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Report

1. I do not believe that any of my classes have any bugs on them. Running the tester and my own tests on each function and class, I had no issues even with running the edge case tests.
2. I believe that all my methods that I had implemented had followed along with the specified delay time necessary. This is assuming that constant values are disregarded and we are looking for the highest power.
3. Find()

Set current node to root node

Get first character as index place

Repeatedly,

If child pointer is not a nullptr,

Access it and recurse

Copy vector values

End if

Break

Return vector values

End function

findHelper() // Recursive function

Set tolerance to 1

If exactMatchOnly is true

Set tolerance to 0

End if

If difference is greater than tolerance

Return empty vector

End if

If key size is zero

Return vector that is held here

End if

Repeatedly

If child pointer is not a nullptr

If child pointer’s character is not current key

Recurse with increased difference and substring of next character to end

Else

Recurse with no difference and substring of next character to end

End if

End if

Break

Return vector

End function

FindGenomesWithThisDNA()

If fragment size is less than minSearchLength OR minimumLength is less than minSearchLength

Return false

End if

Set substring of fragment to be its first character to length of minsearchlength

Find the values of it using constraints of exactmatch only

Sort these values so checking redundancy is efficient

If vector returned is empty

Return false

Else

Iterate through our values found

If exactMatchOnly is true

Iterate through genomes with that value

Check how many times you can iterate before running out of characters to get OR a string is not equal to another

Break at any time one of these happens

Incrementing your distance

Break

Else

Iterate through genomes with that value

If you run out of characters to get, break

Else if you find difference in strings

Increment difference

Increment distance

If difference is greater than one

Break

Break

If our running length is less than minimum searched, continue

If the length is less than back of dnaVector, skip

If the length is greater than or equal to back of dnaVector, pop back of dna

Allocate dna values and push value to vector

Break

End if

Return whether or not dnaVector was changed

End function