DAA Lab Pract5

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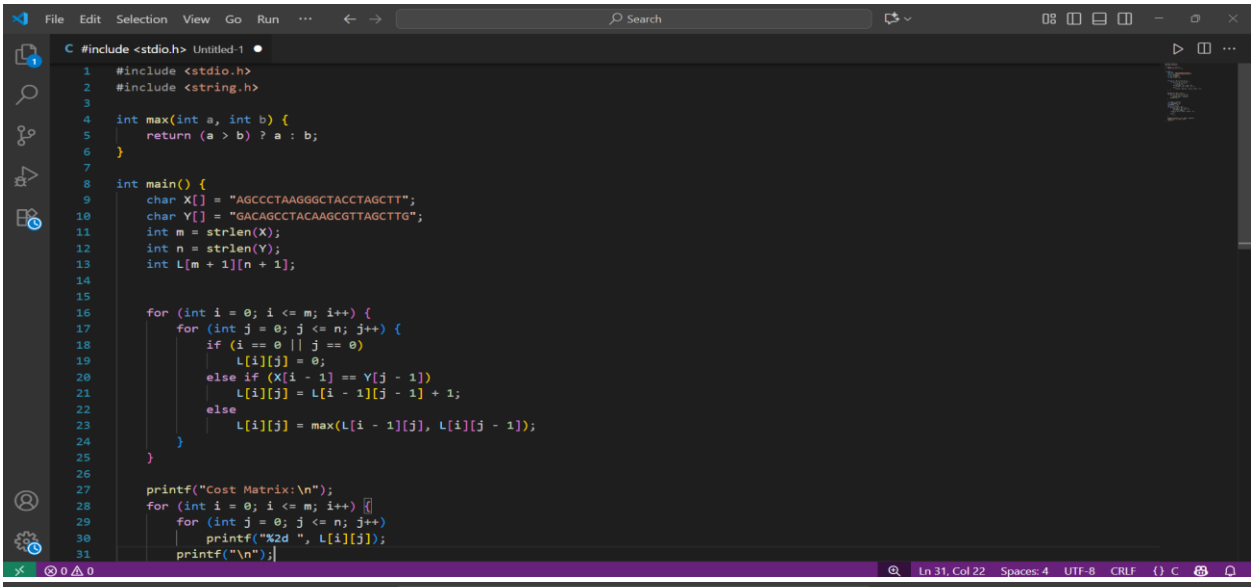
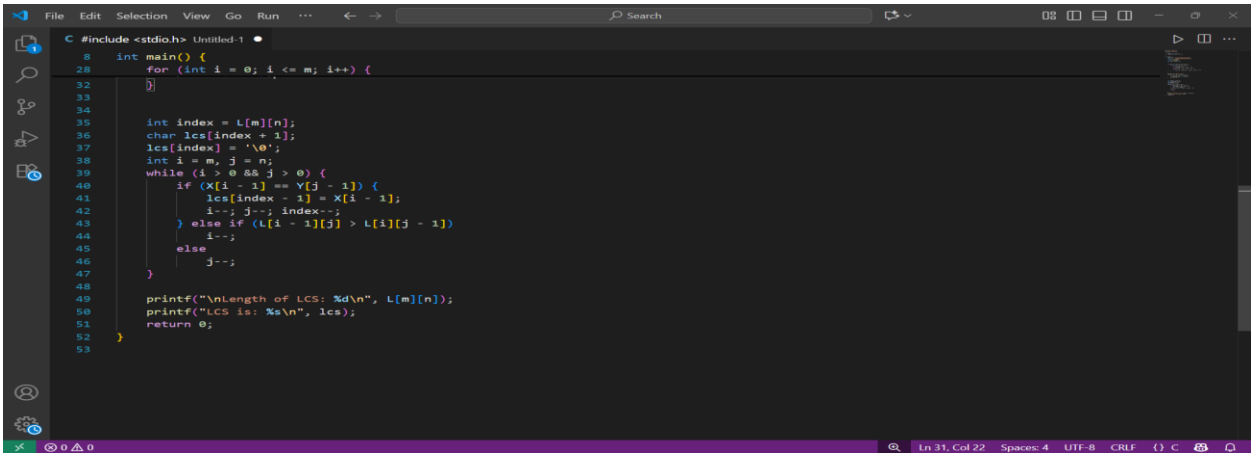
Aim: Implement Longest Common Subsequence (LCS) algorithm to find the length and LCS for DNA sequences.

Task 1 :

Code:

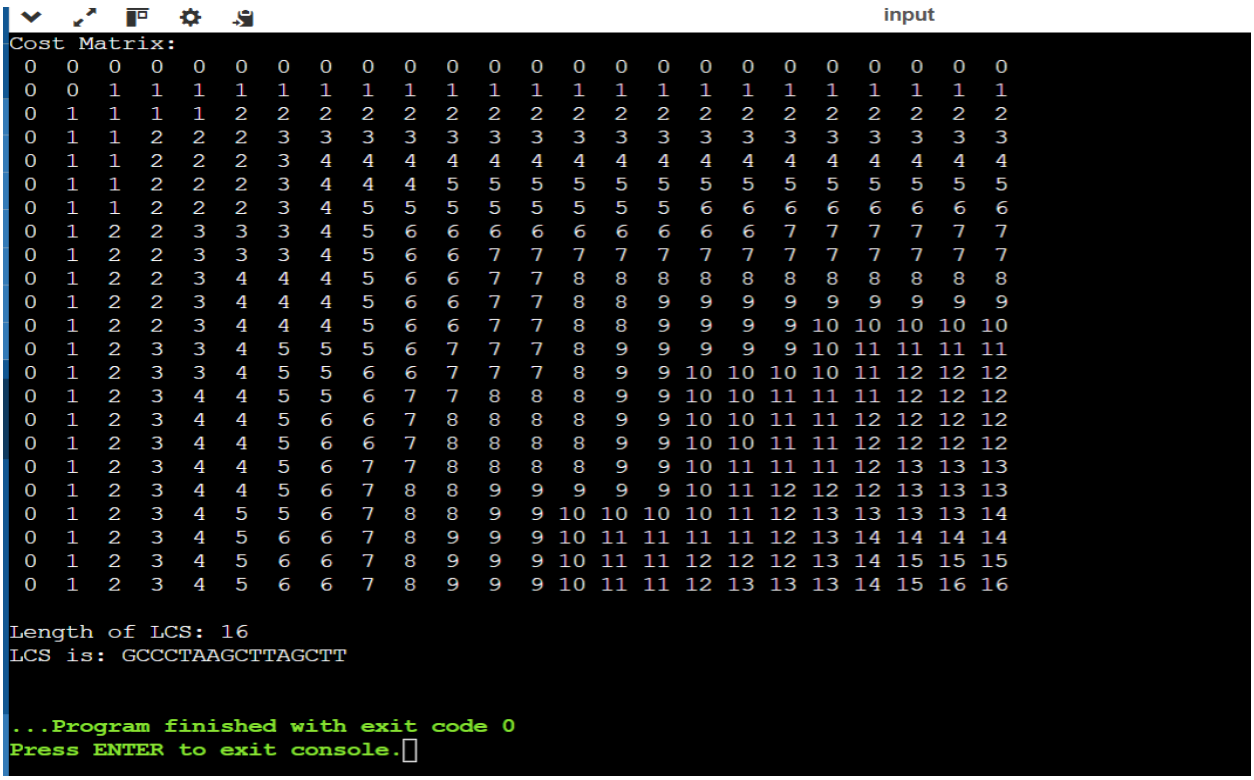


```c
#include <stdio.h>
#include <string.h>

int max(int a, int b) {
    return (a > b) ? a : b;
}

int main() {
    char X[] = "AGCCCTAAGGGCTACCTAGCTT";
    char Y[] = "GACAGCCTACAAGCGTTAGCTTG";
    int m = strlen(X);
    int n = strlen(Y);
    int L[m + 1][n + 1];


    for (int i = 0; i <= m; i++) {
        for (int j = 0; j <= n; j++) {
            if (i == 0 || j == 0)
                L[i][j] = 0;
            else if (X[i - 1] == Y[j - 1])
                L[i][j] = L[i - 1][j - 1] + 1;
            else
                L[i][j] = max(L[i - 1][j], L[i][j - 1]);
        }
    }

    printf("Cost Matrix:\n");
    for (int i = 0; i <= m; i++) {
        for (int j = 0; j <= n; j++)
            printf("%2d ", L[i][j]);
        printf("\n");
```



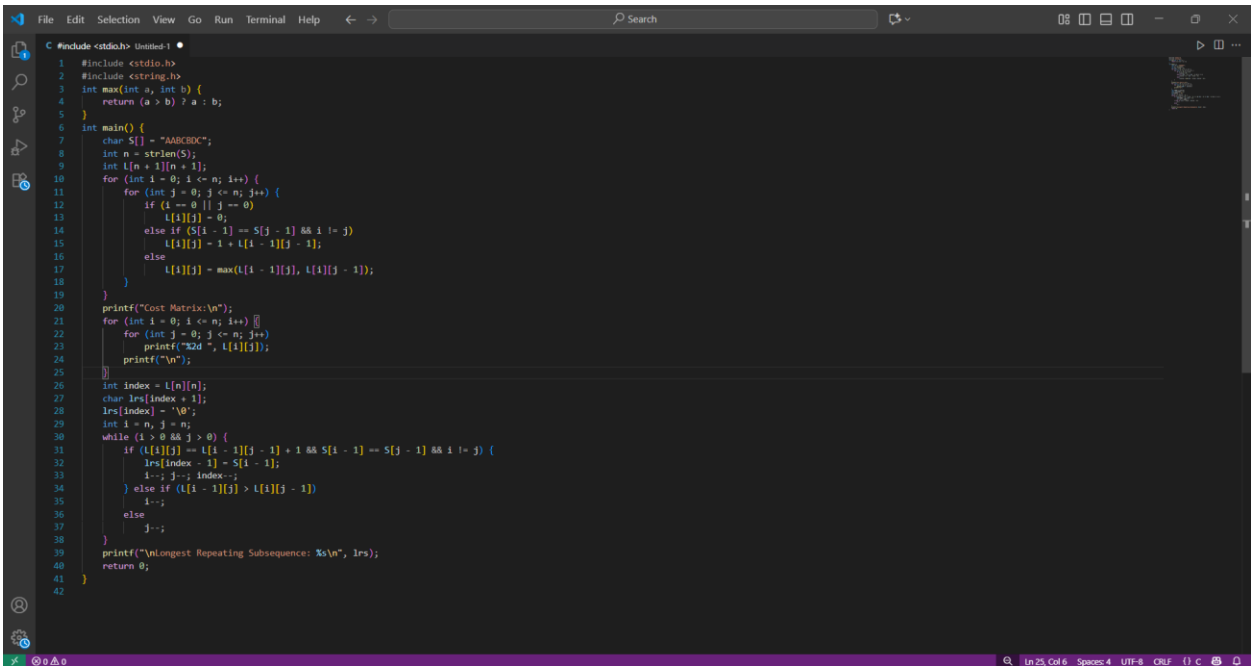
```c
int main() {
    for (int i = 0; i <= m; i++) {
    }


    int index = L[m][n];
    char lcs[index + 1];
    lcs[index] = '\0';
    int i = m, j = n;
    while (i > 0 && j > 0) {
        if (X[i - 1] == Y[j - 1]) {
            lcs[index - 1] = X[i - 1];
            i--; j--; index--;
        } else if (L[i - 1][j] > L[i][j - 1])
            i--;
        else
            j--;
    }

    printf("\nLength of LCS: %d\n", L[m][n]);
    printf("LCS is: %s\n", lcs);
    return 0;
}
```

Output:

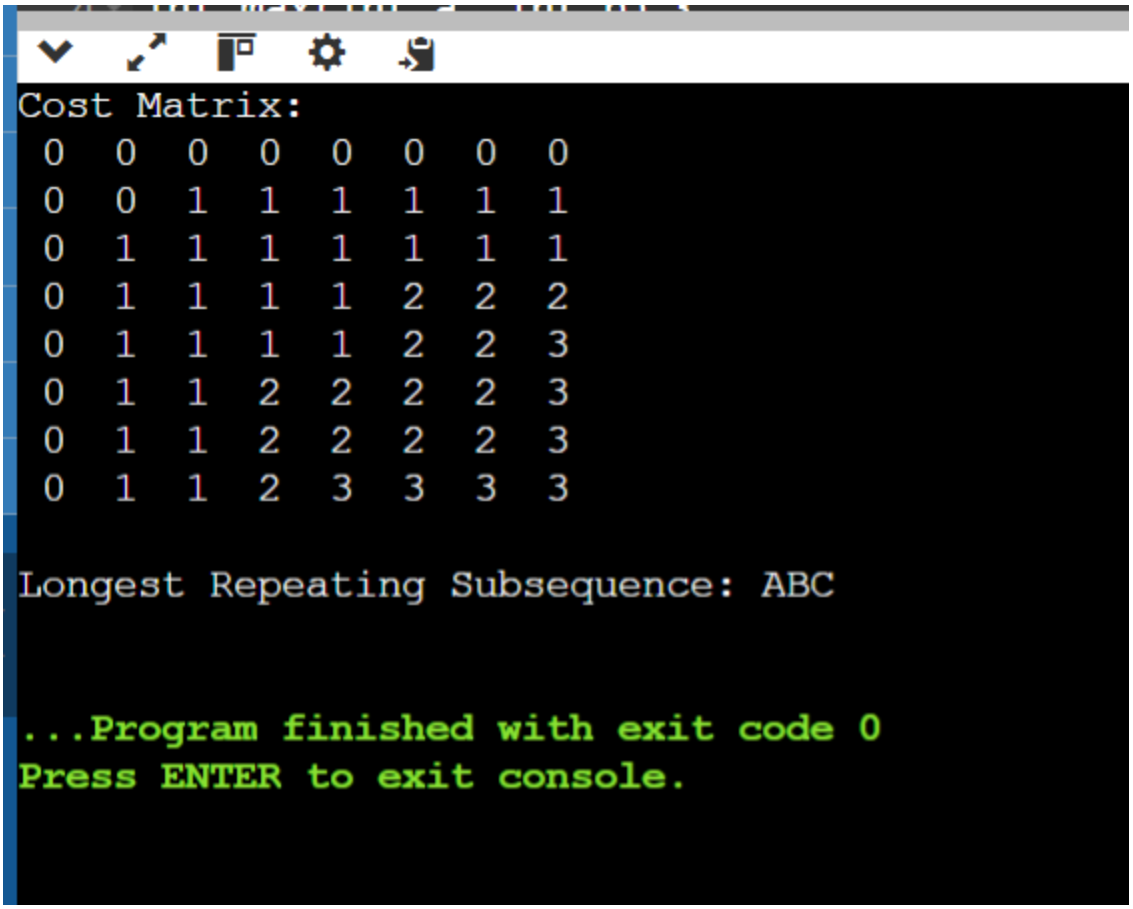


Task : 2

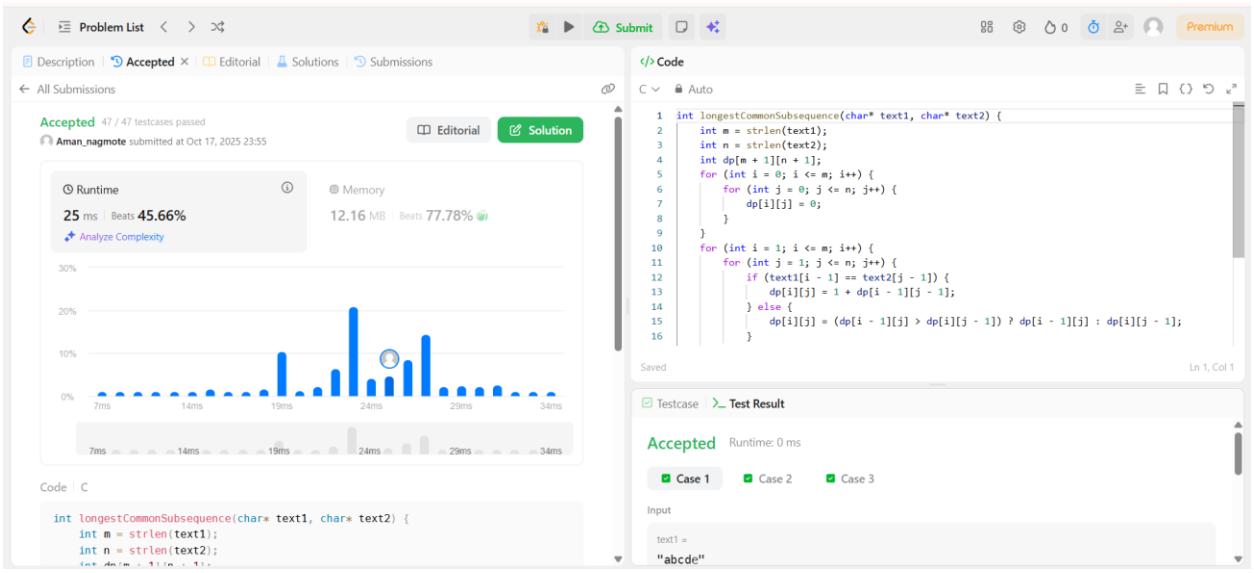
Code :



Code :



Leet code submission:



My git hub link for pract 5 repo : https://github.com/24tiwaria2-code/DAA-