CISC 436/636 Computational Biology and Bioinformatics
Fall 2016
Homework 3

Due date: November 15, 2016

1. Construct the UPGMA tree for the following distance matrix. Show the partial tree at each step, mark edges with their length.

	A	B	C	D
A	0	3	6	5
B	3	0	7	6
C	6	7	0	3
D	5	6	3	0

2. For the same input of problem 1, now reconstruct the tree using the neighbor-joining algorithm. Show the partial tree at each step, mark edges with their length.

3. Use the conventional parsimony method to calculate the most parsimonious cost of the tree ((((I, II), (III, IV)), V), VI) given for the following multiple alignment of 6 species. Mark the internal nodes with the hypothetical sequence that achieves the most parsimonious cost.

```
Sequence   1 2 3 4
    I      T C A A
    II     G C A T
    III    T T T T
    IV     G A T A
    V      G A A C
    VI     A T A G
```

4. For the following tree, calculate the probability $P(A, C| T, t1, t2)$ in the maximum likelihood method as discussed in lecture 15 (slide 8).