

## 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:

```
IDLE Shell 3.9.5
File Edit Shell Debug Options Window Help
Python 3.9.5 (tags/v3.9.5:0a7dcdbd, May 3 2021, 17:27:52) [MSC v.1928 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
===== RESTART: C:\Users\pkk\OneDrive\Documents\bio-pract1.py =====
Enter the first sequence:actgctga
Enter the second sequence:acggcta
enter the position to insert::3
['a', 'c', 't', 'g', 'c', 't', 'g', 'a']
['a', 'c', 'g', '-', 'g', 'c', 't', 'a']
['1', '1', '0', '0', '0', '0', '0', '1']
3
>>>
```

## Practical No: 2

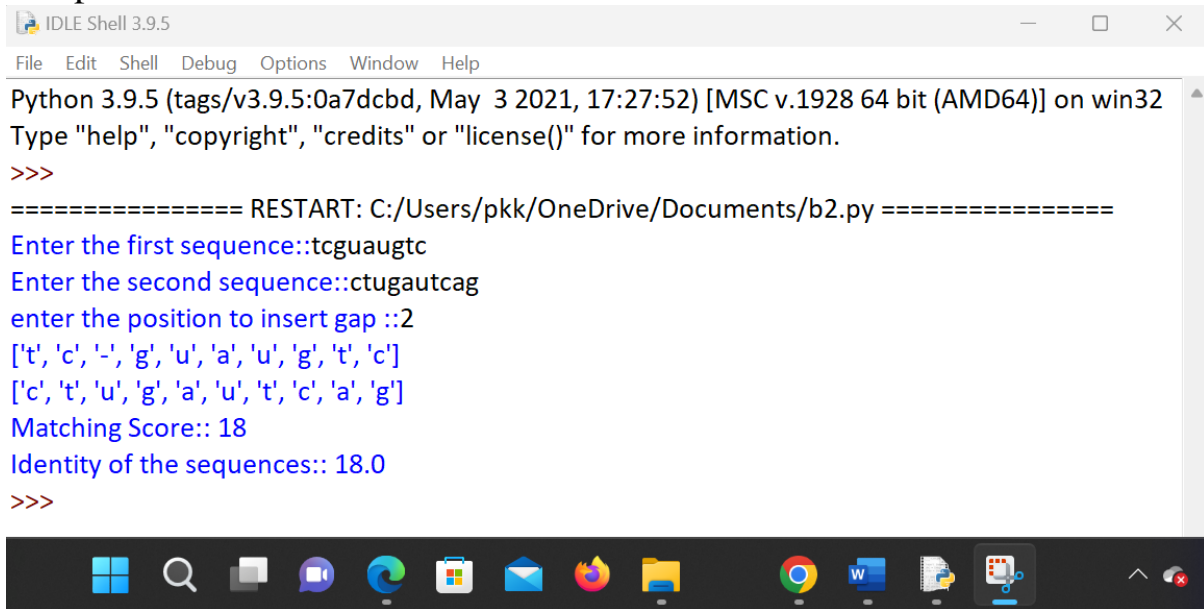
Aim: Write a Python/Java code to find the identity value of a given sequences. Take the sequence from user.

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 from user.

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:

```

IDLE Shell 3.9.5
File Edit Shell Debug Options Window Help
Python 3.9.5 (tags/v3.9.5:0a7dcdb, May 3 2021, 17:27:52) [MSC v.1928 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
===== RESTART: C:/Users/pkk/OneDrive/Documents/b3.py =====
Enter the first sequence: avtcgutca
Enter the second sequence: bdhacutgas
How many elements for similarity condition?2
Enter an element: g
How many elements is it similar to? 2
What is it similar to? c
What is it similar to? u
Enter an element: t
How many elements is it similar to? 2
What is it similar to? a
What is it similar to? h
['a', 'v', 't', 'c', 'g', 'u', 't', 'c', 'a']
['b', 'd', 'h', 'a', 'c', 'u', 't', 'g', 'a', 's']
[['g', 'c', 'u'], ['t', 'a', 'h']]
33.333333333333336 %
>>>

```

## 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:



```
Terminal
Enter the no of Sequences:
3
Enter sequences:
TAGC
CGAT
ATCG
count=1count=1count=1
Max=1index=0
count=1count=1
count=1
Max=1
index=0
count=1count=1
count=1
Max=1index=0
count=1
count=1
count=1Max=1
index=0Consensus=T/C/A A/G/T G/A/C C/T/G
```



## Practical No: 5

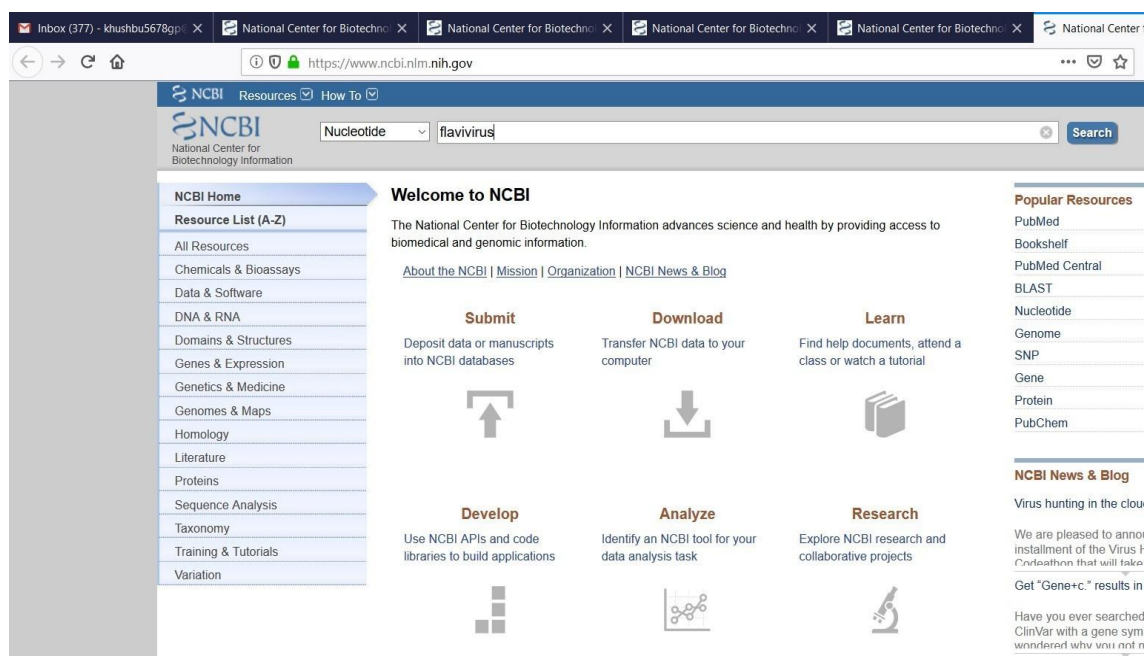
Aim: Perform a BLAST search on a specific gene sequence of a specific organism.

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.



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https://www.ncbi.nlm.nih.gov/nuccore/?term=flavivirus

NCBI Resources How To

Nucleotide Nucleotide Search

Create alert Advanced

Species Summary 20 per page Sort by Default order Send to Filters: Manage Filters

Animals (307)  
Plants (12)  
Fungi (24)  
Protists (20)  
Bacteria (783)  
Archaea (7)  
Viruses (62,020)  
Customize ...

Molecule types  
genomic DNA/RNA (65,124)  
mRNA (1,298)  
Customize ...

Source databases  
INSDC (GenBank) (67,508)  
RefSeq (191)  
Customize ...

Sequence Type  
Nucleotide (67,735)

Genetic compartments  
Mitochondrion (163)  
Plasmid (4)

Sequence length  
Custom range...

Items: 1 to 20 of 67735

1. ☐ Tembusu virus **flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds**  
10,990 bp linear RNA  
Accession: NC\_015843.2 GI: 381333920  
Assembly BioProject Protein PubMed Taxonomy  
GenBank FASTA Graphics

2. ☐ Cacipacore virus **flavivirus polyprotein (flavivirus polyprotein gene) and truncated polyprotein (flavivirus polyprotein gene) genes, complete cds**  
10,284 bp linear RNA  
Accession: NC\_026623.1 GI: 765702699  
Assembly BioProject Protein PubMed Taxonomy  
GenBank FASTA Graphics

3. ☐ Duck **flavivirus KPS54A61/THA, complete genome**  
10,990 bp linear RNA  
Accession: KF573582.1 GI: 673459548  
Protein Taxonomy  
GenBank FASTA Graphics

☐ Duck **flavivirus TA, complete genome**

Results by taxon

Top Organisms [Tree]  
Dengue virus (28466)  
West Nile virus (21550)  
Japanese encephalitis virus  
Tick-borne encephalitis virus  
Zika virus (1694) [viruses]  
All other taxa (10744)  
More...

Find related data  
Database: Select  
Find items

Search details  
"Flavivirus"[Organism]  
flavivirus[All Fields]

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https://www.ncbi.nlm.nih.gov/nuccore/NC\_015843.2

NCBI Resources How To

Nucleotide Nucleotide Search

Advanced

GenBank Send to Change region shown

**Tembusu virus flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds**

NCBI Reference Sequence: NC\_015843.2  
FASTA Graphics

Go to: ☑

LOCUS NC\_015843 10990 bp ss-RNA linear VRL 13-AUG-2018  
DEFINITION Tembusu virus flavivirus polyprotein (flavivirus polyprotein gene) gene, complete cds.  
ACCESSION NC\_015843 NC\_016958 NC\_018670  
VERSION NC\_015843.2  
DBLINK BioProject: PRJNA485481  
KEYWORDS RefSeq.  
SOURCE Tembusu virus (TMUV)  
ORGANISM Tembusu virus  
Viruses; Riboviria; Flaviviridae; Flavivirus.  
REFERENCE 1 (bases 1 to 10990)  
AUTHORS Han,K., Huang,X., Li,Y., Zhao,D., Liu,Y., Zhou,X., You,Y. and Xie,X.  
TITLE Complete genome sequence of goose tembusu virus, isolated from jiangnan white geese in jiangsu, china  
JOURNAL Genome Announc 1 (2), E0023612 (2013)  
PUBMED 23516233  
REMARK Publication Status: Online-Only  
COMMENT 2 (bases 1 to 10990)

Analyze this sequence  
Run BLAST  
Pick Primers  
Highlight Sequence Features  
Find in this Sequence

Related information  
Assembly  
BioProject  
Protein  
PubMed  
Taxonomy  
Full text in PMC  
Functional Class

Run BLAST option we have to select

Align two or more sequences

Choose Search Set

Database: ☐ Human genomic + transcript ☐ Mouse genomic + transcript ☒ Others (nr etc.):  
Nucleotide collection (nr/nt)

Organism:  Enter organism name or id—completions will be suggested ☐ exclude

Exclude: ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to: ☐ Sequences from type material

Entrez Query:  Enter an Entrez query to limit search

Program Selection

Optimize for: ☒ Highly similar sequences (megablast) ☐ More dissimilar sequences (discontiguous megablast) ☐ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

Show results in a new window

Algorithm parameters

BLAST is a registered trademark of the National Library of Medicine

BLAST

Sequences producing significant alignments

Download Manage Columns Show

select all 99 sequences selected

	Description	Max Score	Total Score	Query Cover	E value
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus strain JS804, complete genome</a>	20064	20064	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus strain JS/2010, complete genome</a>	20064	20064	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck egg-drop syndrome virus strain byd1, complete genome</a>	20048	20048	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus isolate Tembusu virus strain, complete genome</a>	20026	20026	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck Tembusu virus isolate df-2, complete genome</a>	20020	20020	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck egg-drop syndrome virus strain JXSP, complete genome</a>	20020	20020	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus isolate YY5, complete genome</a>	20015	20015	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus isolate SDMS, complete genome</a>	20009	20009	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus isolate ZJ-6, complete genome</a>	20009	20009	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus strain AH-F10 from China, complete genome</a>	20004	20004	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck egg-drop syndrome virus strain pigeon, complete genome</a>	20004	20004	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Tembusu virus genomic RNA, complete genome, strain TMUV-YY1Du</a>	19998	19998	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck Tembusu virus strain BZ_2010, complete genome</a>	19998	19998	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck egg-drop syndrome virus strain duan, complete genome</a>	19998	19998	99%	0.0 9
<input checked="" type="checkbox"/>	<a href="#">Duck Tembusu virus strain GDLH01, complete genome</a>	19989	19989	99%	0.0 9

Here the result will be display

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NCBI Blastref|NC

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🔒 https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr\_381283018

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GenBank Graphics

▼ Next ▲ Previous

Tembusu virus strain JS804, complete genome

Sequence ID: [JF895923.2](#) Length: 10990 Number of Matches: 1

Range 1: 1 to 10990

[GenBank](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
20295 bits(10990)	0.0	10990/10990(100%)	0/10990(0%)	Plus/Plus

Query 1

AGAAAGTTGCCTGTGTGAACCTATTCCAAACAGCTTTTGGAGTAGTGCCTGTGAACGTAA

60

|||||

Sbjct 1

AGAAAGTTGCCTGTGTGAACCTATTCCAAACAGCTTTTGGAGTAGTGCCTGTGAACGTAA

60

Query 61

ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACAGGAAGACC

120

|||||

Sbjct 61

ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACAGGAAGACC

120

Query 121

CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCOCGCGGAAATCCGCTAGC

180

|||||

Sbjct 121

CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCOCGCGGAAATCCGCTAGC

180

Query 181

GCGGATAAAGAGGACGATTGATGGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT

240

|||||

Sbjct 181

GCGGATAAAGAGGACGATTGATGGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT

240

Query 241

GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTTGGAATGCTGAAGAG

300

|||||

Sbjct 241

GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTTGGAATGCTGAAGAG

300

Query 301

ATGGAAGCTGGTTGGAGTTAATGAGGCGACCAACATCTGAAAAGCTTCAAGCGTGACAT

360

|||||

Sbjct 301

ATGGAAGCTGGTTGGAGTTAATGAGGCGACCAACATCTGAAAAGCTTCAAGCGTGACAT

360

Query 361

TGGACAGATGCTCGACGGACTGAATAAGCGGAAGCGGAAACCTCgggggggggAGTTGCTC

420

|||||

Sbjct 361

TGGACAGATGCTCGACGGACTGAATAAGCGGAAGCGGAAACCTCGGGGGGGGAGTTGCTC

420

Related Inform

[Gene](#) - associated

## 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+l]):

        str1=r[i:i+l]

        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

```

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

```

Aim: Perform a BLAST search on any genes sequence and write 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
      R T Q L R C D R Y Y Q
      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 of sequence.

### 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: 4

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

G T T   G C

A      C      T      G

4      0      0      0

0      1      2      1

1

2              1

2