# BioInformatics Practicals

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**Class:-Msc CS part 1** **Subject:-BioInformatics**

# Practical No: 1

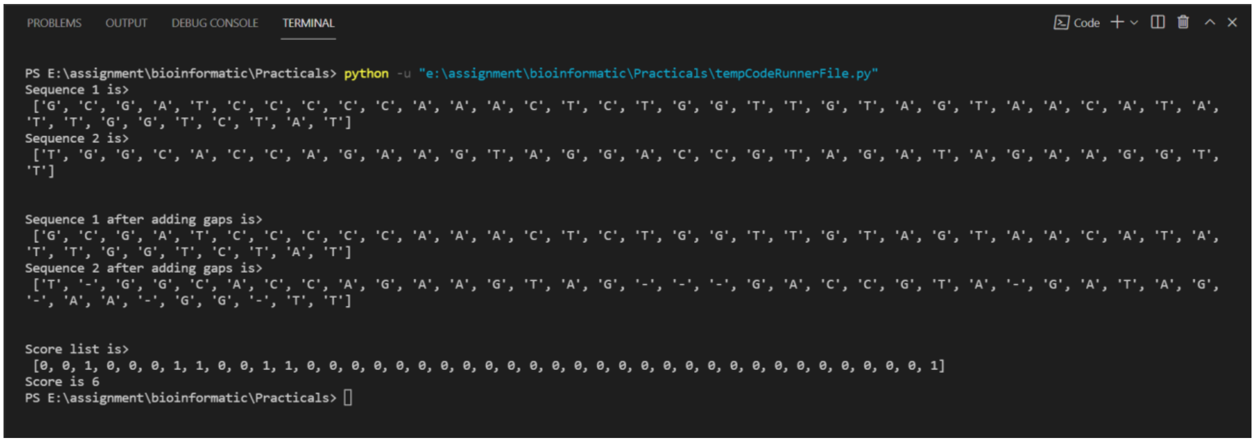
Aim: Write a Python/Java code to perform pairwise alignment. Take 2 sequences from user and calculate the score.

Code:

```
from random import choice, randint
from operator import eq

def get_sequences():
    char_sequence = 'ACTG'
    sequence_1 = [choice(char_sequence) for i in range(randint(10, 50))]
    sequence_2 = [choice(char_sequence) for i in range(randint(10, 50))]

    return sequence_1, sequence_2

def insert_gap(sequence):
    sequence.insert(randint(0, len(sequence) - 1), '-')

    return sequence

def insert_gaps(sequence_1, sequence_2):
    while len(sequence_1) != len(sequence_2):
        if len(sequence_1) < len(sequence_2):
            sequence_1 = insert_gap(sequence_1)
        else:
            sequence_2 = insert_gap(sequence_2)

    return sequence_1, sequence_2

def pairwise_alignment(sequence_1, sequence_2):
    return list(map(eq, sequence_1, sequence_2))

if __name__ == "__main__":
    sequence_1, sequence_2 = get_sequences()
    print("Sequence 1 is>\n", sequence_1)
    print("Sequence 2 is>\n", sequence_2)
    print("\n")
```

```
sequence_1, sequence_2 = insert_gaps(sequence_1, sequence_2)
print("Sequence 1 after adding gaps is>\n", sequence_1)
print("Sequence 2 after adding gaps is>\n", sequence_2)
print("\n")

score_list = pairwise_alignment(sequence_1, sequence_2)
print("Score list is>\n", [1 if i else 0 for i in score_list])
print(f"Score is {sum(score_list)}")
```

Output:



```
PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\tempCodeRunnerFile.py"
Sequence 1 is>
 ['G', 'C', 'G', 'A', 'T', 'C', 'C', 'C', 'C', 'C', 'A', 'A', 'A', 'C', 'T', 'C', 'T', 'G', 'G', 'T', 'T', 'G', 'T', 'A', 'G', 'T', 'A', 'A', 'C', 'A', 'T', 'A',
'T', 'T', 'G', 'G', 'T', 'C', 'T', 'A', 'T']
Sequence 2 is>
 ['T', 'G', 'G', 'C', 'A', 'C', 'C', 'A', 'G', 'A', 'A', 'G', 'T', 'A', 'G', 'G', 'A', 'C', 'C', 'G', 'T', 'A', 'G', 'A', 'T', 'A', 'G', 'A', 'A', 'G', 'G', 'T',
'T']


Sequence 1 after adding gaps is>
 ['G', 'C', 'G', 'A', 'T', 'C', 'C', 'C', 'C', 'C', 'A', 'A', 'A', 'C', 'T', 'C', 'T', 'G', 'G', 'T', 'T', 'G', 'T', 'A', 'G', 'T', 'A', 'A', 'C', 'A', 'T', 'A',
'T', 'T', 'G', 'G', 'T', 'C', 'T', 'A', 'T']
Sequence 2 after adding gaps is>
 ['T', '-', 'G', 'G', 'C', 'A', 'C', 'C', 'A', 'G', 'A', 'A', 'G', 'T', 'A', 'G', '-', '-', '-', 'G', 'A', 'C', 'C', 'G', 'T', 'A', '-', 'G', 'A', 'T', 'A', 'G',
'-', 'A', 'A', '-', 'G', 'G', '-', 'T', 'T']


Score list is>
 [0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1]
Score is 6
PS E:\assignment\bioinformatic\Practicals> []
```

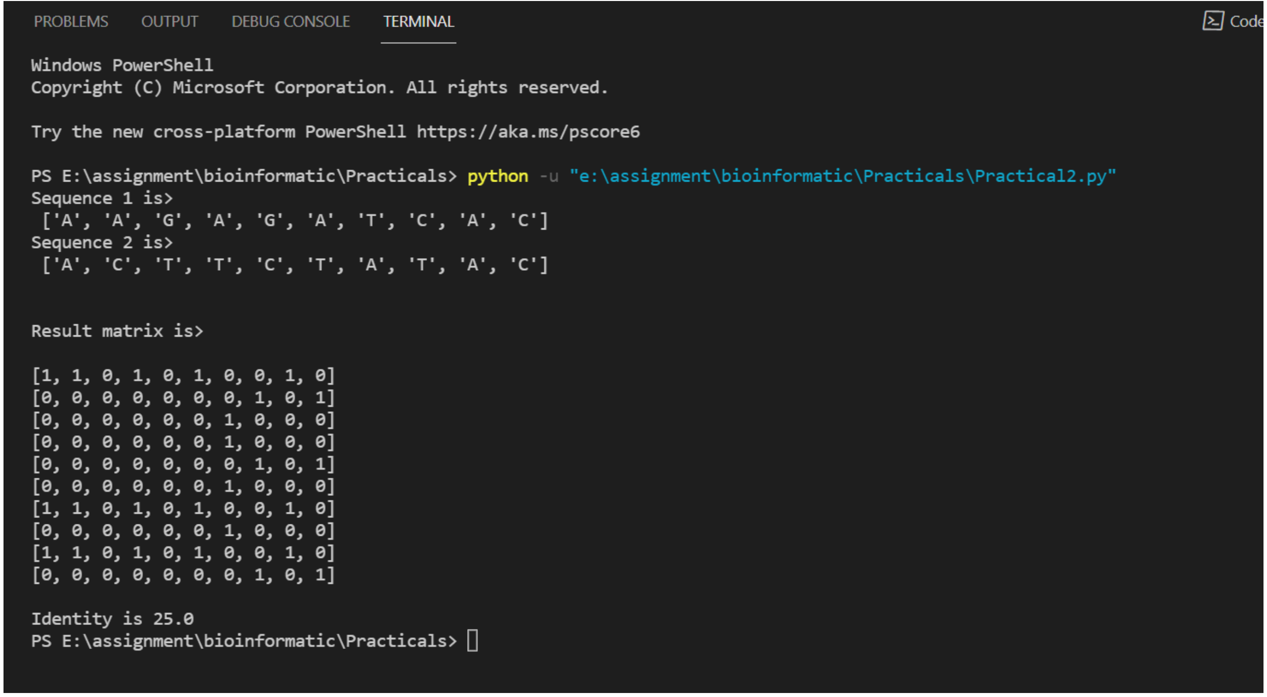
# Practical No:2

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

Code:

```
from random import choice, randint

def get_sequences():
    char_sequence = 'ACTG'
    sequence_length = randint(10, 20)
    sequence_1 = [choice(char_sequence) for i in range(sequence_length)]
    sequence_2 = [choice(char_sequence) for i in range(sequence_length)]

    return sequence_1, sequence_2

def identity(sequence_1, sequence_2):

    result_matrix = [[1 if i == j else 0 for j in sequence_1] for i in sequence_2]
    result = sum([sum(i) for i in result_matrix])

    return result, result_matrix

def print_matrix(matrix):
    for i in matrix:
        print(i)
    print()


if __name__ == "__main__":
    sequence_1, sequence_2 = get_sequences()
    print("Sequence 1 is>\n", sequence_1)
    print("Sequence 2 is>\n", sequence_2)
    print("\n")

    result, result_matrix = identity(sequence_1, sequence_2)
    print("Result matrix is>\n")
    print_matrix(result_matrix)
    print(f"Identity is {round((result / (len(sequence_1) * len(sequence_2))) * 100, 2)}")
```

Output:



```
Windows PowerShell
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PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical2.py"
Sequence 1 is>
 ['A', 'A', 'G', 'A', 'G', 'A', 'T', 'C', 'A', 'C']
Sequence 2 is>
 ['A', 'C', 'T', 'T', 'C', 'T', 'A', 'T', 'A', 'C']


Result matrix is>

[1, 1, 0, 1, 0, 1, 0, 0, 1, 0]
[0, 0, 0, 0, 0, 0, 0, 1, 0, 1]
[0, 0, 0, 0, 0, 0, 1, 0, 0, 0]
[0, 0, 0, 0, 0, 0, 1, 0, 0, 0]
[0, 0, 0, 0, 0, 0, 0, 1, 0, 1]
[0, 0, 0, 0, 0, 0, 1, 0, 0, 0]
[1, 1, 0, 1, 0, 1, 0, 0, 1, 0]
[0, 0, 0, 0, 0, 0, 1, 0, 0, 0]
[1, 1, 0, 1, 0, 1, 0, 0, 1, 0]
[0, 0, 0, 0, 0, 0, 0, 1, 0, 1]

Identity is 25.0
PS E:\assignment\bioinformatic\Practicals> 
```

# Practical No:3

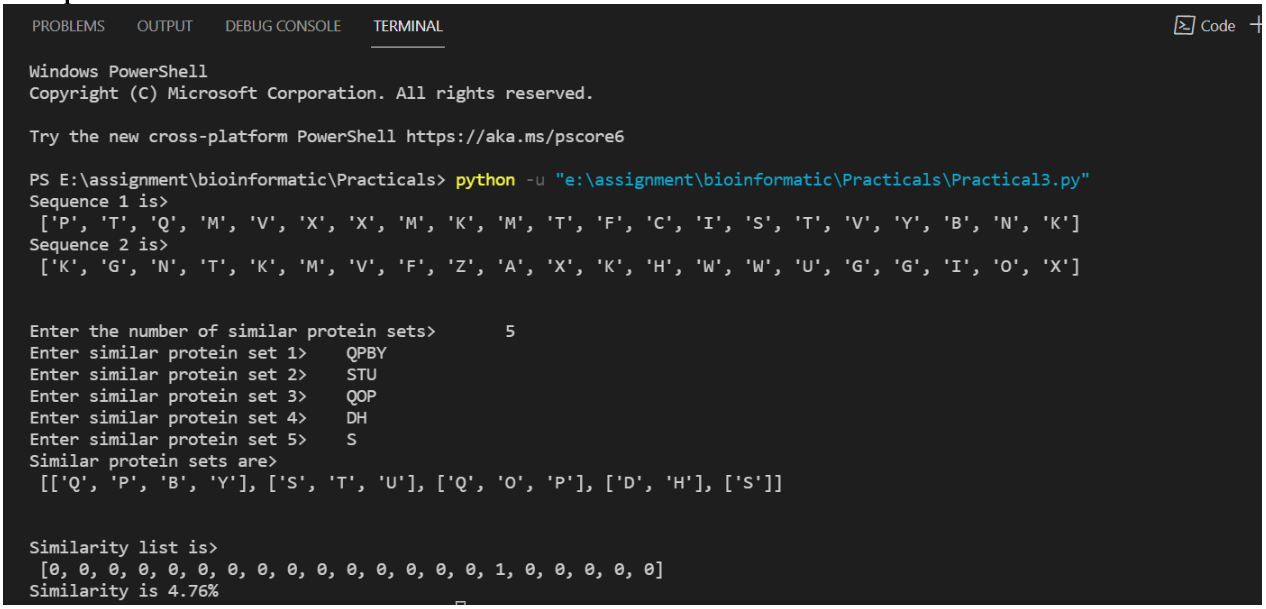
Aim: Write a Python/Java code to find the Similarity value of a given sequences. Take the sequence fromuser.

Code:

```
from random import choice, randint
from string import ascii_uppercase

sequence_list = []

def get_sequences():
        sequence_length = randint(8, 50)
        sequence_1 = [choice(ascii_uppercase) for i in range(sequence_length)]
        sequence_2 = [choice(ascii_uppercase) for i in range(sequence_length)]

        return sequence_1, sequence_2



def get_similar_protein_set():
        sequence_count = int(input("Enter the number of similar protein sets>\t"))

        global sequence_list
        for i in range(sequence_count):
                sequence_list.append(list(input(f"Enter similar protein set {i + 1}>\t")))



def check_similarity(char_1 : str, char_2 : str) -> bool:
        global sequence_list
        for i in sequence_list:
                if (char_1 != char_2):
                        if char_1 in i and char_2 in i:
                                return True

        return False



def similarity(sequence_1, sequence_2):
        similarity_list = [1 if i else 0 for i in list(map(check_similarity, sequence_1,
sequence_2))]
        similarity_value = sum(similarity_list)

        return similarity_value, similarity_list
```

```
if __name__ == "__main__":
    sequence_1, sequence_2 = get_sequences()
    print("Sequence 1 is>\n", sequence_1)
    print("Sequence 2 is>\n", sequence_2)
    print("\n")

    get_similar_protein_set()
    print("Similar protein sets are>\n", sequence_list)
    print("\n")

    similarity_value, similarity_list = similarity(sequence_1, sequence_2)
    print("Similarity list is>\n", similarity_list)
    print(f"Similarity is {round((similarity_value / len(sequence_1)) * 100, 2)}%")
```

Output:



```
Windows PowerShell
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PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical3.py"
Sequence 1 is>
 ['P', 'T', 'Q', 'M', 'V', 'X', 'X', 'M', 'K', 'M', 'T', 'F', 'C', 'I', 'S', 'T', 'V', 'Y', 'B', 'N', 'K']
Sequence 2 is>
 ['K', 'G', 'N', 'T', 'K', 'M', 'V', 'F', 'Z', 'A', 'X', 'K', 'H', 'W', 'W', 'U', 'G', 'G', 'I', 'O', 'X']


Enter the number of similar protein sets>       5
Enter similar protein set 1>    QPBY
Enter similar protein set 2>    STU
Enter similar protein set 3>    QOP
Enter similar protein set 4>    DH
Enter similar protein set 5>    S
Similar protein sets are>
 [['Q', 'P', 'B', 'Y'], ['S', 'T', 'U'], ['Q', 'O', 'P'], ['D', 'H'], ['S']]


Similarity list is>
 [0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0]
Similarity is 4.76%
```

# 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:

```
from random import choice, randint


def get_sequences(no_of_sequences : int):
    sequence_list = []
    print("Enter the sequences (All sequences should have equal length)>\t")

    for i in range(no_of_sequences):
        sequence_list.append(list(input(f"Enter sequence {i + 1}>\t")))

    return sequence_list



def get_random_sequences(no_of_sequences : int):
    sequence_length = randint(8, 20)
    sequence_list = [[choice('ABCDE') for j in range(sequence_length)] for i in
range(no_of_sequences)]
    return sequence_list



def multiple_sequence_alignment(sequence_list):
    output_sequence = []

    for i in range(len(sequence_list[0])):
        char_list = list()

        for j in range(len(sequence_list)):
            char_list.append(sequence_list[j][i])

        char_set = set(char_list)
        char_at_pos = ""

        if len(char_set) == 1:
            char_at_pos = char_set[0]

        elif len(sequence_list) % len(char_set) == 0:
            for i in char_set:
                char_at_pos += f"{i}/"
            char_at_pos = char_at_pos[: -1]

        else:
            largest_count = 0
            largest_char = None

            for i in char_set:
                if char_list.count(i) >= largest_count:
                    largest_char = i
                    largest_count = char_list.count(i)

            char_at_pos = largest_char.lower()

        output_sequence.append(char_at_pos)

    return output_sequence


if __name__ == "__main__":
```

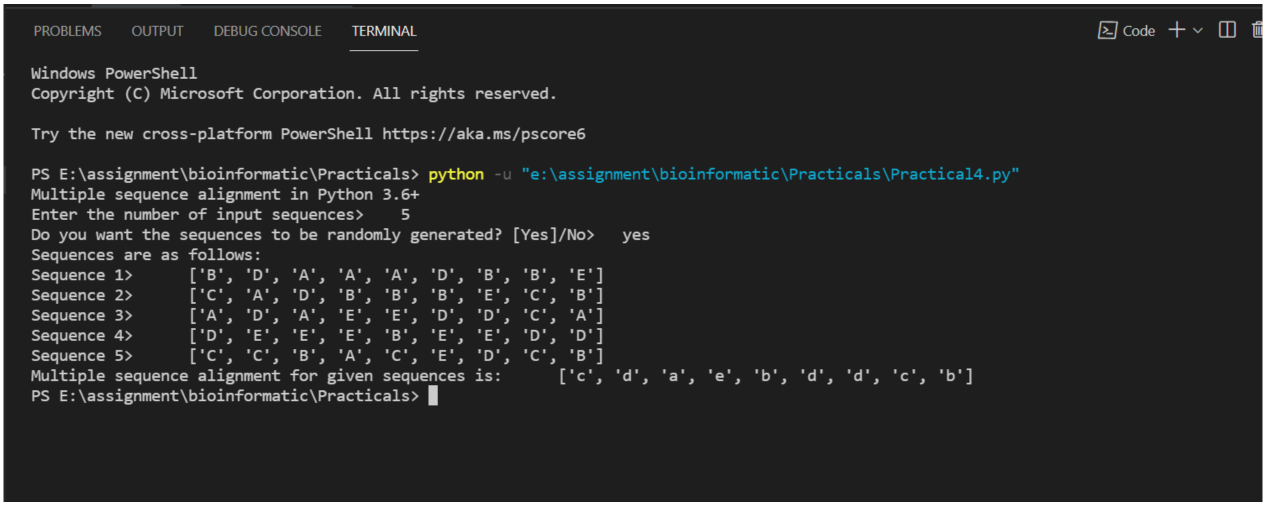
```
print("Multiple sequence alignment in Python 3.6+")
no_of_sequences = int(input("Enter the number of input sequences>\t"))

random_flag = False if input("Do you want the sequences to be randomly generated? [Yes]/No>\t").lower() == "no" else True
sequence_list = get_random_sequences(no_of_sequences) if random_flag else get_sequences(no_of_sequences)

print("Sequences are as follows:")
for i in range(len(sequence_list)):
    print(f"Sequence {i + 1}>\t", sequence_list[i])

print("Multiple sequence alignment for given sequences is:\t", multiple_sequence_alignment(sequence_list))
```

Output:



```
Windows PowerShell
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PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical4.py"
Multiple sequence alignment in Python 3.6+
Enter the number of input sequences>    5
Do you want the sequences to be randomly generated? [Yes]/No>   yes
Sequences are as follows:
Sequence 1>      ['B', 'D', 'A', 'A', 'A', 'D', 'B', 'B', 'E']
Sequence 2>      ['C', 'A', 'D', 'B', 'B', 'B', 'E', 'C', 'B']
Sequence 3>      ['A', 'D', 'A', 'E', 'E', 'D', 'D', 'C', 'A']
Sequence 4>      ['D', 'E', 'E', 'E', 'B', 'E', 'E', 'D', 'D']
Sequence 5>      ['C', 'C', 'B', 'A', 'C', 'E', 'D', 'C', 'B']
Multiple sequence alignment for given sequences is:      ['c', 'd', 'a', 'e', 'b', 'd', 'd', 'c', 'b']
PS E:\assignment\bioinformatic\Practicals> 
```

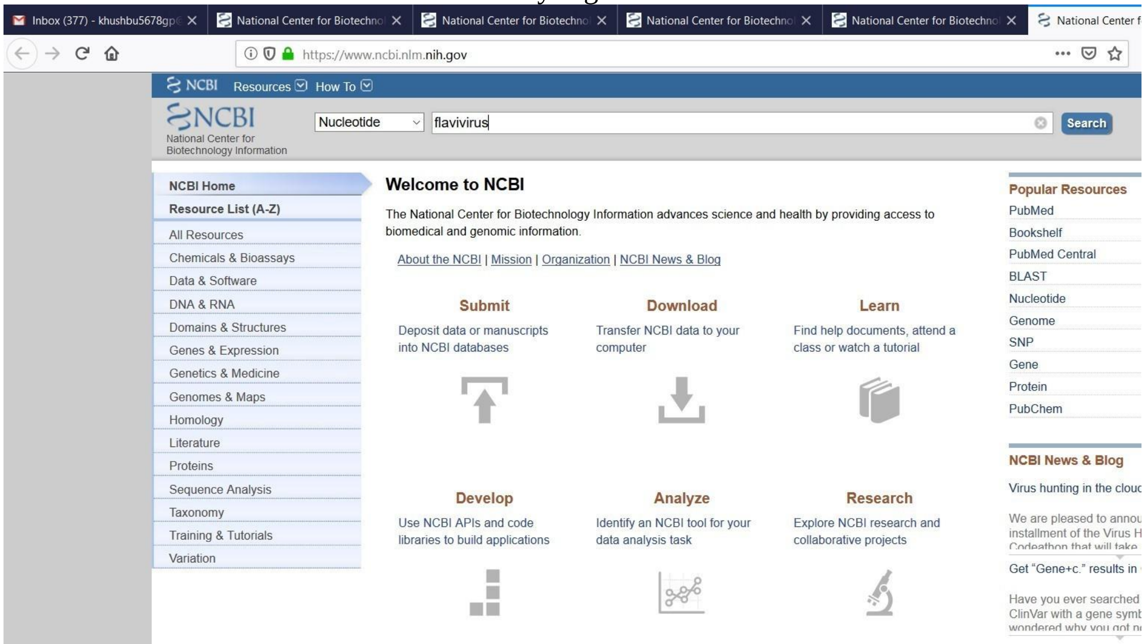
# Practical No:5

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.



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Get "Gene+c." results in
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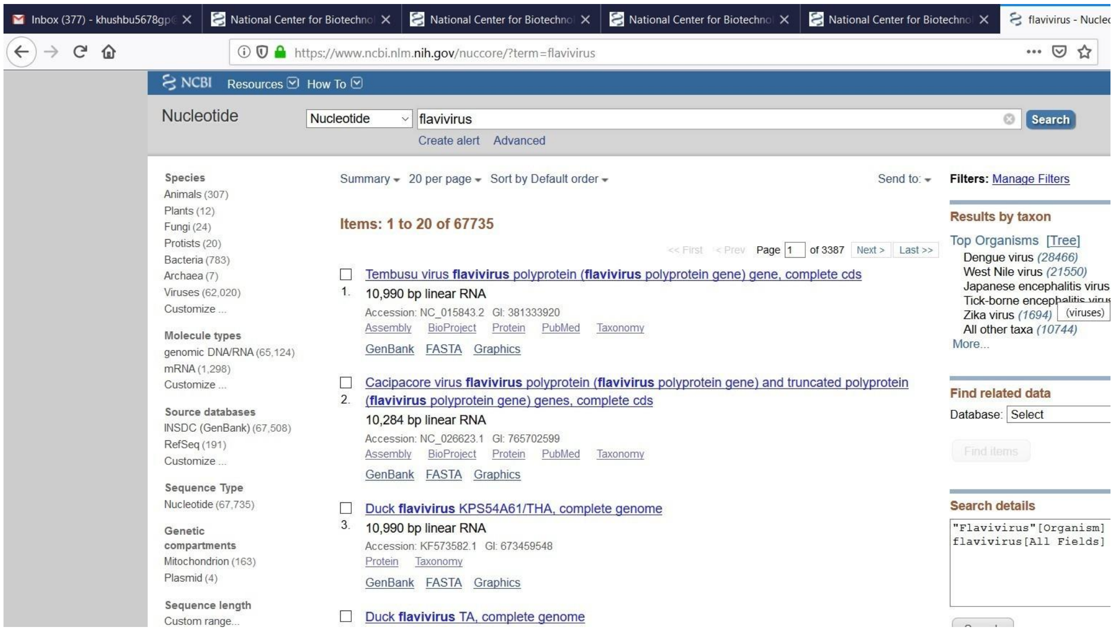


Items: 1 to 20 of 67735

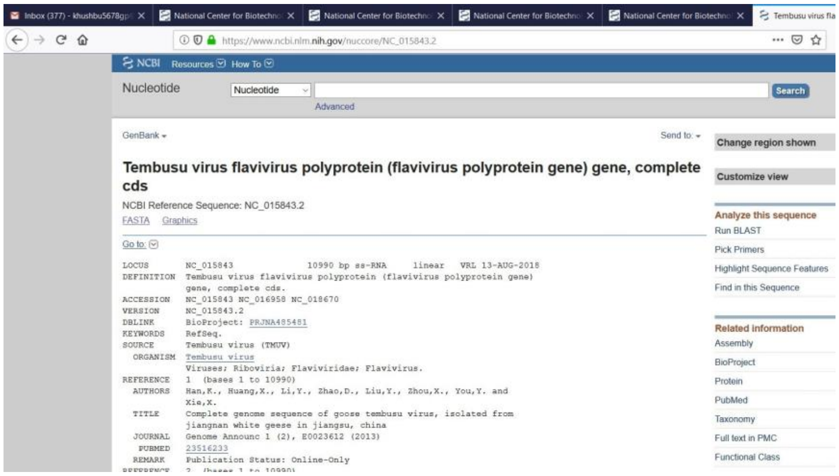
☐ 1. Tembusu virus **flavivirus** polyprotein (**flavivirus** polyprotein gene) gene, complete cds
10,990 bp linear RNA
Accession: NC_015843.2 GI: 381333920
Assembly BioProject Protein PubMed Taxonomy
GenBank FASTA Graphics

☐ 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: 765702599
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

```
"Flavivirus"[Organism]
flavivirus[All Fields]
```



https://www.ncbi.nlm.nih.gov/nuccore/NC_015843.2

Nucleotide | Nucleotide | Search | Advanced

GenBank | Send to:

**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
```

Change region shown

Customize view

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

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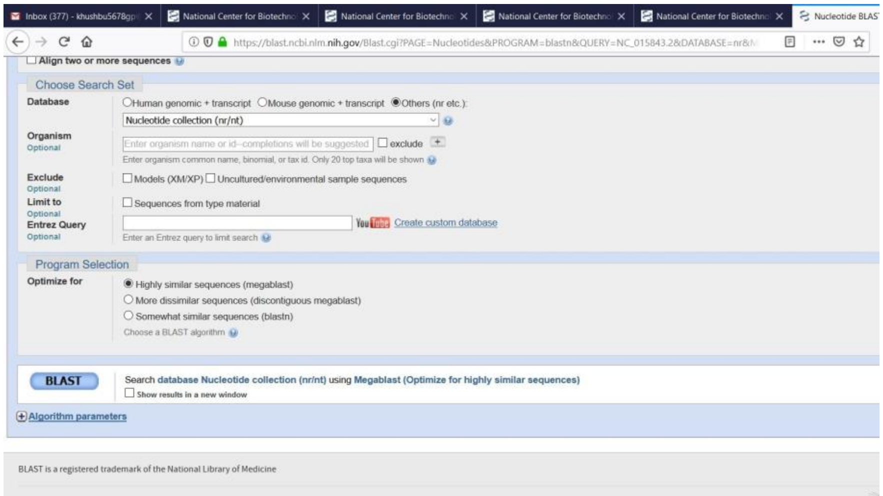
Tembusu virus fla
NCBI
Resources
How To

Run BLAST option we have to select



https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE=Nucleotides&PROGRAM=blastn&QUERY=NC_015843.2&DATABASE=nr&M

□ Align two or more sequences

Choose Search Set

Database: ○Human genomic + transcript ○Mouse genomic + transcript ●Others (nr etc.):

Nucleotide collection (nr/nt)

Organism (Optional): Enter organism name or id--completions will be suggested □ exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

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

Limit to (Optional): □ Sequences from type material

Entrez Query (Optional): Create custom database

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

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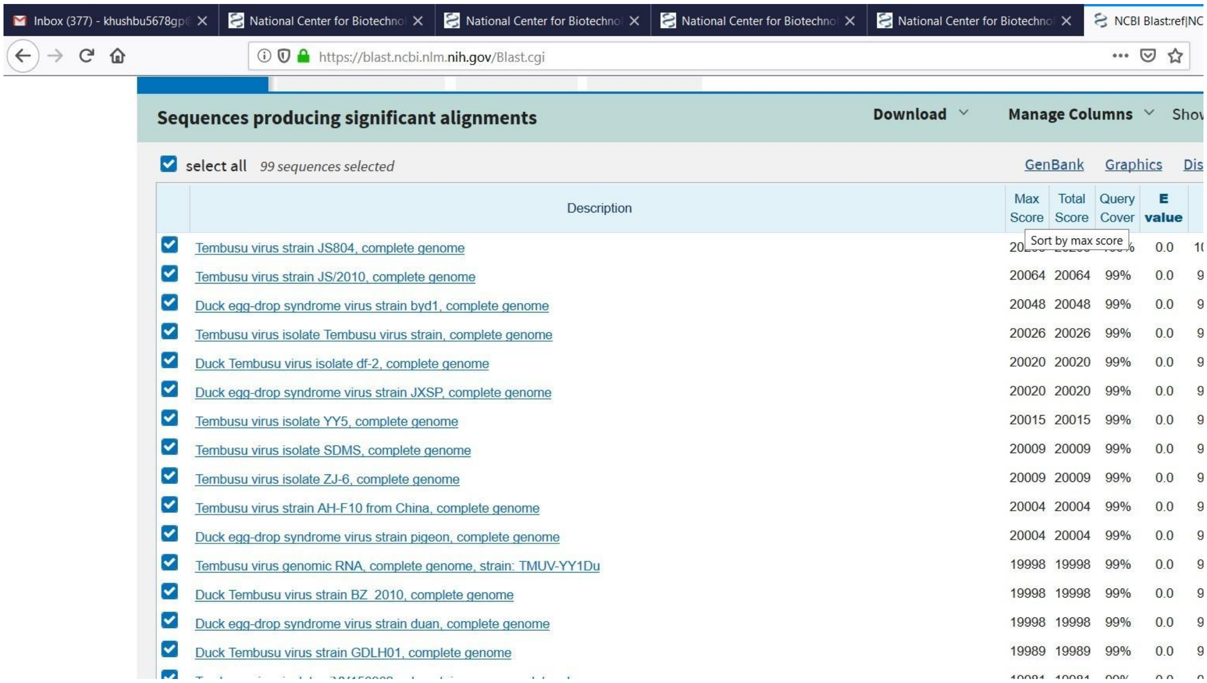
Nucleotide BLAS
BLAST

BLAST



https://blast.ncbi.nlm.nih.gov/Blast.cgi

**Sequences producing significant alignments**

Download | Manage Columns | Sho

☑ select all *99 sequences selected*

GenBank Graphics Dis

| | Description | Max Score | Total Score | Query Cover | E value | |
|---|---|---|---|---|---|---|
| ☑ | Tembusu virus strain JS804, complete genome | 20[illegible] | [illegible] | [illegible]% | 0.0 | 1( |
| ☑ | Tembusu virus strain JS/2010, complete genome | 20064 | 20064 | 99% | 0.0 | 9 |
| ☑ | Duck egg-drop syndrome virus strain byd1, complete genome | 20048 | 20048 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus isolate Tembusu virus strain, complete genome | 20026 | 20026 | 99% | 0.0 | 9 |
| ☑ | Duck Tembusu virus isolate df-2, complete genome | 20020 | 20020 | 99% | 0.0 | 9 |
| ☑ | Duck egg-drop syndrome virus strain JXSP, complete genome | 20020 | 20020 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus isolate YY5, complete genome | 20015 | 20015 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus isolate SDMS, complete genome | 20009 | 20009 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus isolate ZJ-6, complete genome | 20009 | 20009 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus strain AH-F10 from China, complete genome | 20004 | 20004 | 99% | 0.0 | 9 |
| ☑ | Duck egg-drop syndrome virus strain pigeon, complete genome | 20004 | 20004 | 99% | 0.0 | 9 |
| ☑ | Tembusu virus genomic RNA, complete genome, strain: TMUV-YY1Du | 19998 | 19998 | 99% | 0.0 | 9 |
| ☑ | Duck Tembusu virus strain BZ_2010, complete genome | 19998 | 19998 | 99% | 0.0 | 9 |
| ☑ | Duck egg-drop syndrome virus strain duan, complete genome | 19998 | 19998 | 99% | 0.0 | 9 |
| ☑ | Duck Tembusu virus strain GDLH01, complete genome | 19989 | 19989 | 99% | 0.0 | 9 |

Sort by max score

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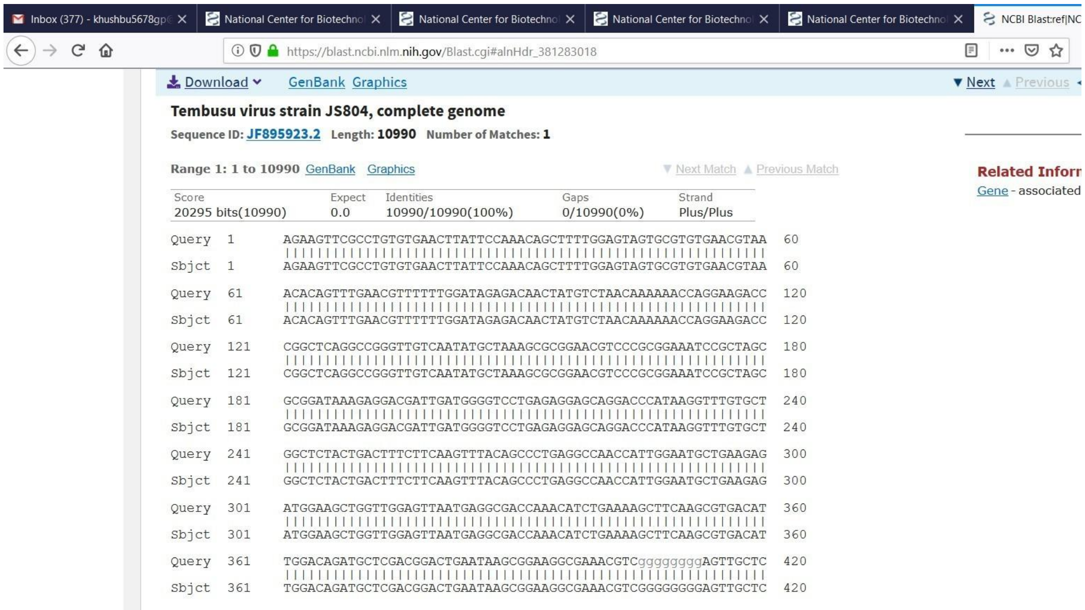
Here the result will be display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NCBI Blast:ref|NC
https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_381283018
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GenBank
Graphics
▼ Next
▲ Previous

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

Related Inforr

Gene - associated

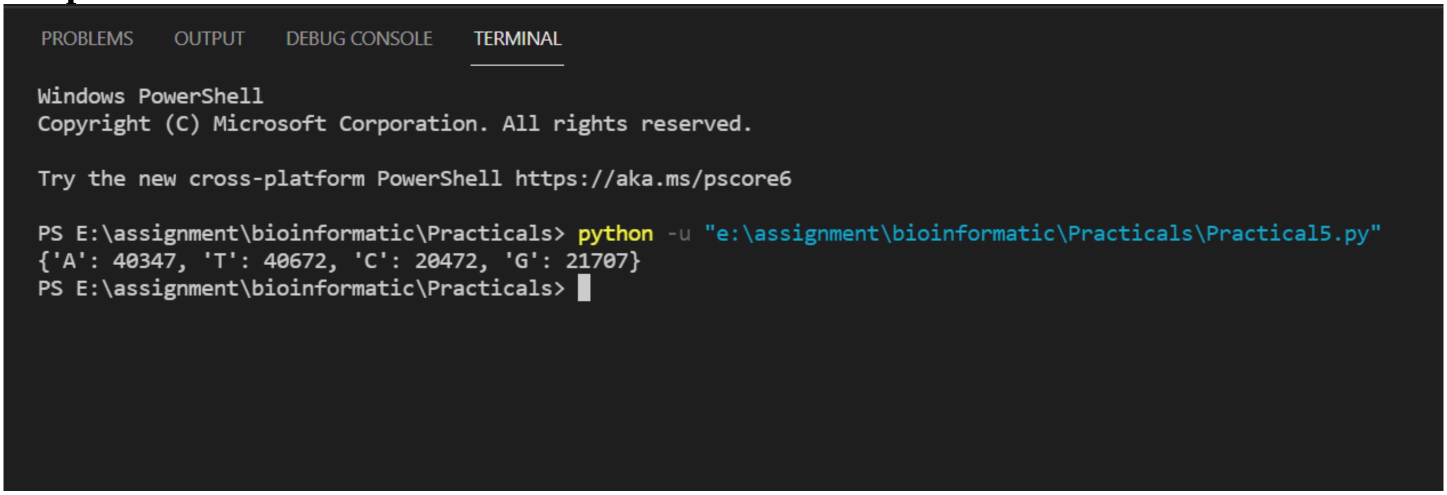
| Score | Expect | Identities | Gaps | Strand |
|---|---|---|---|---|
| 20295 bits(10990) | 0.0 | 10990/10990(100%) | 0/10990(0%) | Plus/Plus |

```
Query  1      AGAAGTTCGCCTGTGTGAACTTATTCCAAACAGCTTTTGGAGTAGTGCGTGTGAACGTAA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      AGAAGTTCGCCTGTGTGAACTTATTCCAAACAGCTTTTGGAGTAGTGCGTGTGAACGTAA  60

Query  61     ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACCAGGAAGACC  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     ACACAGTTTGAACGTTTTTTGGATAGAGACAACTATGTCTAACAAAAAACCAGGAAGACC  120

Query  121    CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCCCGCGGAAATCCGCTAGC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    CGGCTCAGGCCGGGTTGTCAATATGCTAAAGCGCGGAACGTCCCGCGGAAATCCGCTAGC  180

Query  181    GCGGATAAAGAGGACGATTGATGGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    GCGGATAAAGAGGACGATTGATGGGGTCCTGAGAGGAGCAGGACCCATAAGGTTTGTGCT  240

Query  241    GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTGGAATGCTGAAGAG  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    GGCTCTACTGACTTTCTTCAAGTTTACAGCCCTGAGGCCAACCATTGGAATGCTGAAGAG  300

Query  301    ATGGAAGCTGGTTGGAGTTAATGAGGCGACCAAACATCTGAAAAGCTTCAAGCGTGACAT  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    ATGGAAGCTGGTTGGAGTTAATGAGGCGACCAAACATCTGAAAAGCTTCAAGCGTGACAT  360

Query  361    TGGACAGATGCTCGACGGACTGAATAAGCGGAAGGCGAAACGTCggggggggAGTTGCTC  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    TGGACAGATGCTCGACGGACTGAATAAGCGGAAGGCGAAACGTCGGGGGGGGAGTTGCTC  420
```

## Code:-

```
fasta=open('seqdump.txt','r')
seq=fasta.read()
data={'A':seq.count('A'),'T':seq.count('T'),'C':seq.count('C'),'G':seq.count('G')}
print(data)
```

## Output:-



```
Windows PowerShell
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Try the new cross-platform PowerShell https://aka.ms/pscore6

PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical5.py"
{'A': 40347, 'T': 40672, 'C': 20472, 'G': 21707}
PS E:\assignment\bioinformatic\Practicals> 
```
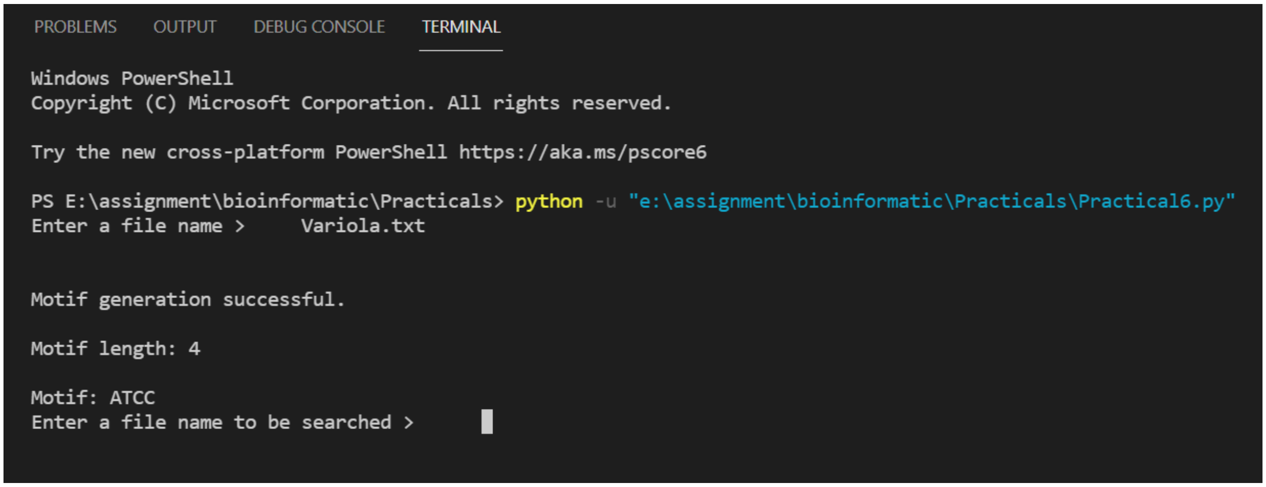

# Practical No:6

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

```
from random import randint

def motif(input_file_name : str) -> str:

    with open(input_file_name) as input_file_handle:

        input_file_data = input_file_handle.read()

        input_file_handle.close()



    input_file_data = input_file_data.replace("\n", "")



    #motif_length = randint(2, len(input_file_data) - 1)

    motif_length = randint(2, 10)

    start_index = randint(0, len(input_file_data) - motif_length)



    return input_file_data[start_index : start_index + motif_length]
```

```
def search_for_motif(motif : str, search_file_name : str) -> int:
    with open(search_file_name) as search_file_handle:
        search_file_data = search_file_handle.read()
        search_file_handle.close()

    search_file_data = search_file_data.replace("\n", "")

    index = search_file_data.find(motif)

    return index

if __name__ == "__main__":
    input_file_name = input("Enter a file name >\t")
    generated_motif = motif(input_file_name)
    print("\n\nMotif generation successful.")
    print(f"\nMotif length: {len(generated_motif)}")
    print(f"\nMotif: {generated_motif}")

    search_file_name = input("Enter a file name to be searched >\t")
    index = search_for_motif(generated_motif, search_file_name)



    if index > 0:

        print("Given motif is found at index:\t", index)

    else:

        print("Motif not found in document")
```

Output:



```
Windows PowerShell
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Try the new cross-platform PowerShell https://aka.ms/pscore6

PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical6.py"
Enter a file name >     Variola.txt


Motif generation successful.

Motif length: 4

Motif: ATCC
Enter a file name to be searched >
```
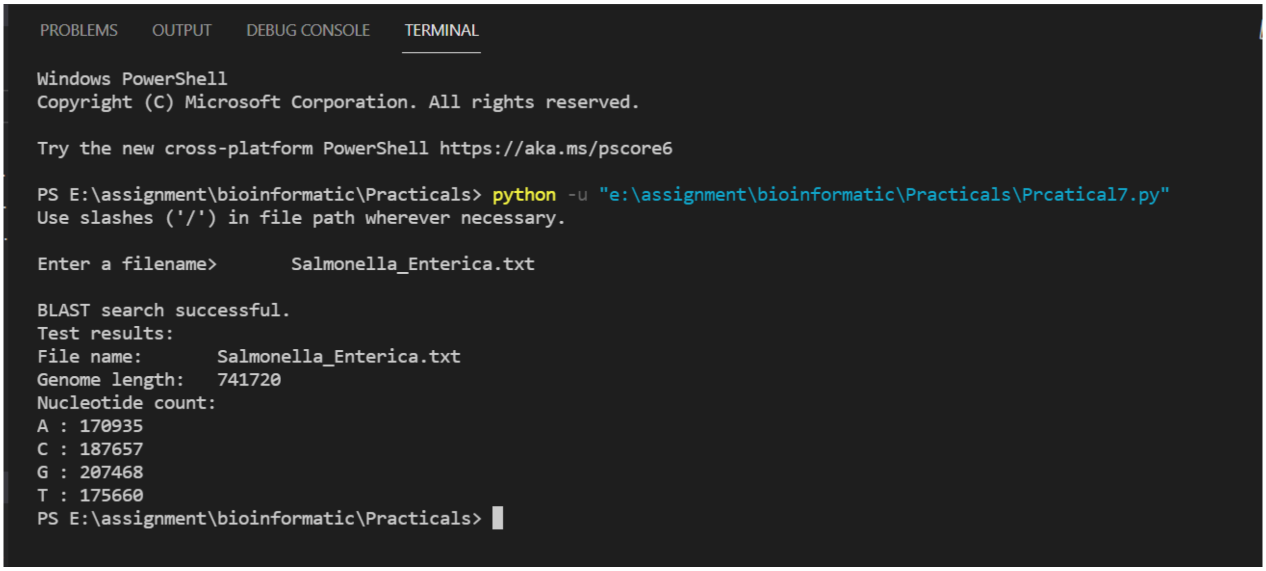

# Practical No:7

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:

```
if __name__ == "__main__":

    print("Use slashes ('/') in file path wherever
necessary.\n")

    file_handle = open(input("Enter a
filename>\t"))

    file_data = file_handle.read()

    file_handle.close()



    base_dict = {}



    for i in "ACGT":

        base_dict[i] = file_data.count(i)



    print("\nBLAST search successful.\nTest
results:")

    print(f"File name:\t
{file_handle.name.split('/')[- 1]}")

    print(f"Genome length:\t

{sum(base_dict.values())}")

    print(f"Nucleotide count:")



    for i in "ACGT":

        print(f"{i} : {base_dict[i]}")
```

Output:



```
Windows PowerShell
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Try the new cross-platform PowerShell https://aka.ms/pscore6

PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Prcatical7.py"
Use slashes ('/') in file path wherever necessary.

Enter a filename>       Salmonella_Enterica.txt

BLAST search successful.
Test results:
File name:       Salmonella_Enterica.txt
Genome length:   741720
Nucleotide count:
A : 170935
C : 187657
G : 207468
T : 175660
PS E:\assignment\bioinformatic\Practicals> 
```
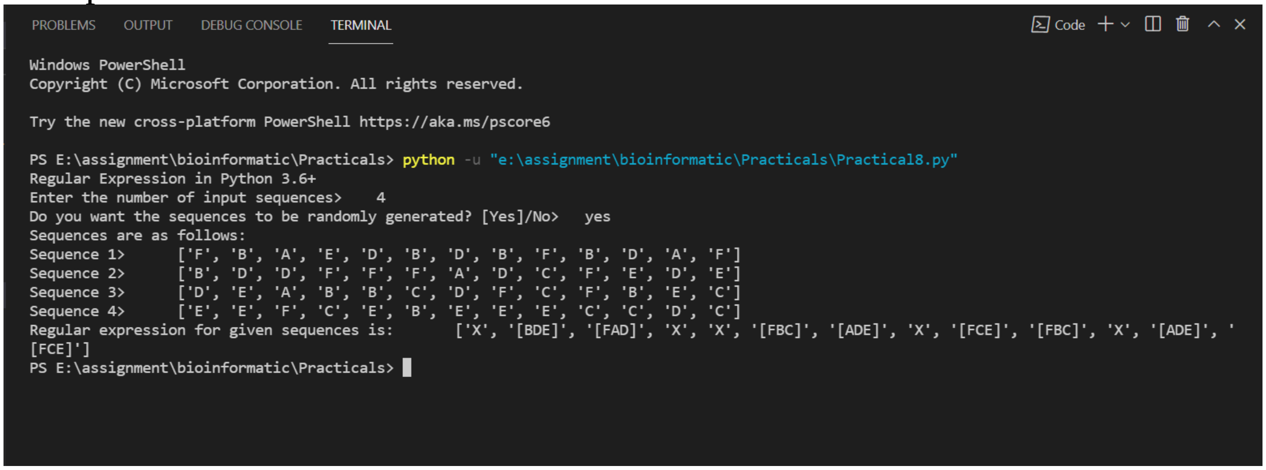

# Practical No:8

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:

```
from random import choice, randint
from string import ascii_uppercase

def get_sequences(no_of_sequences : int):
    sequence_list = []
    print("Enter the sequences (All sequences should have equal length)>\t")

    for i in range(no_of_sequences):
        sequence_list.append(list(input(f"Enter sequence {i + 1}>\t")))

    return sequence_list


def get_random_sequences(no_of_sequences : int):
    sequence_length = randint(8, 20)
    sequence_list = [[choice(ascii_uppercase[: 6]) for j in range(sequence_length)] for i in
range(no_of_sequences)]
    return sequence_list


def get_regular_expression(sequence_list):
    output_sequence = []

    for i in range(len(sequence_list[0])):
        char_column = set()

        for j in range(len(sequence_list)):
            if sequence_list[j][i] != '-':
                char_column.add(sequence_list[j][i])

        char_at_i = ""
        if len(char_column) == 1:
            char_at_i = char_column[0]

        else:
            if len(char_column) == len(sequence_list):
                char_at_i = 'X'
            else:
                char_at_i += "["
                for i in char_column:
                    char_at_i += i
                char_at_i += "]"

        output_sequence.append(char_at_i)

    return output_sequence

if __name__ == "__main__":
    print("Regular Expression in Python 3.6+")
    no_of_sequences = int(input("Enter the number of input sequences>\t"))

    random_flag = False if input("Do you want the sequences to be randomly generated?
[Yes]/No>\t").lower() == "no" else True
    sequence_list = get_random_sequences(no_of_sequences) if random_flag else
get_sequences(no_of_sequences)

    print("Sequences are as follows:")
    for i in range(len(sequence_list)):
        print(f"Sequence {i + 1}>\t", sequence_list[i])

    print("Regular expression for given sequences is:\t", get_regular_expression(sequence_list))
```

Output:



```
Windows PowerShell
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Try the new cross-platform PowerShell https://aka.ms/pscore6

PS E:\assignment\bioinformatic\Practicals> python -u "e:\assignment\bioinformatic\Practicals\Practical8.py"
Regular Expression in Python 3.6+
Enter the number of input sequences>    4
Do you want the sequences to be randomly generated? [Yes]/No>   yes
Sequences are as follows:
Sequence 1>      ['F', 'B', 'A', 'E', 'D', 'B', 'D', 'B', 'F', 'B', 'D', 'A', 'F']
Sequence 2>      ['B', 'D', 'D', 'F', 'F', 'F', 'A', 'D', 'C', 'F', 'E', 'D', 'E']
Sequence 3>      ['D', 'E', 'A', 'B', 'B', 'C', 'D', 'F', 'C', 'F', 'B', 'E', 'C']
Sequence 4>      ['E', 'E', 'F', 'C', 'E', 'B', 'E', 'E', 'E', 'C', 'C', 'D', 'C']
Regular expression for given sequences is:       ['X', '[BDE]', '[FAD]', 'X', 'X', '[FBC]', '[ADE]', 'X', '[FCE]', '[FBC]', 'X', '[ADE]', '
[FCE]']
PS E:\assignment\bioinformatic\Practicals> 
```
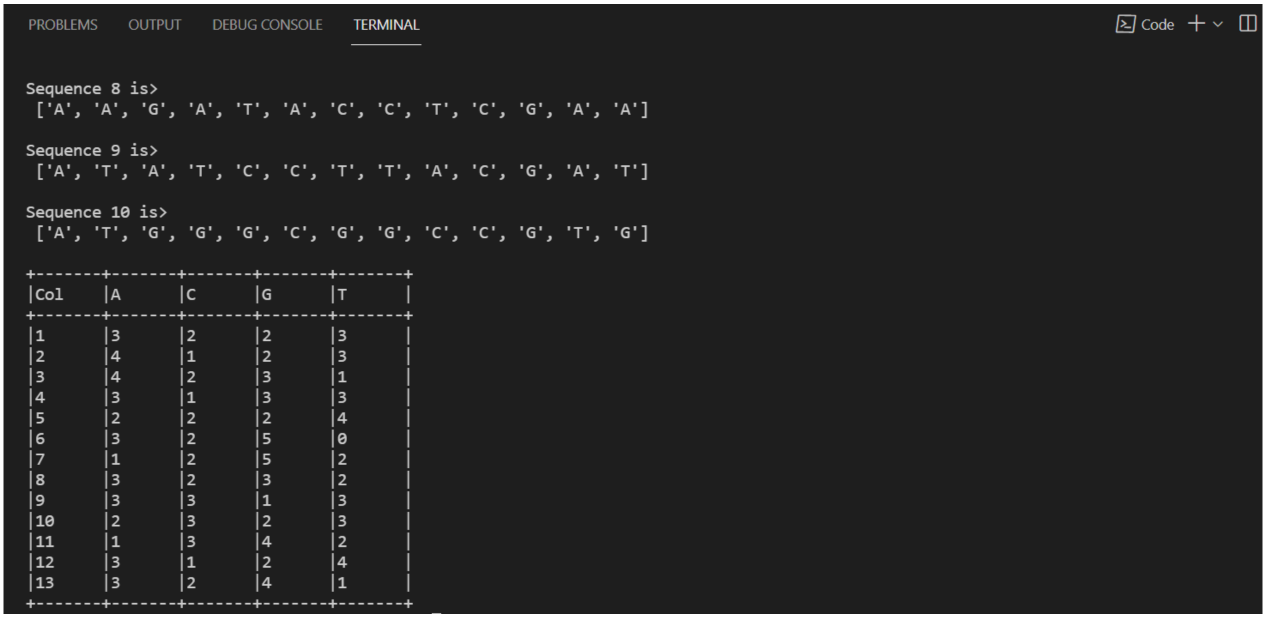

# Practical No:9

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

Code:

```
from random import choice, randint
import sys

def generate_sequences():
    sequence_length = randint(8, 20)
    sequence_count = randint(8, 20)

    return [[choice("ACTG") for i in range(sequence_length)] for j in
range(sequence_count)]


def calculate_fingerprint(sequence_list):
    fingerprint_list = []

    for j in range(len(sequence_list[0])):
        finger_print_dict = dict()

        for i in range(len(sequence_list)):
            finger_print_dict[sequence_list[i][j]] =
finger_print_dict.get(sequence_list[i][j], 0) + 1

        for i in 'ACTG':
            if i not in finger_print_dict:
                finger_print_dict[i] = 0
            fingerprint_list.append(finger_print_dict)

    return fingerprint_list


def print_result(fingerprint_list):

    print("+-------+-------+-------+-------+-------+")
    print("|Col\t|A\t|C\t|G\t|T\t|")
    print("+-------+-------+-------+-------+-------+")

    for i in range(len(fingerprint_list)):
        print(f"|{i + 1}\t|{fingerprint_list[i]['A']}\t|{fingerprint_list[i]['C']}\t|{fingerprint_list[i]['G']}\t|{fingerprint_list[i]['T']}\t|")

    print("+-------+-------+-------+-------+-------+")


if __name__ == "__main__":
    sequence_list = generate_sequences()

    for i in range(len(sequence_list)):
        print(f"Sequence {i + 1} is>\n", sequence_list[i], "\n")

    fingerprint_list = calculate_fingerprint(sequence_list)
    print_result(fingerprint_list)
```

Output:



```
Sequence 8 is>
 ['A', 'A', 'G', 'A', 'T', 'A', 'C', 'C', 'T', 'C', 'G', 'A', 'A']

Sequence 9 is>
 ['A', 'T', 'A', 'T', 'C', 'C', 'T', 'T', 'A', 'C', 'G', 'A', 'T']

Sequence 10 is>
 ['A', 'T', 'G', 'G', 'G', 'C', 'G', 'G', 'C', 'C', 'G', 'T', 'G']

+-------+-------+-------+-------+-------+
|Col    |A      |C      |G      |T      |
+-------+-------+-------+-------+-------+
|1      |3      |2      |2      |3      |
|2      |4      |1      |2      |3      |
|3      |4      |2      |3      |1      |
|4      |3      |1      |3      |3      |
|5      |2      |2      |2      |4      |
|6      |3      |2      |5      |0      |
|7      |1      |2      |5      |2      |
|8      |3      |2      |3      |2      |
|9      |3      |3      |1      |3      |
|10     |2      |3      |2      |3      |
|11     |1      |3      |4      |2      |
|12     |3      |1      |2      |4      |
|13     |3      |2      |4      |1      |
+-------+-------+-------+-------+-------+
```