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PA05

Project Report

In this project I found the longest sequence of the gene sequence and returned its length. I created an adjacency matrix of size [n x n] and marked the respective [row][column] indices with 1's and 0's depending on whether they represented a sequence of elements present in all the given sequences. Based off the traversal lengths obtained from jumping from a [row][col] marked as 1 to its respective row and finding if the sequence terminated I was able to determine the longest sequence. I used a depth first search algorithm to assist me in this process.

The time complexity of the code came out to be O(n^2 \* m) where m is the number of sequences and n is the number of columns.