Homework Assignment #4
Due: 10/27/2004 in class

1. (7 points) What is phylogeny?

2. (6 points) Textbook, question 4.1.

3. (10 points) Textbook, question 4.8.

4. (7 points) In a few sentences discuss pros and cons for using UPGMA as a method for phylogeny.

5. (5 points) How many rooted evolutionary trees are there for 6 (six) species?

6. (6 points) What is the purpose of an outgroup?

7. (5 points) What is a “maximum parsimony” tree?

8. (6 points) What are informative and uninformative sites? What is the rule of thumb to extract them from the multiple sequence alignment?

9. (7 points) Textbook, question 5.1.

10. (15 points) Draw a maximum parsimony tree for the 5 sequences from question 5.1. Hint: One way to solve this problem is to use the algorithm provided in lecture notes.

11. (6 points) What is a consensus tree in maximum parsimony?

12. (10 points) Explain use of bootstrapping in phylogeny? Make 3 bootstrapping iterations and estimate confidence of the tree from question 10. Use only informative positions.

13 (10 points) Textbook, question 5.4.