**Class:MSC-I** **SEM:I**
**Subject:BioInfomatics** **Paper:III**
**AcademicYear:2022-2023** **RollNo:509**

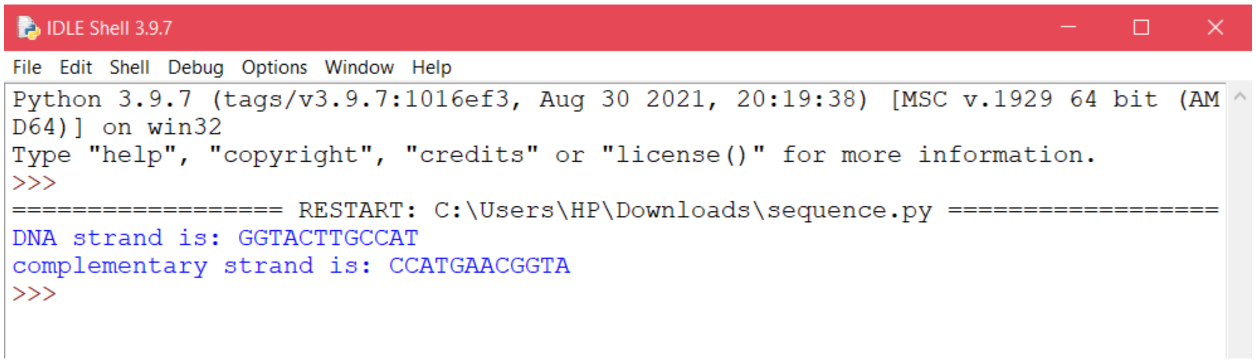
**Aim: Write a Python/Java code to perform Complementary sequence Take 2 sequences from user and calculate the score**

**Code:**

```
def complementary_strand_find(dna_strand):
   complementary_strand = ""
   for base in dna_strand:
      if base == "A" :
         complementary_strand += "T"
      elif base == "T" :
         complementary_strand += "A"
      elif base == "U" :
         complementary_strand += "A"
      elif base == "G" :
         complementary_strand += "C"
      elif base == "C" :
         complementary_strand += "G"
      elif base == "Y" :
         complementary_strand += "R"
      elif base == "R" :
         complementary_strand += "Y"
      else :
         print("Wrong input")
         complementary_strand = None
         break
   return complementary_strand
if __name__ == "__main__":
  dna_strand = "GGTACTTGCCAT"
print("DNA strand is:",
        dna_strand)
```

```
print("complementary strand is:",
        complementary_strand_find(dna_strand))
```

**OUTPUT:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
================== RESTART: C:\Users\HP\Downloads\sequence.py ==================
DNA strand is: GGTACTTGCCAT
complementary strand is: CCATGAACGGTA
>>>
```

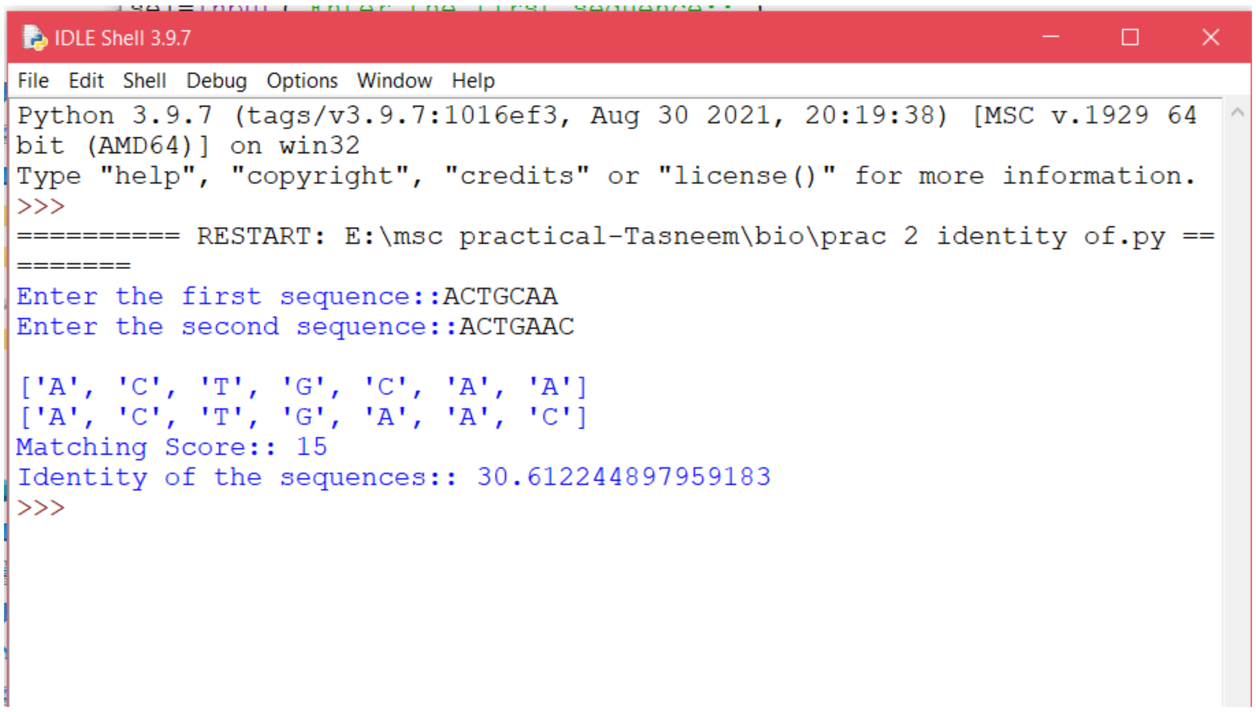
## Practical No: 2

**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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64
bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
========== RESTART: E:\msc practical-Tasneem\bio\prac 2 identity of.py ==
=======
Enter the first sequence::ACTGCAA
Enter the second sequence::ACTGAAC

['A', 'C', 'T', 'G', 'C', 'A', 'A']
['A', 'C', 'T', 'G', 'A', 'A', 'C']
Matching Score:: 15
Identity of the sequences:: 30.612244897959183
>>>
```

**Practical No: 3**

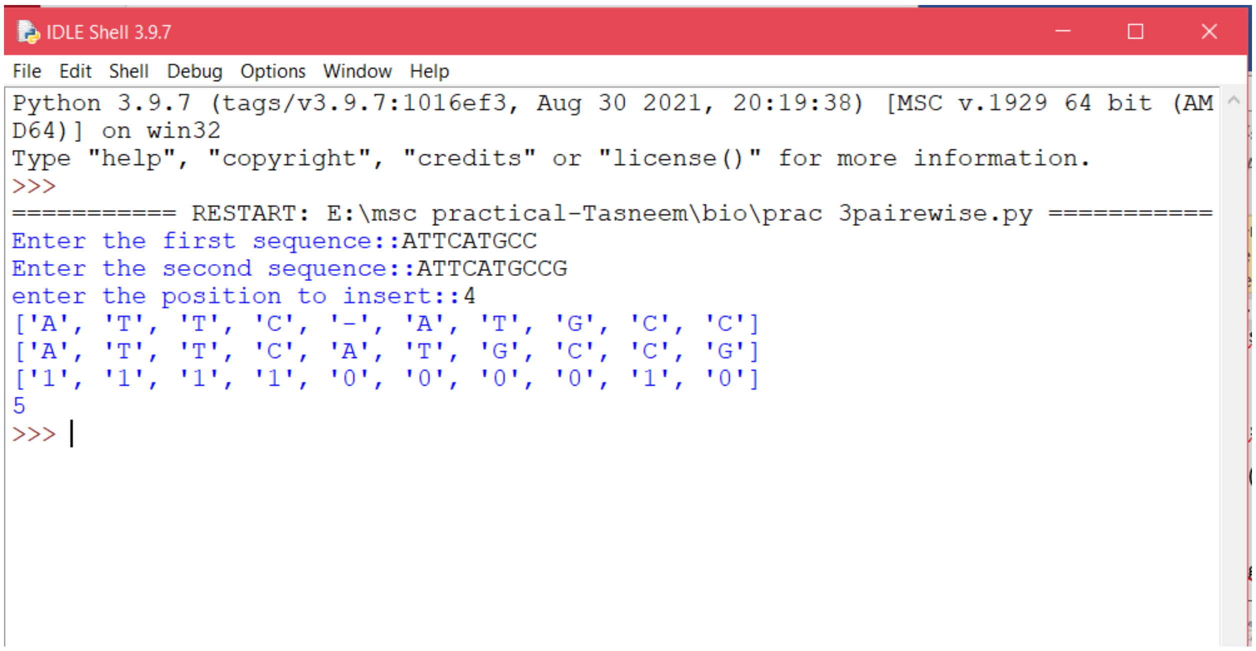
**Aim: Write a Python/Java code to perform pairwise alignment. Take 2 sequences from user and calculate the score**

**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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
=========== RESTART: E:\msc practical-Tasneem\bio\prac 3pairewise.py ===========
Enter the first sequence::ATTCATGCC
Enter the second sequence::ATTCATGCCG
enter the position to insert::4
['A', 'T', 'T', 'C', '-', 'A', 'T', 'G', 'C', 'C']
['A', 'T', 'T', 'C', 'A', 'T', 'G', 'C', 'C', 'G']
['1', '1', '1', '1', '0', '0', '0', '0', '1', '0']
5
>>> 
```

## Practical No: 4

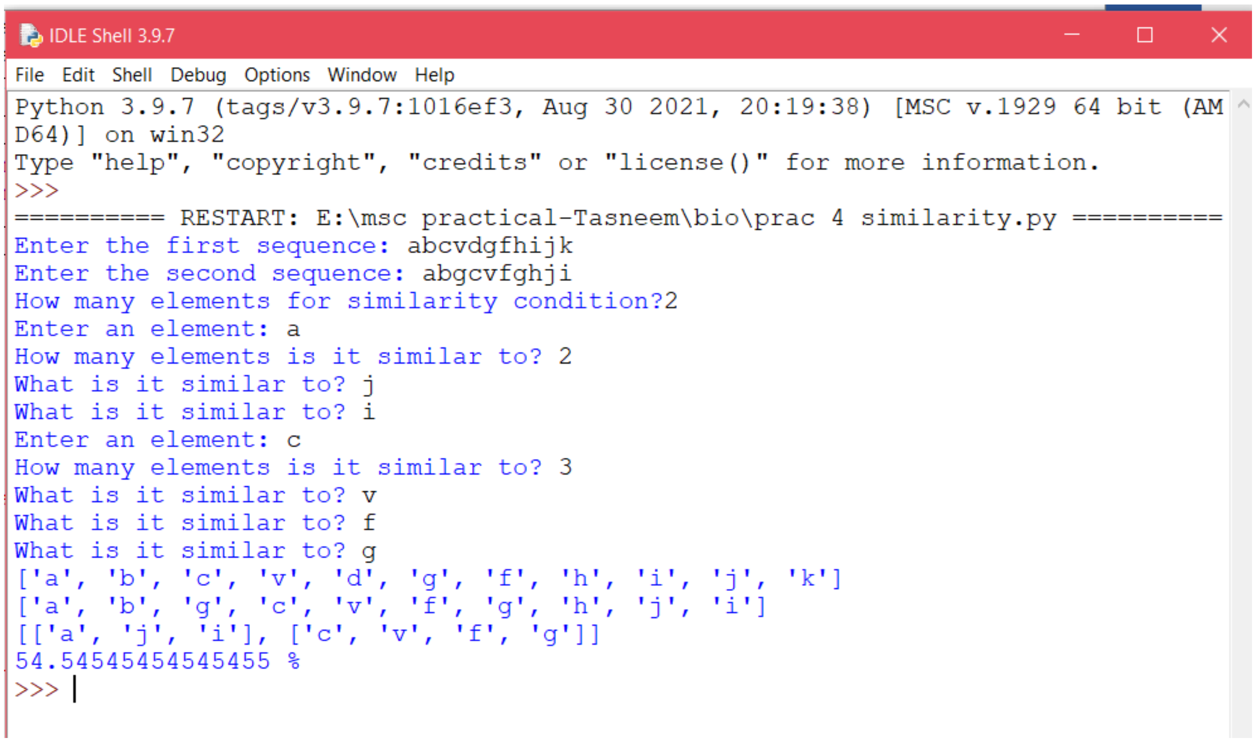
**Aim: Write a Python/Java code to find the Similarity value of a given sequences. Take the sequence from user:**

**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)
            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
            similarity= (score*100)/len(o)
            return similarity
print(compare(list(sequence_one),list(sequence_two),similarities),"%")
```

**OUTPUT:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
========== RESTART: E:\msc practical-Tasneem\bio\prac 4 similarity.py ==========
Enter the first sequence: abcvdgfhijk
Enter the second sequence: abgcvfghji
How many elements for similarity condition?2
Enter an element: a
How many elements is it similar to? 2
What is it similar to? j
What is it similar to? i
Enter an element: c
How many elements is it similar to? 3
What is it similar to? v
What is it similar to? f
What is it similar to? g
['a', 'b', 'c', 'v', 'd', 'g', 'f', 'h', 'i', 'j', 'k']
['a', 'b', 'g', 'c', 'v', 'f', 'g', 'h', 'j', 'i']
[['a', 'j', 'i'], ['c', 'v', 'f', 'g']]
54.54545454545455 %
>>> |
```

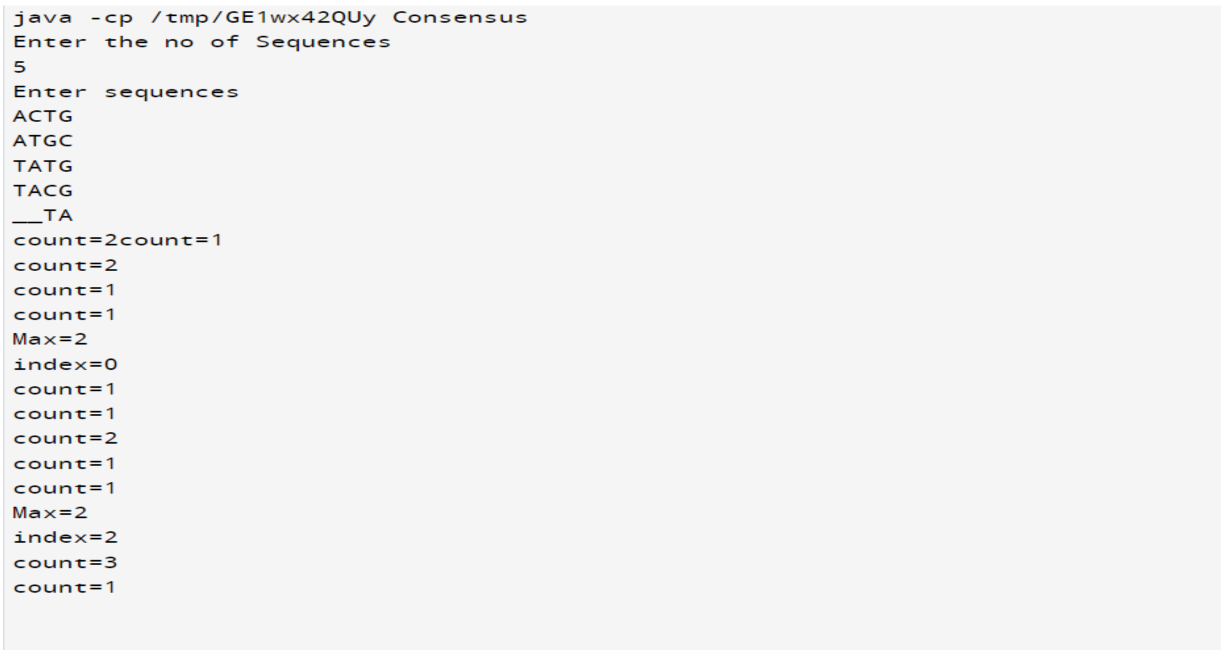
## Practical No: 5

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

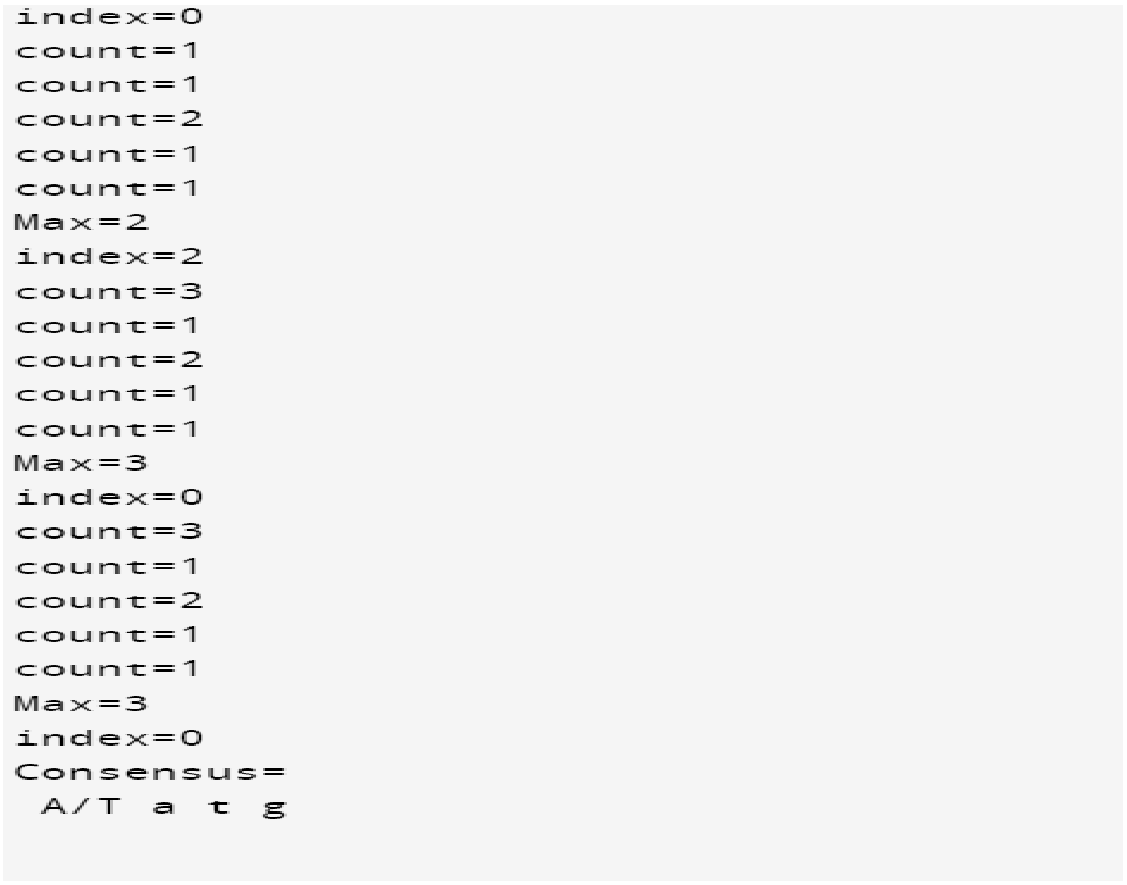
**Code:**

```
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]);
}
}
}
```



```
java -cp /tmp/GE1wx42QUy Consensus
Enter the no of Sequences
5
Enter sequences
ACTG
ATGC
TATG
TACG
__TA
count=2count=1
count=2
count=1
count=1
Max=2
index=0
count=1
count=1
count=2
count=1
count=1
Max=2
index=2
count=3
count=1
```



```
index=0
count=1
count=1
count=2
count=1
count=1
Max=2
index=2
count=3
count=1
count=2
count=1
count=1
Max=3
index=0
count=3
count=1
count=2
count=1
count=1
Max=3
index=0
Consensus=
 A/T a t g
```

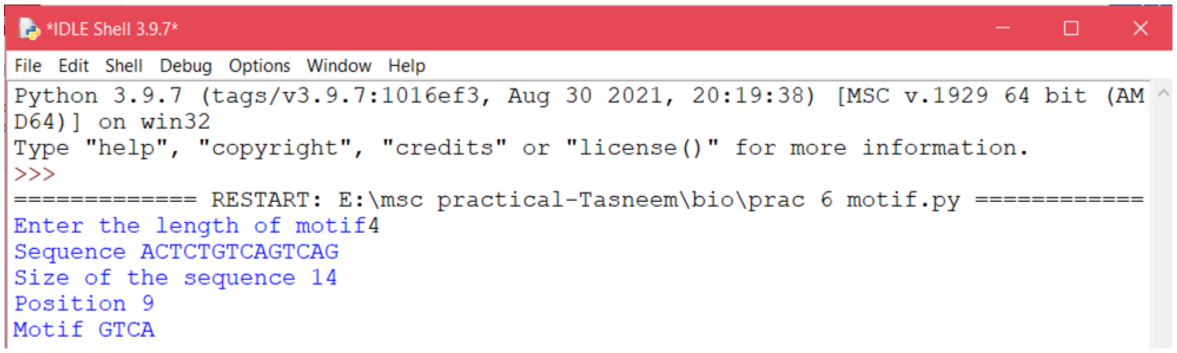
**Practical No: 6**

**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)

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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
============= RESTART: E:\msc practical-Tasneem\bio\prac 6 motif.py ============
Enter the length of motif4
Sequence ACTCTGTCAGTCAG
Size of the sequence 14
Position 9
Motif GTCA
```

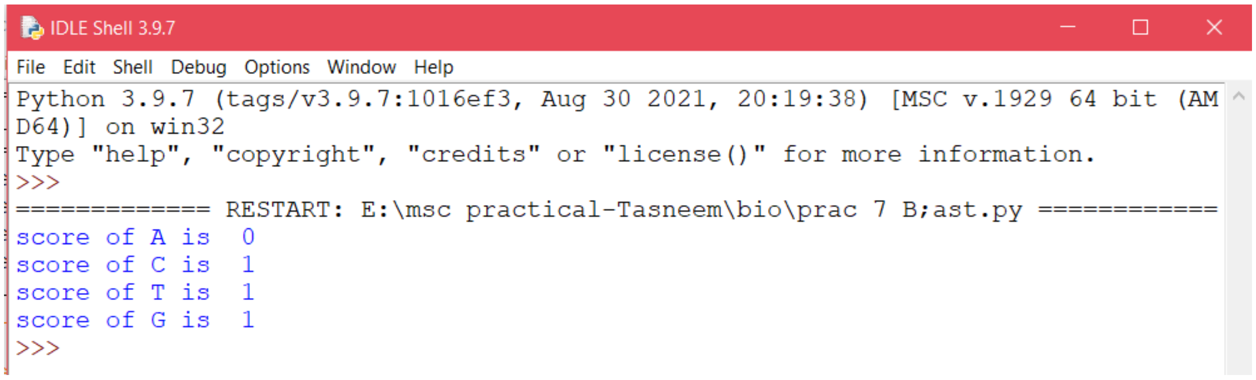
## Practical No: 7

**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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
============= RESTART: E:\msc practical-Tasneem\bio\prac 7 B;ast.py ============
score of A is  0
score of C is  1
score of T is  1
score of G is  1
>>>
```

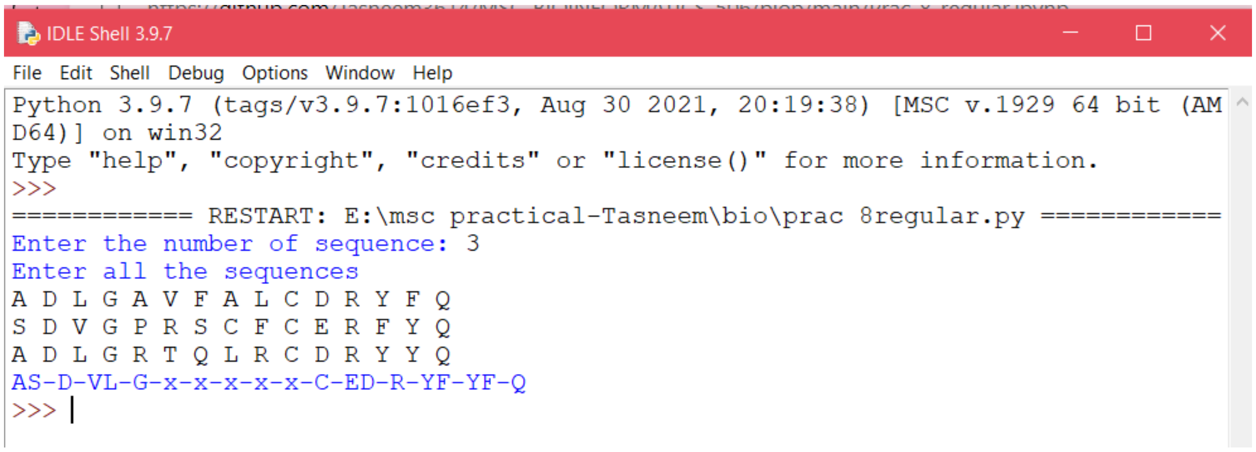
**Practical No: 8**

**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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
============ RESTART: E:\msc practical-Tasneem\bio\prac 8regular.py ============
Enter the number of sequence: 3
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
AS-D-VL-G-x-x-x-x-x-C-ED-R-YF-YF-Q
>>>
```

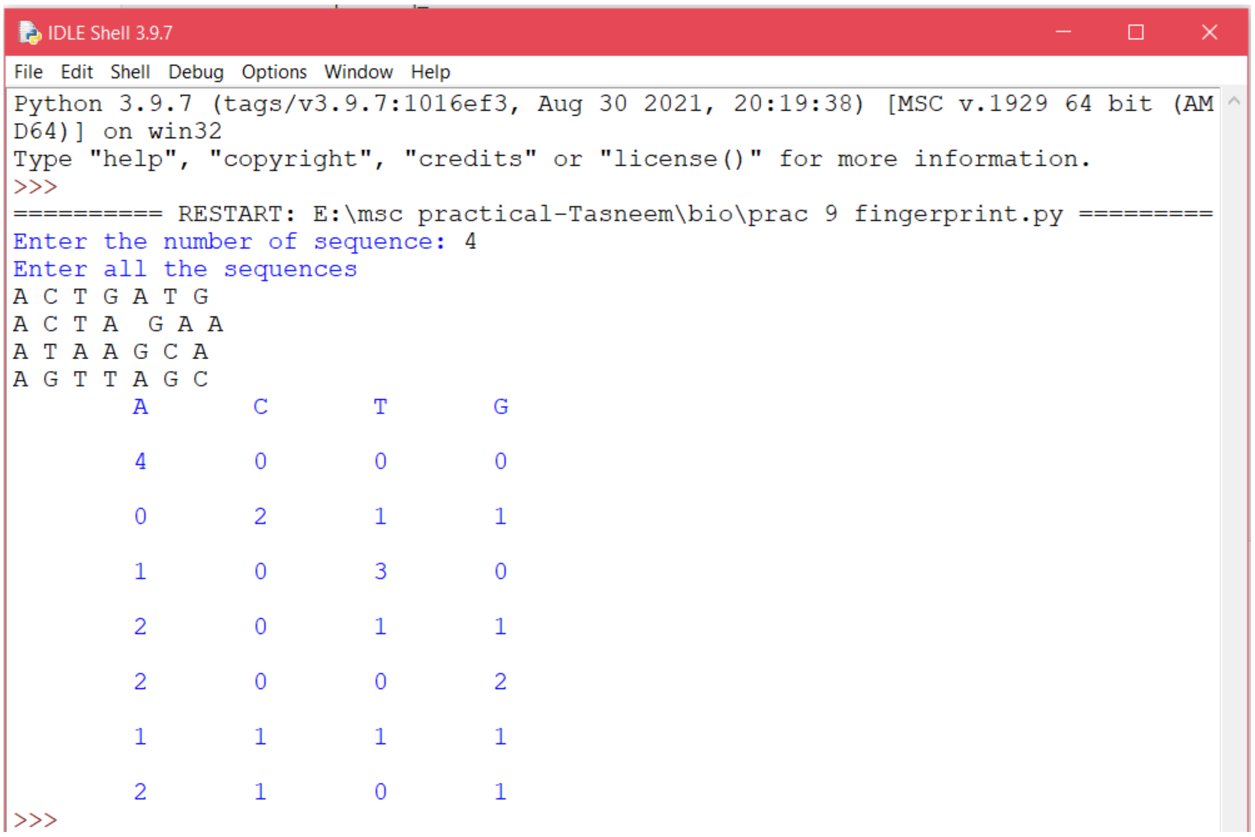
## Practical No: 9

**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:**



```
Python 3.9.7 (tags/v3.9.7:1016ef3, Aug 30 2021, 20:19:38) [MSC v.1929 64 bit (AM
D64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
========== RESTART: E:\msc practical-Tasneem\bio\prac 9 fingerprint.py =========
Enter the number of sequence: 4
Enter all the sequences
A C T G A T G
A C T 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       2       1       1

        1       0       3       0

        2       0       1       1

        2       0       0       2

        1       1       1       1

        2       1       0       1
>>>
```