PRACTICAL NO: 05

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Date: 07/10/25

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.

[Note that a subsequence might not include consecutive elements of the original sequence.]

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

X=AGCCCTAAGGGCTACCTAGCTT

Y= GACAGCCTACAAGCGTTAGCTTG

```
Code:
#include <stdio.h>
#include <string.h>
#define MAX 100
void printMatrix(int dp[][MAX], int m, int n, char *X, char *Y)
{
printf("Cost matrix (LCS lengths):\n ");
for (int j = 0; j < n; j++)
printf("%c ", Y[j]);
printf("\n");
for (int i = 0; i \le m; i++) {
if (i == 0)
printf(" ");
else
printf("%c ", X[i-1]);
for (int j = 0; j <= n; j++) {
printf("%d ", dp[i][j]);
printf("\n");
}
```

```
void findLCS(char *X, char *Y, int m, int n, int dp[][MAX], char
*lcs) {
int index = dp[m][n];
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 (dp[i-1][j] > dp[i][j-1]) {
i--;
} else {
j--;
}
}
int main() {
char X[] = "AGCCCTAAGGGCTACCTAGCTT";
char Y[] = "GACAGCCTACAAGCGTTAGCTTG";
```

```
int m = strlen(X);
int n = strlen(Y);
int dp[MAX][MAX];
for (int i = 0; i <= m; i++)
for (int j = 0; j <= n; j++)
dp[i][j] = 0;
for (int i = 1; i \le m; i++) {
for (int j = 1; j \le n; j++) {
if (X[i-1] == Y[j-1])
dp[i][j] = dp[i - 1][j - 1] + 1;
else
dp[i][j] = (dp[i-1][j] > dp[i][j-1]) ? dp[i-1][j] : dp[i][j-1];
}
}
printMatrix(dp, m, n, X, Y);
printf("\nLength of Longest Common Subsequence: %d\n",
dp[m][n]);
char lcs[MAX];
findLCS(X, Y, m, n, dp, lcs);
printf("Longest Common subsequence: %s\n", lcs);
return 0;
```

```
}
A
```

Output:

```
Cost matrix (LCS lengths):
 GACAGCCTACAAGCGTTAGCTTG
7 8 9 9 9 10 11 11 12 12 12 13 14 15 15 15
T 0 1 2 3 4 5 6 6 7 8 9 9 9 10 11 11 12 13 13 13 14 15 16 16
Length of Longest Common Subsequence: 16
Longest Common subsequence: GCCCTAAGCTTAGCTT
```

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:
```

```
} else if (dp[i - 1][j] >= dp[i][j - 1]) {
       i--;
     } else {
       j--;
     }
  }
  printf("\nLongest Repeating Subsequence: %s\n", Irs);
  printf("Length of LRS: %d\n", dp[n][n]);
}
void LRS(char str[]) {
  int n = strlen(str);
  int dp[MAX][MAX];
  for (int i = 0; i <= n; i++)
     for (int j = 0; j \le n; j++)
       dp[i][j] = 0;
  for (int i = 1; i \le n; i++) {
     for (int j = 1; j \le n; j++) {
       if (str[i-1] == str[j-1] \&\& i != j)
          dp[i][j] = dp[i - 1][j - 1] + 1;
       else
          dp[i][j] = (dp[i-1][j] > dp[i][j-1]) ? dp[i-1][j] : dp[i][j]
- 1];
```

```
}
}
printLRS(str, n, dp);
}
int main() {
  char str[] = "AABCBDC";
  LRS(str);
  return 0;
}
```

Output:

```
Longest Repeating Subsequence: ABC

Length of LRS: 3

=== Code Execution Successful ===
```

Leet Code: https://leetcode.com/problems/longest-common-subsequence/



