Project 4 Report

Andrew Kan 305125178

Bugs: n/a

Big-O: all of my functions satisfy the big-O requirements

Pseudocode:

**Trie’s find():**

Iterate through key

If exactMatchOnly is false and the mismatch might be the last char in the key, insert all of their values

If its a mismatch for this char and this isn’t the first char, insert all the non-mismatches for its children

If the values match, keep moving through the key

If the key position iterator is at the end of the key, insert all of the values of the node

Return the vector

**GenomeMatcher’s findGenomeWithThisDNA():**

Using the Trie find function on minSearchLength of fragment, store the positions and genomes in a vector

Iterate through this vector

The bound is the size of the fragment and the remaining chars left in the genome sequence

If you can extract the genome sequence within the bound onto a compareString

Compare compareString and fragment up to mininumLength

If it works up to min length,

Continue comparing up to the bound

You found a match, and compare the match with an unordered map for matches of the same name

Insert the matches from the map into the matches vector

Return if you found a match or not