Maggie Huang

105116127

Project 4 Report

1. I do not know of any bugs in my program.

2. I believe my methods follow all big O requirements.

3. Pseudocode:

vector Trie::find(key, exactMatch)

{

if exactMatch is true:

return findExactlyMatch(root\_node, key)

else:

if first char of key does not exist in root\_node.children:

return an empty vector

else:

return findSnipMatch(root\_node, key,exactMatch)

}

vector Trie::findExactlyMatch(node, key)

{

for char in key:

if char is in node.children:

set node to node.children[char]

else:

return

return node.values

}

vector Trie::findSnipMatch(node, key, exactMatch)

{

if exactMatch is true:

return findExactlyMatch(node, key)

define an vector v1

if key.length is 1

for child in node.children:

if child is leaf:

increment vector v1 by child.values

return v1

for char in key:

for child in node.children:

define a vector v2

if child is null:

skip rest of code in this loop

else:

if char equals child:

v2 = findSnipMatch(child,key\_substring,false)

else:

v2 = findSnipMatch(child,key\_substring,true)

increment v1 by v2

return v1

}

bool GenomeMatcher::findGenomesWithThisDNA(fragment, minimumLength, exactMatchOnly, matches\_vector)

{

find match position and genome from Trie, and save to a vector of pair<genome,position>

for each pair<genome,position>

if matches with at least minimumLength:

if no previous match exists for this genome:

add new match<genome,length,position> to matches\_vector

else:

if the current match has longer length:

replace existed match with this match

else

keep the original match and ignore this match

else:

goto next genome

if matches\_vector is empty:

return false

else:

return true

}