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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                                    Code

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, 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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                Code

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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                    Code

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, 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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                   Code

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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>
```

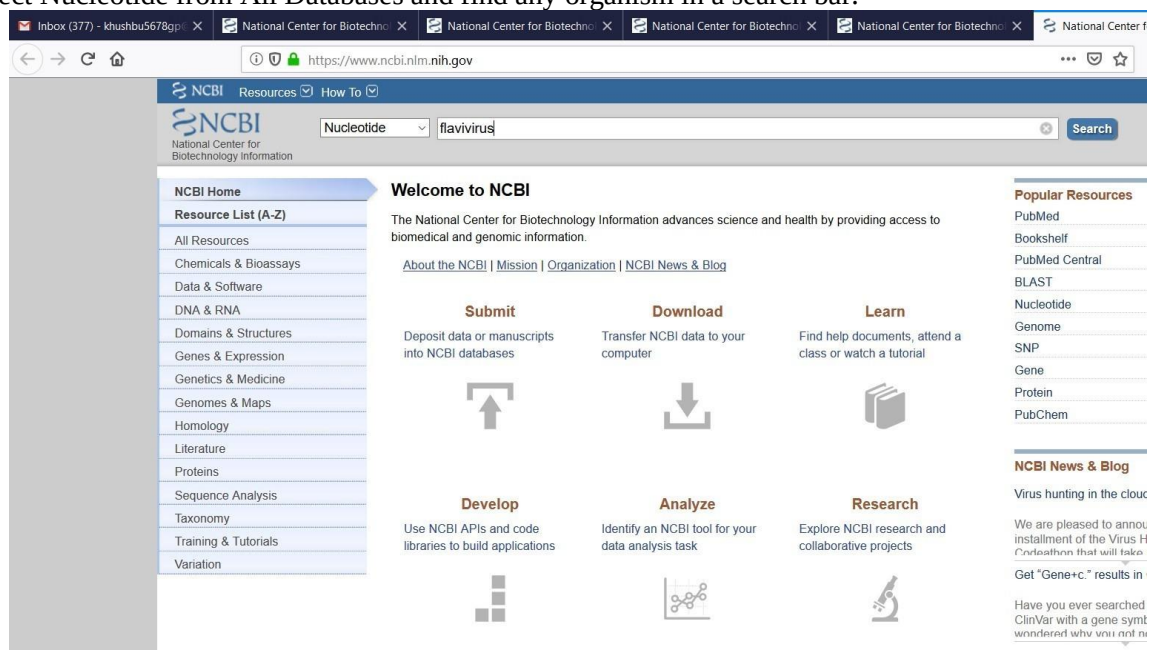
Practical No:5

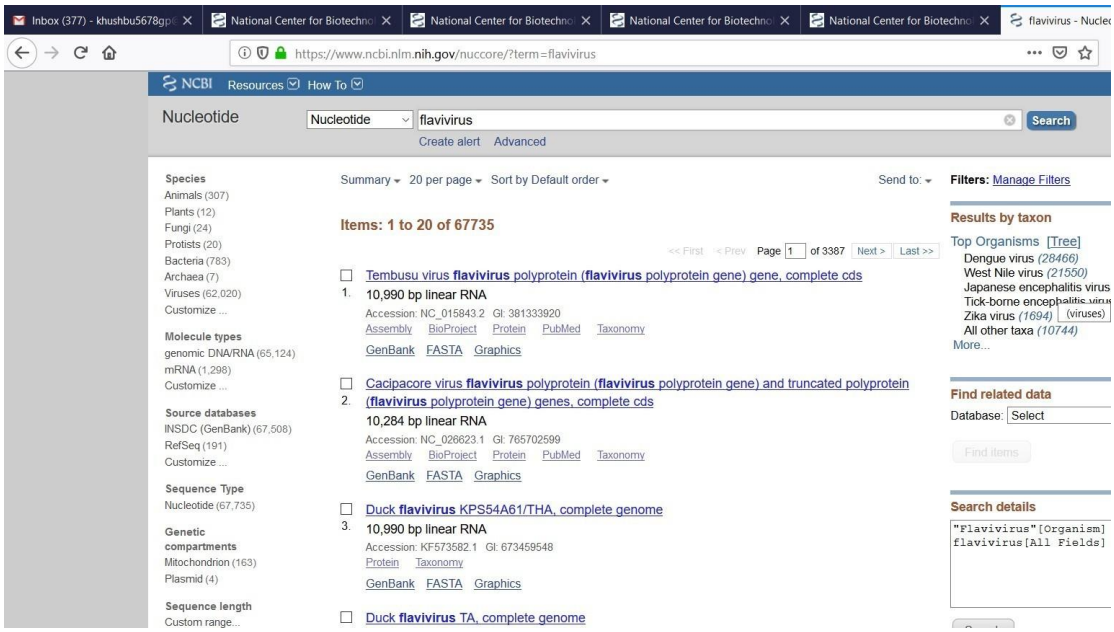
Aim: Perform a BLAST search on a specific gene sequence of a specify organism.

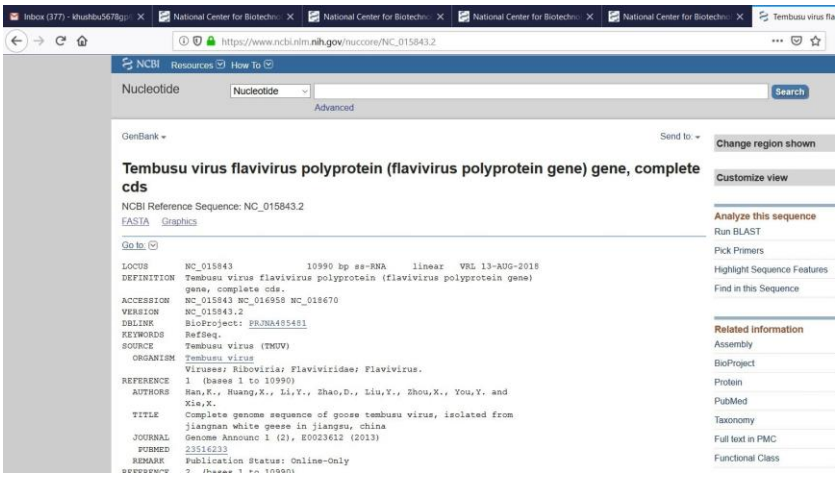
Steps:

Go to the National Center for Biotechnology Information Site https://www.ncbi.nlm.nih.gov/

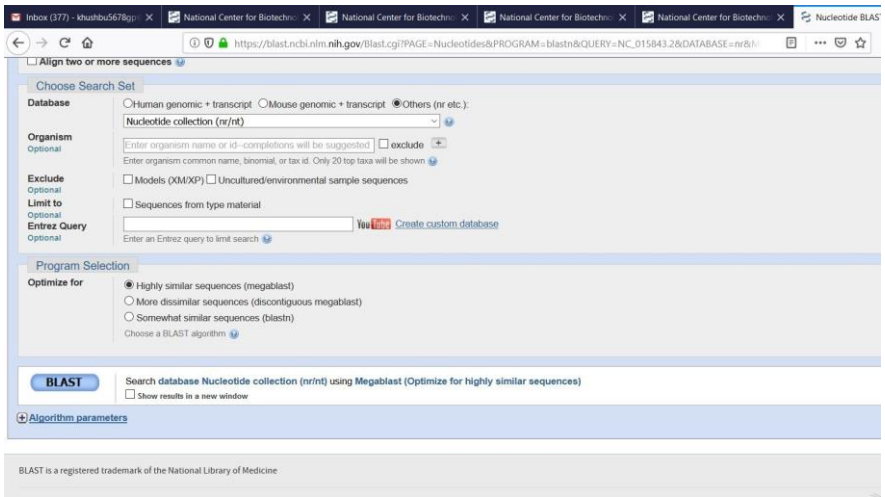
Select Nucleotide from All Databases and find any organism in a search bar.



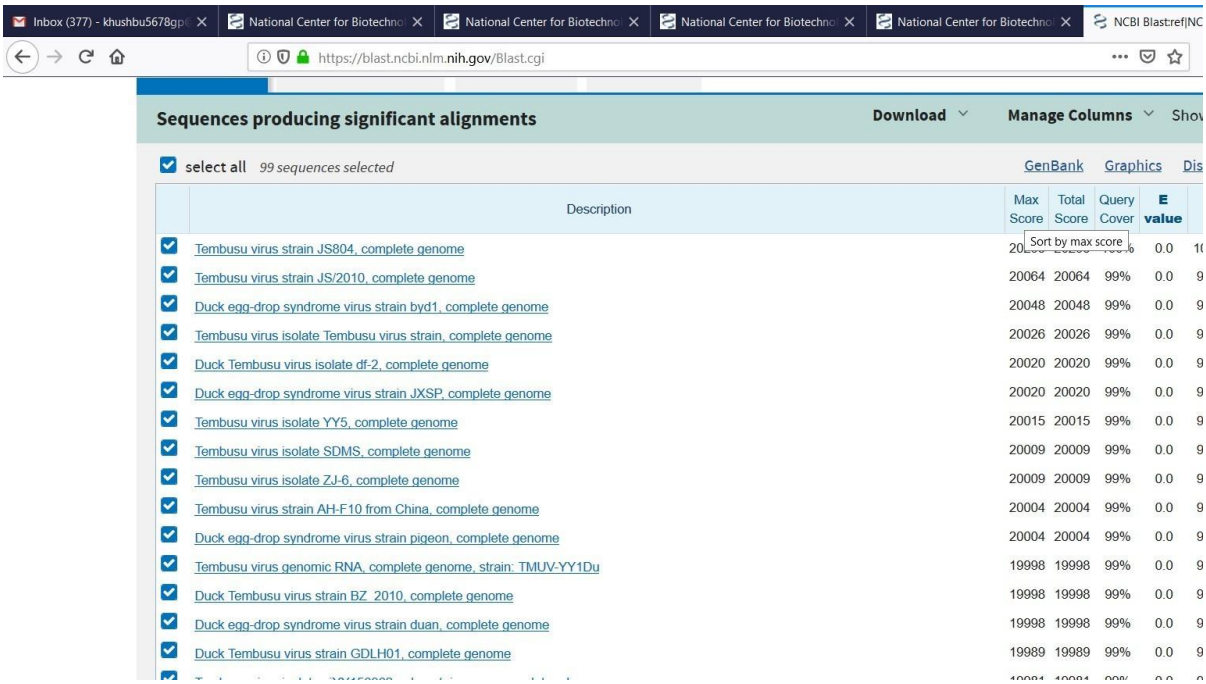




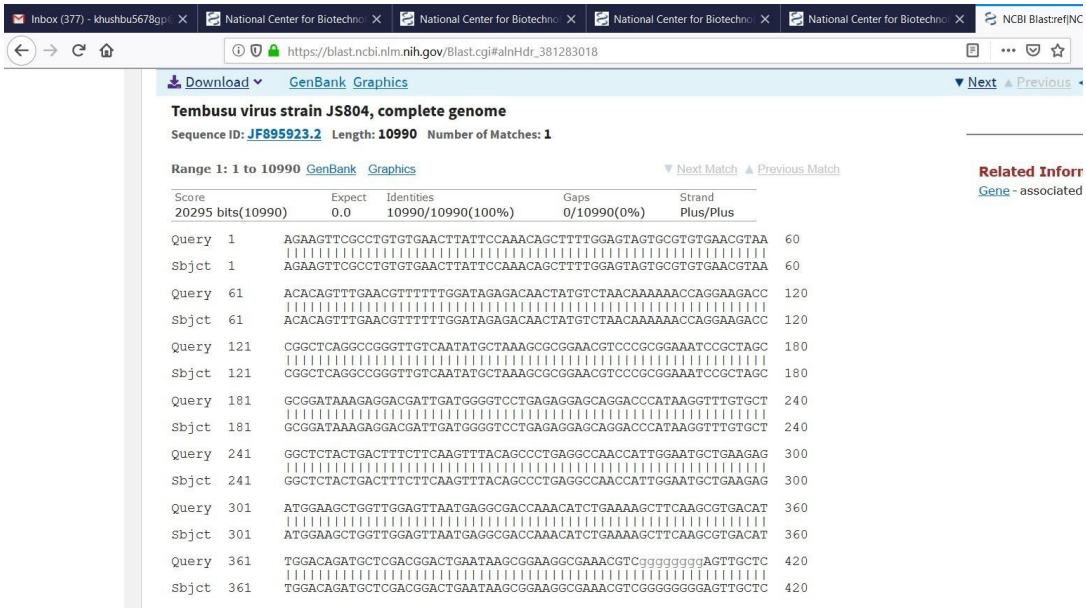
Run BLAST option we have to select



BLAST



Here the result will be display



Inbox (377) - khushbu5678gp | National Center for Biotechno | National Center for Biotechno | National Center for Biotechno | National Center for Biotechno | NCBI Blast:ref|NC

https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_381283018

Download 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    TGGACAGATGCTCGACGGACTGAATAAGCGGAAGGCGAAACGTCgggggggAGTTGCTC  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:-

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL

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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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL

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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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL

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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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                                    Code

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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|{fin
gerprint_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:

```
PROBLEMS    OUTPUT    DEBUG CONSOLE    TERMINAL                                   Code

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      |
+-------+-------+-------+-------+-------+
```