**Practical 5**

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Class – A4 (B3)

Roll no. – 45

Aim: Implement a dynamic algorithm for Longest Common Subsequence (LCS) to find the

length and LCS for DNA sequences.

Problem Statement:

DNA sequences can be viewed as strings of A, C, G, and T characters, which

represent nucleotides. Finding the similarities between two DNA sequences are an

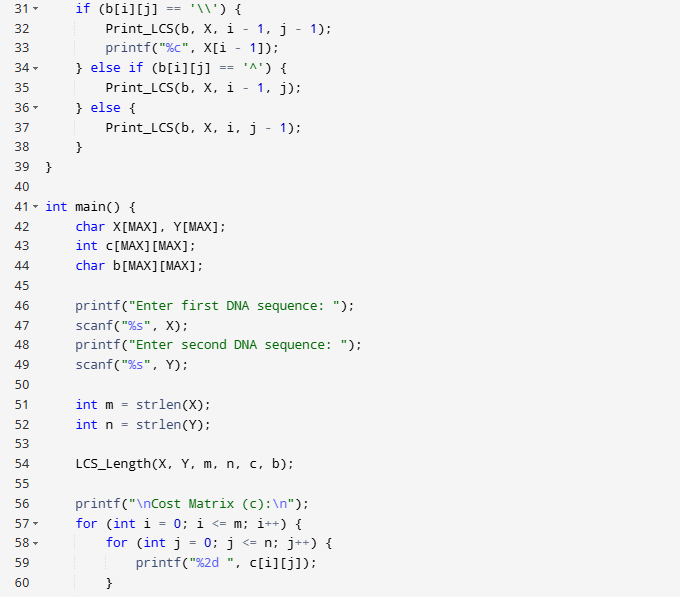
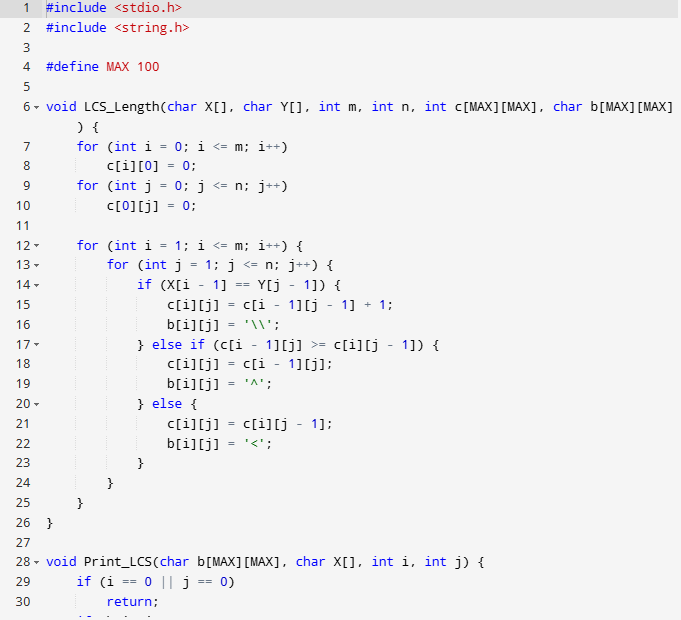
important computation performed in bioinformatics.

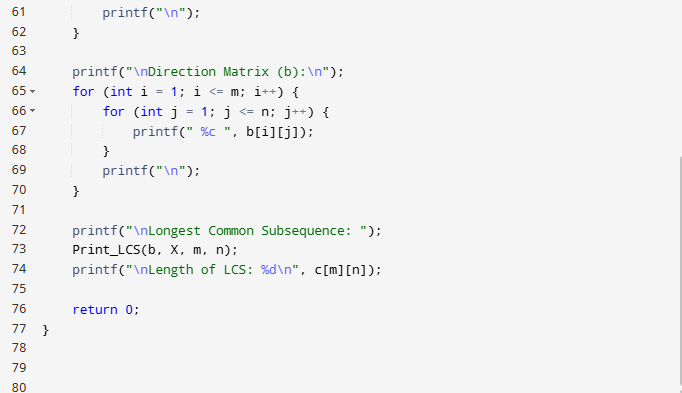
TASK 1: Find the similarity between the given X and Y sequence.

X=AGCCCTAAGGGCTACCTAGCTT

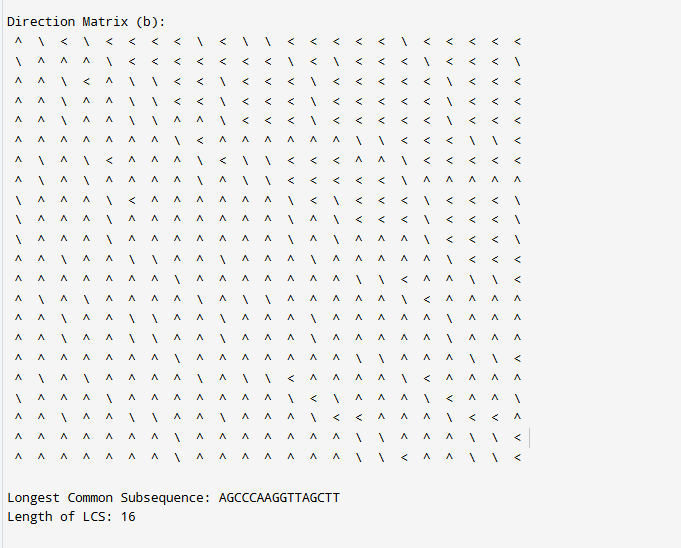
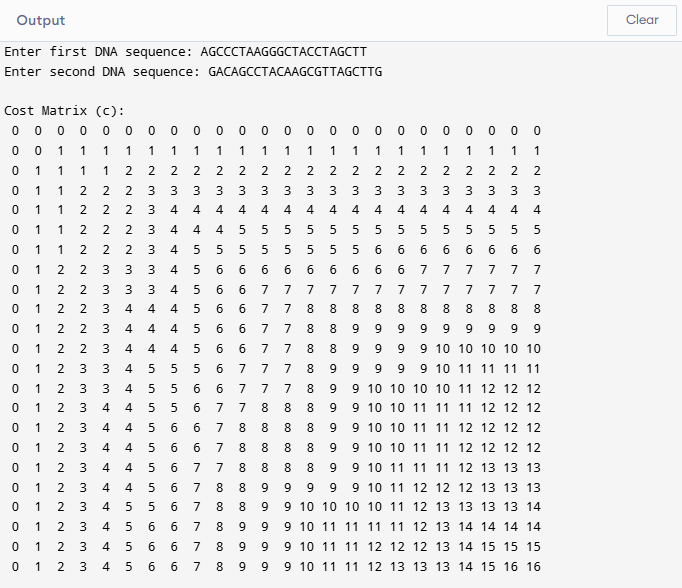
Y= GACAGCCTACAAGCGTTAGCTTG

Code -





Output –



TASK-2: Find the longest repeating subsequence (LRS). Consider it as a variation of the

longest common subsequence (LCS) problem.

Let the given string be S. You need to find the LRS within S. To use the LCS framework, you

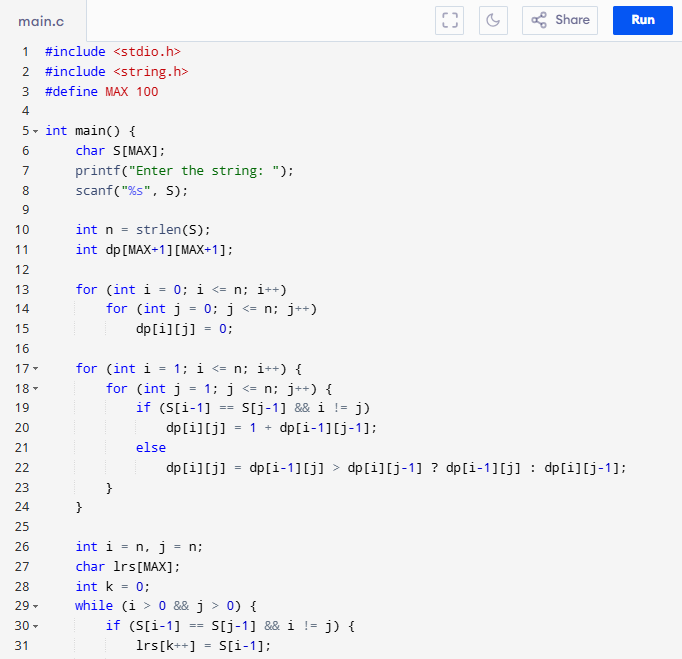
effectively compare S with itself. So, consider string1 = S and string2 = S.

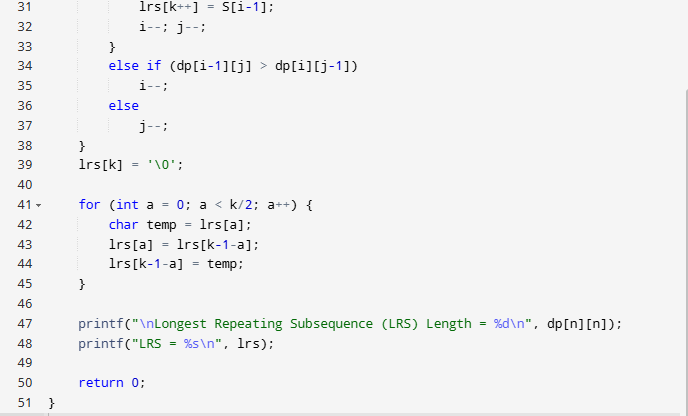
Example:

AABCBDC

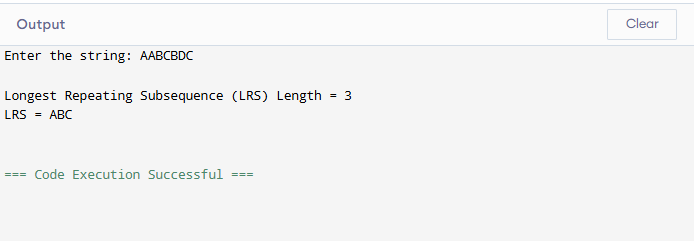
LRS= ABC or ABD

Code –

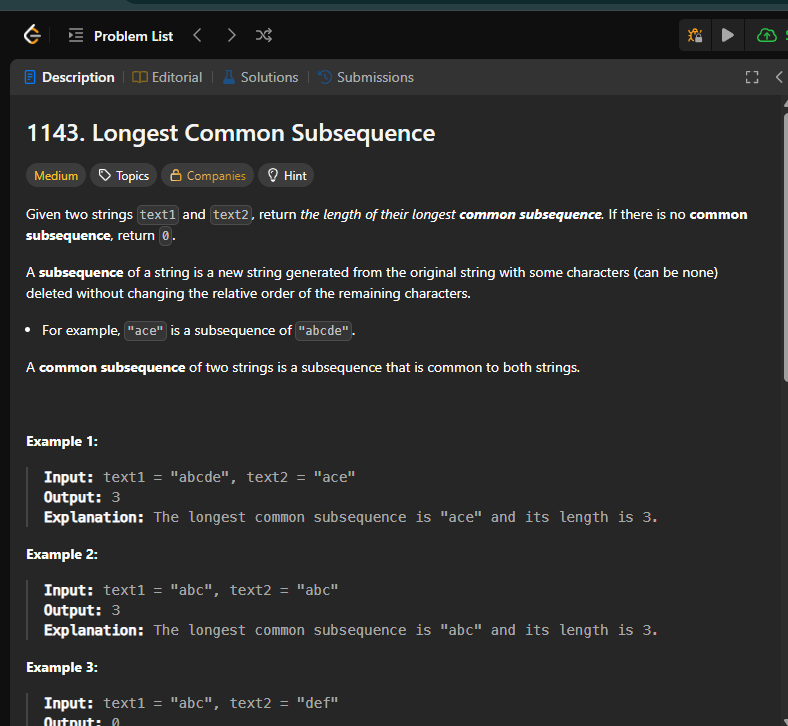


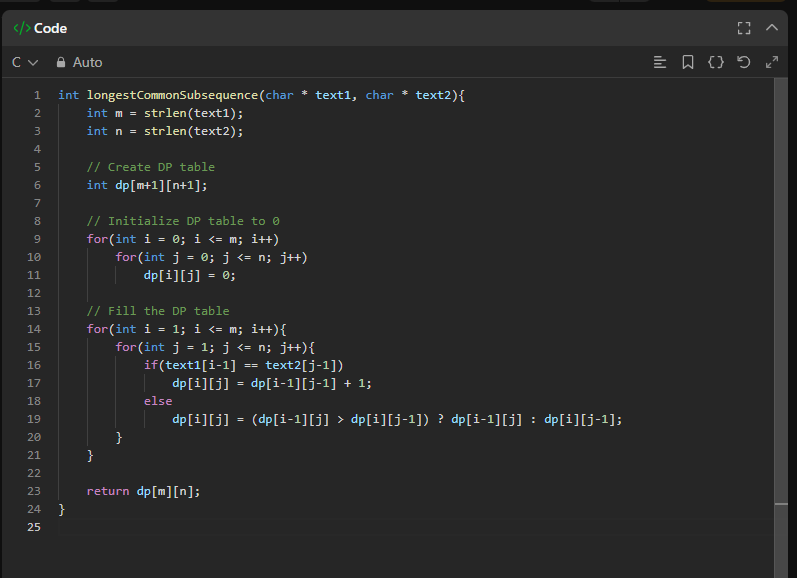


Output –



Leetcode Submission –





Output-

