BNFO 236 second exam review sheet (Spring 2017)

1. Newick representation of trees
2. Tree data structure used in the UPGMA Python program
3. UPGMA algorithm: running it through an input by hand
4. UPGMA variants:
    a. Update distance matrix to be the shortest distance between two clusters
    b. Update distance matrix to be the largest distance between two clusters
    c. Update distance matrix to be the median distance between two clusters
5. Comparison of phylogenies with bipartitions
6. Calculation of Jukes-Cantor distances
7. Calculation of evolutionary distances for whole genome sequences
8. Neighbor joining (NJ) algorithm
    a. Running it by hand
    b. Difference between NJ and UPGMA