

Practical 5

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Class-A-4

Batch-B3

Aim-

(i) 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

Output: Cost matrix with all costs and direction, final cost of LCS and the LCS.

Length of LCS=16

```
#include <iostream>
```

```
#include <string>
```

```
using namespace std;
```

```
#include <iostream>
```

```
#include <string>
```

```
using namespace std;
```

```
string printLCS(string x, string y) {
```

```
    int m = x.length();
```

```
    int n = y.length();
```

```
    int dp[100][100] = {0};
```

```
    // Fill dp table
```

```
    for (int i = 1; i <= m; i++) {
```

```
        for (int j = 1; j <= n; j++) {
```

```

        if (x[i - 1] == y[j - 1]) {
            dp[i][j] = dp[i - 1][j - 1] + 1;
        } else {
            dp[i][j] = max(dp[i - 1][j], dp[i][j - 1]);
        }
    }
}

// Reconstruct LCS from dp table
int i = m, j = n;
string lcsStr = "";

while (i > 0 && j > 0) {
    if (x[i - 1] == y[j - 1]) {
        lcsStr = x[i - 1] + lcsStr;
        i--;
        j--;
    } else if (dp[i - 1][j] > dp[i][j - 1]) {
        i--;
    } else {
        j--;
    }
}

return lcsStr;
}

int main() {
    string x = "AGCCCTAAGGGCTACCTAGCTT";
    string y = "GACAGCCTACAAGCGTTAGCTTG";

```

```

string lcsStr = printLCS(x, y);

cout << "The length of the LCS is " << lcsStr.length() << endl;

cout << "The LCS is: " << lcsStr << endl;

return 0;
}

```

Output

```

The length of the LCS is 16
The LCS is: GCCCTAAGCTTAGCTT

```

Leetcode Problem-

Accepted 47 / 47 testcases passed
 Huzail Nazim Baig submitted at Sep 25, 2025 15:20

Runtime: 23 ms | Beats: 81.41%
 Memory: 27.20 MB | Beats: 80.10%

Code | C++

```

class Solution {
public:
    int longestCommonSubsequence(string text1, string text2) {

```

```

1 class Solution {
2 public:
3     int longestCommonSubsequence(string text1, string text2) {
4
5
6
7
8
9     int m = text1.length();
10    int n = text2.length();
11
12    vector<vector<int>> dp(m + 1, vector<int>(n + 1, 0));
13
14
15    for (int i = 1; i <= m; i++) {
16        for (int j = 1; j <= n; j++) {
17            if (text1[i - 1] == text2[j - 1]) {
18                dp[i][j] = dp[i - 1][j - 1] + 1;
19            } else {
20                dp[i][j] = max(dp[i - 1][j], dp[i][j - 1]);
21            }
22        }
23    }
24    return dp[m][n];
25
26
27
28
29
30 }

```

LRS Part 2

Code-

```

#include <iostream>

#include <vector>

#include <string>

using namespace std;

int main() {

    string s1, s2;

    cin >> s1 >> s2;

    int n = s1.length();

    vector<vector<int>> dp(n + 1, vector<int>(n + 1, 0));

    vector<vector<char>> result(n + 1, vector<char>(n + 1, ' '));

    for (int i = 1; i <= n; i++) {

        for (int j = 1; j <= n; j++) {

            if (s1[i-1] == s2[j-1] && i != j) {

                dp[i][j] = 1 + dp[i-1][j-1];

                result[i][j] = s1[i-1];

            } else {

                dp[i][j] = max(dp[i-1][j], dp[i][j-1]);

                result[i][j] = ' ';

            }

        }

    }

    cout << "DP Matrix:" << endl;

    for (int i = 0; i <= n; i++) {

        for (int j = 0; j <= n; j++) {

            cout << dp[i][j] << " ";


```

```

    }

    cout << endl;
}

cout << "Repeated Characters Matrix:" << endl;
for (int i = 0; i <= n; i++) {
    for (int j = 0; j <= n; j++) {
        cout << result[i][j] << " ";
    }
    cout << endl;
}

cout << "LRS Length: " << dp[n][n] << endl;

return 0;
}

```

Output-

```

AABEBCDD
AABEBCDD
DP Matrix:
0 0 0 0 0 0 0 0 0
0 0 1 1 1 1 1 1 1
0 1 1 1 1 1 1 1 1
0 1 1 1 1 2 2 2 2
0 1 1 1 1 2 2 2 2
0 1 1 2 2 2 2 2 2
0 1 1 2 2 2 2 2 2
0 1 1 2 2 2 2 2 3
0 1 1 2 2 2 2 3 3
Repeated Characters Matrix:
      A
     A
    A
   B
  B
 D
D
LRS Length: 3

```