Homework 2
BINF 730 Biological Sequence Analysis
September 27, 2021
Due October 11, 2021

1. In class we discussed how to develop phylogenetic trees from a matrix of distance data. For example, assume we have sequences A, B, C, D. We can put the distances between them into a distance matrix.

	A	B	C	D
A	0			
B		0		
C			0	
D				0

Please give two ways by which someone might determine the distances that will fill this distance matrix. For example, if A=ACTGGGCT and B=CGTGAGCT, how would you determine the distance between sequences A and B?

2. Write code to implement, UPGMA, WPGMA, and neighbor joining algorithms. You code should produce output from which you will draw a phylogenetic tree for some sample data. Please used the example from the lecture and the primate data from the lecture. Also pick you own set of short sequences.