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Project 4 Report

1. No known bugs

2. Satisfies all Big-O Requirements

3.

find()

{  
 create a result vector of ValueType

Create an iterator through the Trie’s root node’s children vector

While(we have not reached end of children vector)

{  
 if(the current node’s label is equal to the first letter of key)

{  
 set result equal to findHelper with parameters: all of key after

the first character, exactMatchOnly bool, pointer to current node

Break the while loop

}

Increment iterator

}

Return result vector

}

findHelper(string key, bool exactMatchOnly, Node\* root)

{  
 create a result vector of ValueType

Copy the key string into a keyCopy string

If(keyCopy’s size equals zero)

{

Insert the root node’s values vector into result vector

Return result

}

Create iterator through root node’s children vector

For(every node in children vector)

{  
 if(Node’s label equals first character of key)

{  
 set a temp vector of ValueTypes equal to result of calling findHelper with

parameters: all of keyCopy after first character, exactMatchOnly, pointer to

current node

Insert temp vector into result vector;

}

Else if(exactMatchOnly is false)

{  
 set a temp vector of ValueTypes equal to result of calling findHelper with

parameters: all of keyCopy after first character, not(exactMatchOnly), pointer to current node

Insert temp vector into result vector;

}

}

Return result vector

}

findGenomesWithThisDNA()

{

If(fragment size is smaller than minimumLength or minimumLength is smaller than

minimumSearchLength)

return false

create string newFragment of beginning of fragment to minimumSearchLength

create string restOfFrag of minimumSearchLength to end of fragment

if(exactMatchOnly is false)  
{  
 create a vector of all the genome snips that potentially match fragment, allowing

for snips

for(each genome in vector)

{  
 extract the rest of that genome’s sequence into string restOfSeq

Check if the sequence matches the rest of fragment with no mismatches

If(the matching sequence meets minimumLength)

{  
 check if a longer sequence of same genome already exists

If new sequence is longer, replace old sequence

If not, add a new DNAMatch of this sequence to matches vector

}

}  
}

Create a vector of all genome snips that potentially match fragment with no snips

For(each genome in vector)

{

Extract the rest of that genome’s sequence into string restOfSeq

Check if the sequence matches the rest of fragment with no mismatches

If(the matching sequence meets minimumLength)

{  
 Check if a longer sequence of the same genome already exists

If new sequence is longer, replace old sequence

If not, add a new DNAMatch of this sequence to matches vector

}

If(exactMatchOnly is false)

{  
 create a usedmismatch bool

While(restOfFrag matches restOfSeq or a mismatch is found and usedmismatch is

false)

{

If(a mismatch is found)

Set usedmismatch to true

}

If(the matching sequence meets minimumLength)

{

Check if a longer sequence from same genome already exists

If new sequence is longer, replace old sequence

If not, add a new DNAMatch of this sequence to matches vector

}

}

}

If(matches vector is empty)

Return false

Return true

}