Assignment 3 (Phylogenetic analysis)

Construct a phylogenetic relationship for the given nucleotide sequences (sequence.txt).

- Write a script to generate a distance matrix (.csv file) for the sequences present in the data file. Name the distance matrix file as 'Ndistance.txt'.
  For example,
  seq1 = 'ATGAATGCAA'
  seq2 = 'ATGCATGCTA'
  Distance (seq1, seq2) = Mismatches/total length = 2/10 = 0.2.

- Write a script that uses 'Ndistance.txt' and generate the phylogenetic relationship between the organisms using the UPGMA method.
- What do you infer from the above analysis?