**504 – Sejal Pawar**

**MSc. (Computer Science) Semester – I**

**Paper III (Bioinformatics)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **INDEX** |  |  |
| **NO** | **DATE** | **TITLE** | **PAGE NO** | **SIGN** |
|  |  |  |  |  |
| 1 | 08/08/22 | Complementary DNA Sequence | 2 |  |
| 2 | 08/08/22 | Identity of Two protein sequence | 3 |  |
| 3 | 26/08/22 | Pairwise Sequence Alignment | 5 |  |
| 4 | 21/09/22 | Similarity between two protein sequence | 7 |  |
| 5 | 21/09/22 | Multiple Sequence Alignment | 9 |  |
| 6 | 13/10/22 | Motif Finding | 13 |  |
| 7 | 29/08/22 | Perform a BLAST search on any gene sequence and write a code to count the no of repetition of each nucleotide in the sequence | 14 |  |
| 8 | 29/08/22 | Regular Expression | 15 |  |
| 9 | 22/09/22 | Fingerprint | 16 |  |
| 10 | 13/10/22 | Retrieving 3D structure from PDB | 18 |  |

**Practical 1**

Aim: Complementary DNA Sequence.

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:

Graphical user interface, text

Description automatically generated with medium confidence

**Practical 2**

Aim: Identity of Two protein sequence

Code:

se1=input("Enter the first sequence: ")

se2=input("Enter the second sequence: ")

seq1=list(se1)

seq2=list(se2)

def find\_identity(a,b):abcvfdg

  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,'-')

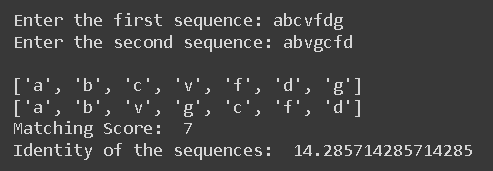
    else:

      b.insert(k,'-')

  return(a,b)

find\_identity(seq1,seq2)

Output:



**Practical 3**

Aim: Pairwise Sequence Alignment

Code:

seq1=list(input("Enter the first sequence: "))

seq2=list(input("Enter the second sequence: "))

score=[]

def pairwise(a,b):

    gap(a,b)

    print(a)

    print(b)

    value=1

    length=len(a)

    for i in range(0,length):

        if a[i]==b[i]:

            score.append('1')

            value+=0

        else:

            score.append('0')

    print("Score ",score)

    print("Value ",value)

def gap(a,b):

    if (len(a)==len(b)):

        print()

    else:

        k=int(input("Enter the position to insert the gap: "))

        if (len(a)<len(b)):

            a.insert(k,'-')

        else:

            b.insert(k,'-')

        return (a,b)

pairwise(seq1,seq2)

Output:

Text

Description automatically generated

**Practical 4**

Aim: Similarity between two protein sequence

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)

  print("The similarity is: ",similarity)

print(compare(list(sequence\_one),list(sequence\_two),similarities),"%")

Output:

Text

Description automatically generated

**Practical 5**

Aim: Multiple Sequence Alignment

Code: prac\_5.java

import java.io.BufferedReader;

import java.io.IOException;

import java.io.InputStreamReader;

import java.util.ArrayList;

import java.util.Collections;

import java.util.HashSet;

import java.util.Set;

public class prac\_5{

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));

}

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:

Table

Description automatically generated

**Practical 6**

Aim: Motif Finding

Code:

*prac\_6.py*

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 is: ",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

*mot.txt*

ACTGAATTCAGG

Output:

Text

Description automatically generated

**Practical 7**

Aim: Perform a BLAST search on any gene sequence and write a code to count the no of repetition of each nucleotide in the sequence.

Code:

*prac\_7.py*

file=open("gene.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)

*gene.txt*

ACTGAATTCAGG

Output:

Text

Description automatically generated

**Practical 8**

Aim: Regular Expression

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:

Text

Description automatically generated

**Practical 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:

A screenshot of a computer

Description automatically generated with low confidence