

Introduction to Bioinformatics
Problem Set 7: Metagenome Sequence Analysis Part 2

1. Draw a phylogenetic tree of sequences evolving by your own hand. Define a parent sequence composed of random DNA 40 nucleotides long. Then define child1, INSERTing a mutation at a random location within the DNA. Define child2 in the same way. Then define child1a and child1b by mutating child1 and define child2a and child2b by mutating child2. To do this, define a function called MUTATE that will take any sequence and put a mutation at a random location. Align all the parent, children and grandchildren and from the alignment, figure out a phylogenetic tree. Check your result using TREE-OF.