## Practical No: 1

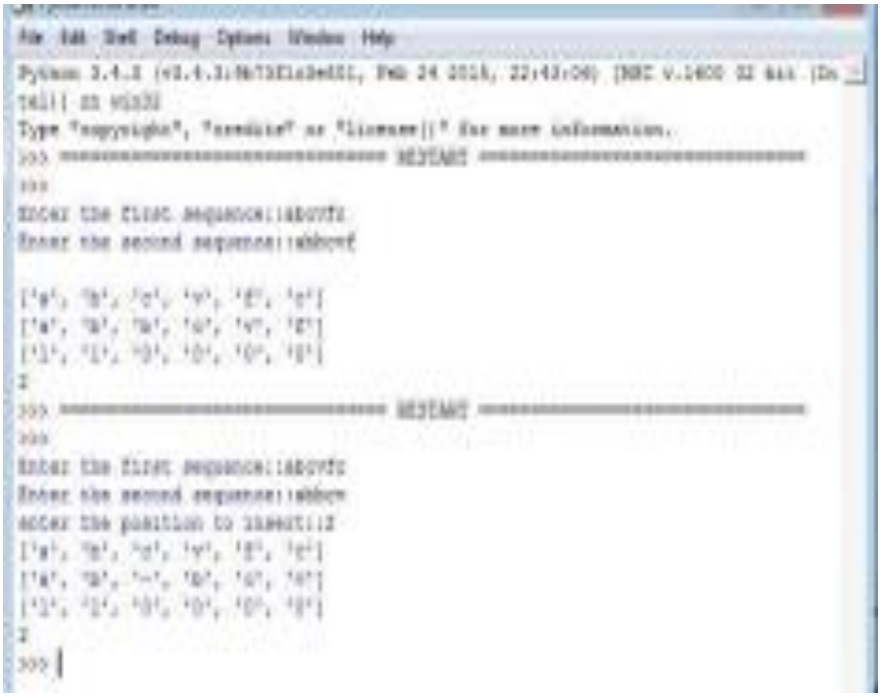
Aim: Write a Python/Java code to perform pairwise alignment. Take 2 sequences from user and calculate the score.

Code:

```
se1=input("Enter the first sequence::")
se2=input("Enter the second sequence::")
seq1=list(se1)
seq2=list(se2)
score=[]

def Pairwise_alignment(a,b):
    gap(a,b)
    print(a)
    print(b)
    value=0
    length=len(a)
    for i in range(0,length):
        if(a[i]==b[i]):
            score.append('1')
            value=value+1
        else:
            score.append('0')
    print(score)
    print(value)

def gap(a,b):
    if(len(a)==len(b)):
        print()
    else:
```

```
        k=int(input("enter the position to insert::"))
        if (len(a)<len(b)):
            a.insert(k,'-')
        else:
            b.insert(k,'-')
    return(a,b)

Pairwise_alignment(seq1,seq2)
```

Output:



Practical No: 2

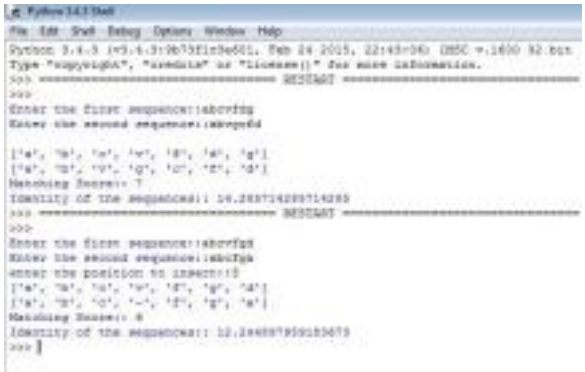
Aim: Write a Python/Java code to find the identity value of a given sequences. Take the sequence fromuser.

Code:

```
se1=input("Enter the first sequence::")
se2=input("Enter the second sequence::")

seq1=list(se1)
seq2=list(se2)
def find_identity(a,b):
    gap(a,b)
    print(a)
    print(b)
    score=0
    length=len(a)
    total_elements=len(a)*len(b)
    for i in range(0,length):
        for j in range(0,length):
            if(a[i]==b[j]):
                score=score+1
    identity=(score/total_elements)*100
    print("Matching Score::",score)
    print("Identity of the sequences::",identity)
def gap(a,b):
    if(len(a)==len(b)):
        print()
    else:
        k=int(input("enter the position to insert gap ::"))
        if (len(a)<len(b)):
            a.insert(k,'-')
        else:
```

```
        b.insert(k,'-')

    return(a,b)

find_identity(seq1,seq2)
```

Output:



Practical No: 3

Aim: Write a Python/Java code to find the Similarity value of a given sequences. Take the sequence fromuser.

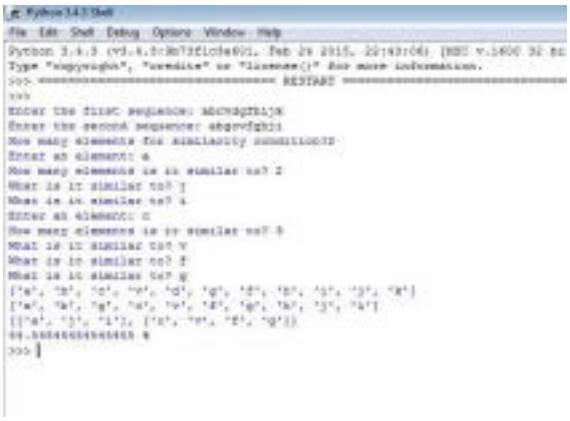
Code:

```
sequence_one=input("Enter the first sequence: ")
sequence_two=input("Enter the second sequence: ")
how_many=int(input("How many elements for similarity condition?"))
similarities=[]
for i in range(0,how_many):
    a=input("Enter an element: ")
    c=int(input("How many elements is it similar to? "))
    similarities.append([])
    similarities[i].append(a)
    for j in range(0,c):
        b=input("What is it similar to? ")
        similarities[i].append(b)
def compare(o,t,s):
    print(o)
    print(t)
    print(s)
    #checking if similar
    score=0
    for i in range(len(o)):
        for j in range(len(s)):
            if o[i] in s[j] and t[i] in s[j] and o[i] != t[i]:
                score+=1
    #calculating similarity
```

similarity= (score*100)/len(o) return similarity

print(compare(list(sequence_one),list(sequence_two),similarities),"%")

Output:



Practical No: 4

Aim: Enter genome of five different organism and write a python/java program to find consensus sequence using Multiple Sequence Alignment (MSA) technique.

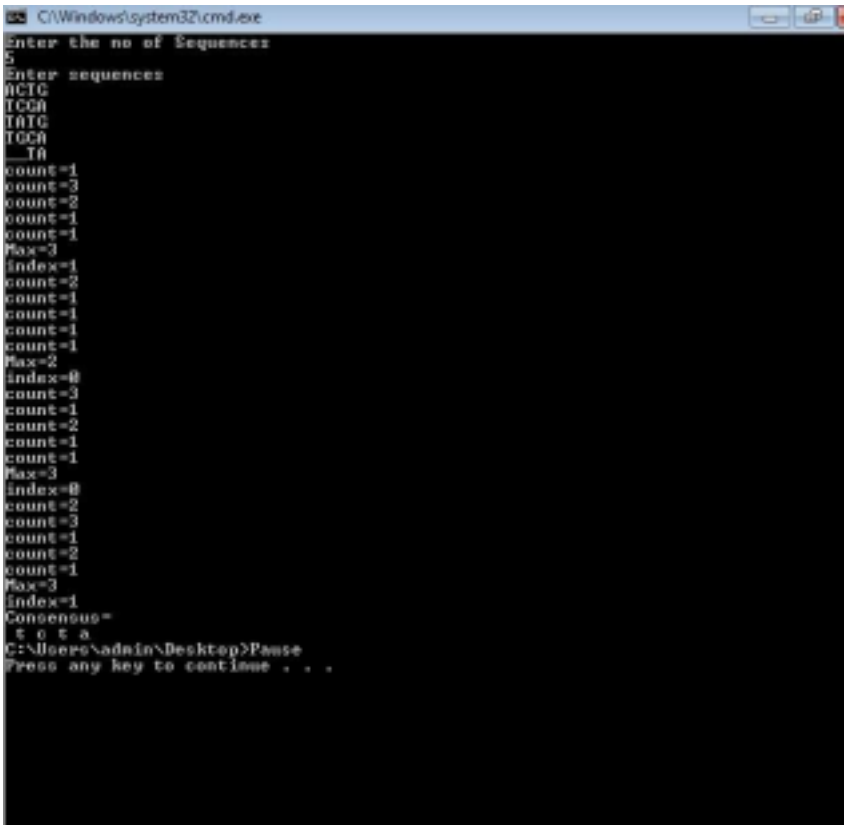
Code:

```
import java.io.*;

import java.util.*;

public class Consensus

{

  public static void main(String str[]) throws IOException

   {

    int n, i,j,k,count;

    String seq[],cons[];

    ArrayList<Integer> a = new ArrayList<Integer>();

    ArrayList s = new ArrayList();

    BufferedReader br=new BufferedReader(new InputStreamReader(System.in));

    System.out.println("Enter the no of Sequences");

    n=Integer.parseInt(br.readLine());

    seq=new String[n];



    System.out.println("Enter sequences");

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

    seq[i]=br.readLine();

    cons=new String[seq[0].length()];

    for(j=0;j<seq[0].length();j++)

    cons[j]=" ";

    for(j=0;j<seq[0].length();j++)

     {

      a.clear();
```

```
s.clear();
for(i=0;i<n;i++)
{
  count=1;
  for(k=i+1;k<n;k++)
  {

    if(seq[i].charAt(j)==seq[k].charAt(j))
    count++;

  }
  System.out.println("count="+count);
  a.add(count);
  s.add(seq[i].charAt(j));
}
/**Updated Snippet 1**/
Set<String> set = new HashSet<>(s);
ArrayList setlist = new ArrayList(set);
Collections.sort(setlist);

if (setlist.contains('-') &&setlist.size()==2){
cons[j]+="-"+setlist.get(1);

}
else if (setlist.size()==1){
cons[j]+="-"+setlist.get(0);
}
else{
int m = Collections.max(a);

int index=a.indexOf(m);
System.out.println("Max="+m);
cons[j]+=s.get(index);
System.out.println("index="+index);
for(i=index+1;i<a.size();i++)
```

```
        {
        if(a.get(i)==m)
        cons[j]+="/"+s.get(i);
        }
        }
      }
      System.out.println("Consensus=");
      for(j=0;j<seq[0].length();j++){
        /**Updated Snippet 2**/
      if(cons[j].length()==2)
      System.out.print(cons[j].toLowerCase());
      else if(cons[j].length()==3)
      System.out.print(cons[j].replace("-",""));
      else
      System.out.print(cons[j]);
      }
    }
  }
```

Output:


C:\Windows\system32\cmd.exe
Enter the no of Sequences:
5
Enter sequences:
ACTG
TCGA
TATG
TGCA
__TA
count=1
count=3
count=2
count=1
count=1
Max=3
index=1
count=2
count=1
count=1
count=1
count=1
Max=2
index=0
count=3
count=1
count=2
count=1
count=1
Max=3
index=0
count=2
count=3
count=1
count=2
count=1
Max=3
index=1
Consensus=
t c t a
C:\Users\admin\Desktop>Pause
Press any key to continue . . .

Practical No: 5

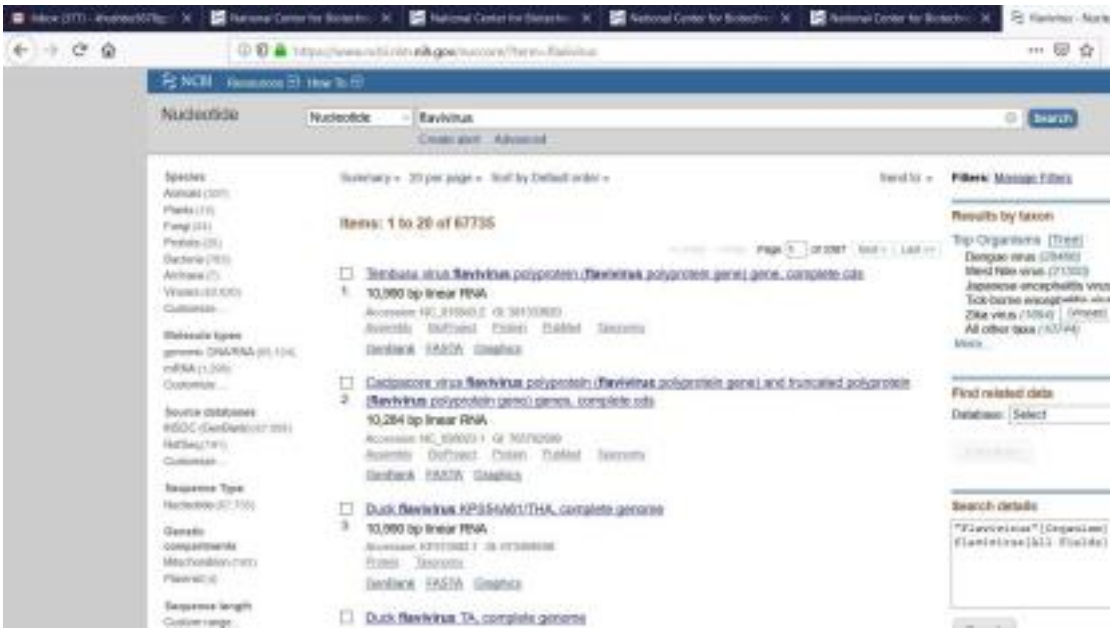
Aim: Perform a BLAST search on a specific gene sequence of a specify organism.

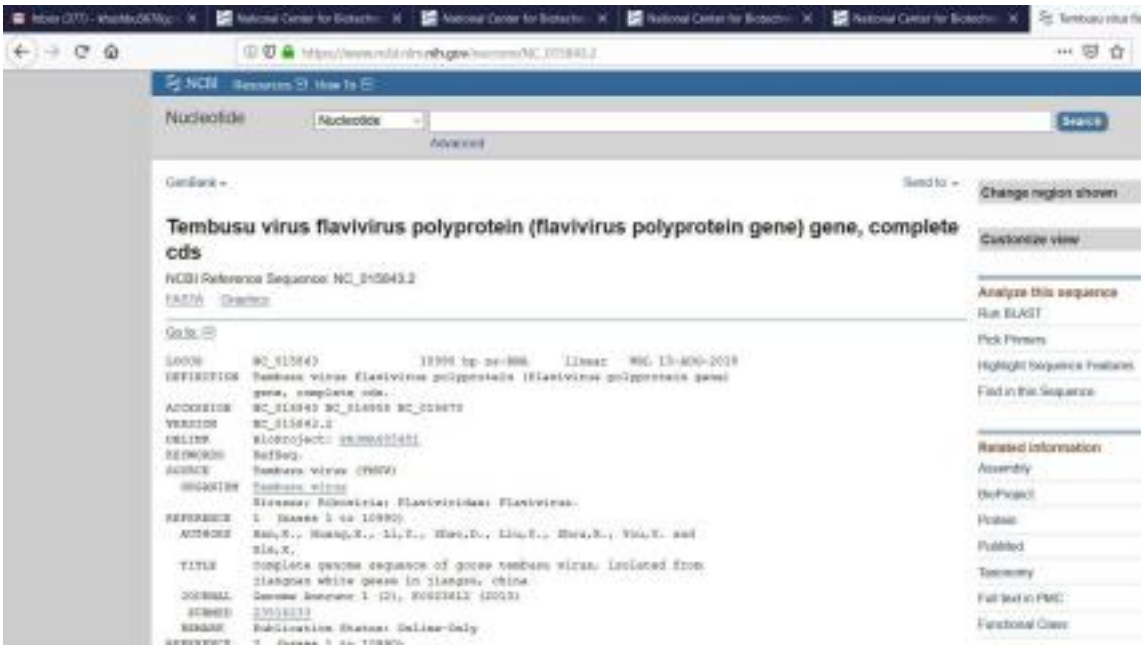
Steps:

Go to the National Center for Biotechnology Information Site

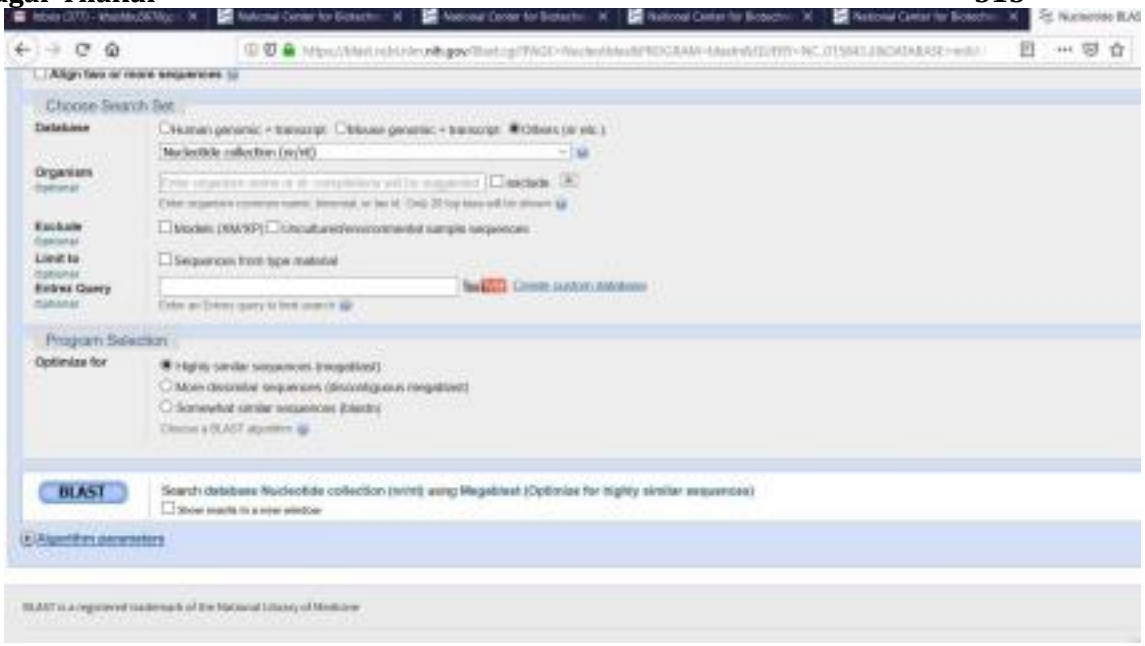
https://www.ncbi.nlm.nih.gov/

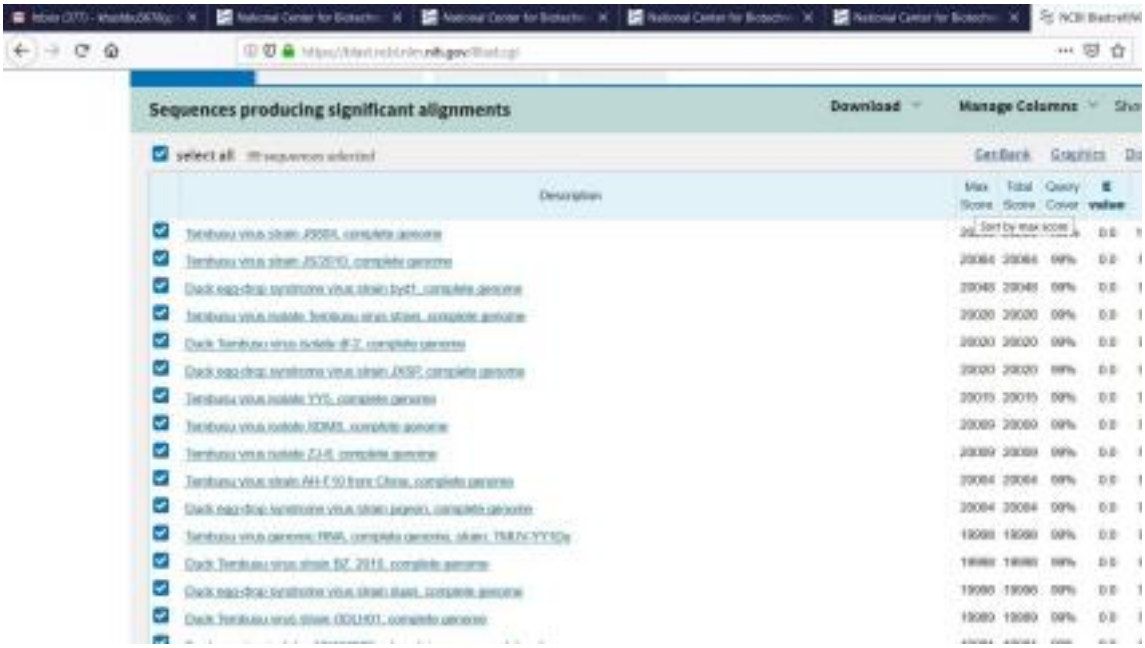
Select Nucleotide from All Databases and find any organism in a search bar.




Run BLAST option we have to select




Here the result will be display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Practical No: 6

Aim: Write a Python/Java code to find motif in a given sequence.

Code:

```
import random

l=int(input("Enter the length of motif"))
file=open("mot.txt","r")
r=file.read()
print("Sequence",r)
size=len(r)
print("Size of the sequence",size)
pos=random.randint(0,len(r)-5)
#pos=1
print("Position",pos)
motif=r[pos:pos+l]
print("Motif",motif)
i=pos+1
while(i<=size-1):
    if(motif==r[i:i+1]):
        str1=r[i:i+1]
        print("Match motif",str1)
        file1=open("motoutput.txt","a")
        file1.write(str1+" ")
    i+=1
```

Output:

```
Enter the length of motif4
Sequence AGAAGTTCGAGAAGCCGTAGT
```

Size of the sequence 21

Position 0

Motif AGAA

Practical No: 7

Aim: Perform a BLAST search on any genes sequence and writer a java/python code to count the no of repetition of each nucleotide in the sequence.

Code:

```
file=open("genes.txt","r")
r=file.read()
size=len(r)
score_A=0
score_C=0
score_T=0
score_G=0
for i in range(size):
    if(r[i]=='A'):
        score_A+=1
    elif (r[i]=='C'):
        score_C+=1
    elif (r[i]=='T'):
        score_T+=1
    elif (r[i]=='G'):
        score_G+=1
print("score of A is ",score_A)
print("score of C is ",score_C)
print("score of T is ",score_T)
print("score of G is ",score_G)
```

Output:

```
score of A is 6
score of C is 4
```

score of T is 7

score of G is 6

Practical No: 8

Aim: Generate a regular expression enter three protein sequence of three different organism. Write Python/Java code to find regular expression for this sequences.

Code:

```
def gen_reg_exp(seq_list, no_of_col):
    final_list=[]
    for colnum in range(no_of_col):
        collist=[]
        for colseq in seq_list:
            collist.append(colseq[colnum])
        if len(set(collist))==len(collist):
            #print(final_list)
            final_list.append('x')
        else:
            if len(set(collist))==1:
                final_list.append(collist[0])
            else:
                final_list.append(''.join(set(collist)))
    display_output(final_list)

def display_output(final_list):
    print(*final_list, sep='-')


no_of_seq=int(input("Enter the number of sequence: "))
print("Enter all the sequences")
seq_list=[]
for _ in range(no_of_seq):
    seq_list.append(list(map(str, input("").split())))
```

```
gen_reg_exp(seq_list, len(seq_list[0]))
```

## Output:

Enter the number of sequence: 4

Enter all the sequences

A D L G A V F A L C D R Y F Q

S D V G P R S C F C E R F Y Q

A D L G R T Q L R C D R Y Y Q

A D I G Q P H S L C E R Y F Q

SA-D-IVL-G-x-x-x-x-FRL-C-ED-R-YF-YF-Q

Practical No: 9

Aim: Enter six protein sequence of different organism and write a program to find a fingerprint ofsequence.

Code:

```
def solve_fingerprint(seq_list, no_of_col):
    seq_dict=dict()
    for colnum in range(no_of_col):
        counta,countc,countt,countg=0,0,0,0
        for colseq in seq_list:
            if colseq[colnum]=='A':
                counta+=1
            elif colseq[colnum]=='T':
                countt+=1
            elif colseq[colnum]=='C':
                countc+=1
            elif colseq[colnum]=='G':
                countg+=1
        seq_dict[colnum]=[counta,countc,countt,countg
    ] display_results(seq_dict)


def display_results(seq_dict):
    print("\tA \tC \tT \tG")
    for key in seq_dict:
        print("\n",*seq_dict[key],sep="\t")


no_of_seq=int(input("Enter the number of sequence: "))
print("Enter all the sequences")

seq_list=[]
```

```
for _ in range(no_of_seq):
    seq_list.append(list(map(str, input("").split())))
solve_fingerprint(seq_list,len(seq_list[0]))
```

Output: Enter the number of sequence:

Enter all the sequences

A C T G A T G

A T C A G A A

A T A A G C A

A G T T A G C

A C T G 4 0 0 0

0 1 2 1

1 1 2 0

2 0 1 1

2 0 0 2

2 1 0 1