Practical 6

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Subject: DAA Lab

Problem Statement:

DNA sequences can be viewed as a string of A, C, G, and T characters, which represent nucleotides. Finding the similarities between two DNA sequences is an important computation performed in bioinformatics. Find the similarity between the given X and Y sequence.

X=AGCCCTAAGGGCTACCTAGCTT

Y=GACAGCCTACAAGCGTTAGCTTG

Code:

```
#include <stdio.h>
#include <stdlib.h>
struct node {
   int val;
   char dir;
};
void print_lcs(int n, char a[], struct node C[][n], int i, int j) {
   if(i==0 || j==0) {
      return;
   }
   if(C[i][j].dir=='D') {
      print_lcs(n,a,C,i-1,j-1);
   }
}
```

```
printf("%c",a[i]);
    }
  else {
    if(C[i][j].dir=='U'){
       print lcs(n,a,C,i-1,j);
     }
    else {
       print_lcs(n,a,C,i,j-1);
     }
  }
}
int main(){
  char a[]="AGCCCTAAGGGCTACCTAGCTT";
  char b[]="GACAGCCTACAAGCGTTAGCTTG";
  printf("First string: %s\n",a);
  printf("Second string: %s\n",b);
  struct node C[22][23];
  for(int i=0; i<22; i++){
    for(int j=0;j<23;j++){
       if(a[i]==0 || b[j]==0){
         C[i][j].val=0;
         C[i][j].dir='H';
```

```
if(a[i]!=b[j])\{\\
        C[i][j].val = C[i-1][j].val > C[i][j-1].val ? \ C[i-1][j].val : C[i][j-1].val;
        if(C[i-1][j].val \ge C[i][j-1].val){
            C[i][j].dir='U';
        }else{
            C[i][j].dir='S';
if(a[i]==b[j]){}
C[i][j].val=C[i-1][j-1].val+1;
C[i][j].dir='D';
print_lcs(23,a,C,21,22);
```

Output: