome versus its "expressed-genome". (5 points).
12. By what method/process do you assign statistical significance to a phylogenetic tree? Briefly, explain how this method works. (10 points)

Bonus credit for this question. (3pts.)
 What does this method assume?

13. List and briefly describe "The Five Steps of Tree Making". (10 points)
15. Of the two alignments presented below which is the best alignment? What could be the evolutionary cause for the difference between the two sequences? If you were preparing these sequences for phylogenetic analysis what would you do with the regions containing the dashes? (5 points)

Alignment #1

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-GALVIFYWGV TMTVLGGAFYILITAVGLWAKVLI SRDECTMHKRPDE-
-GALVIFYWGV LIAVLGGAFYI--M-----HK----R-----PNE-
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Alignment #2

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-GALVIFYWGV TMTVLGGAFYILITAVGLWAKVLI SRDECTMHKRPDE-
-GALVIFYWGV LIAVLGGAFYI-----MHKRPNE-
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