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Practical 1

Aim: Write a Python3/Java program to perform pairwise alignment.

Code:

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


def get_sequences() → tuple[list[str]]:
    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 : list[str]) → list[str]:
    sequence.insert(randint(0, len(sequence) - 1), '-')


    return sequence
```

```
def insert_gaps(sequence_1 : list[str], sequence_2 :
list[str]) → tuple[list[str]]:
    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 : list[str],
sequence_2 : list[str]) → list[str]:
    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:

```
C:\Temp\Bioinformatics>python pairwise_alignment.py
Sequence 1 is>
 ['C', 'C', 'T', 'G', 'G', 'G', 'A', 'C', 'C', 'C', 'G', 'G', 'C', 'T', 'T', 'C', 'A', 'G', 'T', 'A', '
T', 'C', 'A', 'G', 'C', 'T', 'G', 'T', 'T', 'T', 'C', 'C', 'G', 'C', 'G', 'A', 'C', 'T', 'A', 'T', 'T',
 'C', 'G', 'C', 'T', 'T', 'A', 'A', 'C']
Sequence 2 is>
 ['A', 'T', 'T', 'A', 'T', 'G', 'G', 'A', 'T', 'C', 'C', 'T', 'G', 'G', 'G', 'T', 'A', 'A', 'A', 'G', '
C', 'T', 'T', 'C', 'C', 'G', 'G', 'T', 'A', 'G', 'T', 'G', 'A', 'A', 'C', 'A', 'A']


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


Score list is>
 [0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 1, 1, 0, 0,
 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0]
Score is 13
```

Practical 2

Aim: Write a Python3/Java program to calculate identity of two sequences.

Code:

```
from random import choice, randint


def get_sequences() → tuple[list[str]]:
    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 : list[str], sequence_2 :
list[str]) → tuple[int, list[list[int]]]:


    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 : list[list[int]]):
    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:

```
C:\Temp\Bioinformatics>python identity.py
Sequence 1 is>
 ['A', 'A', 'C', 'A', 'C', 'A', 'C', 'C', 'C', 'A', 'T', 'A']
Sequence 2 is>
 ['T', 'A', 'A', 'C', 'T', 'A', 'G', 'C', 'G', 'A', 'A', 'C']


Result matrix is>

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

Identity is 32.64
```

Practical 3

Aim: Write a Python3/Java program to calculate similarity of two sequences.

Code:

```
from random import choice, randint

from string import ascii_uppercase


sequence_list = []


def get_sequences() → tuple[list[str]]:

    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 : list[str], sequence_2 :
list[str]) → tuple[int, list[str]]:
```

```
    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:

```
C:\Temp\Bioinformatics>python similarity.py
Sequence 1 is>
 ['B', 'T', 'P', 'P', 'H', 'G', 'H', 'N', 'T', 'Z', 'I', 'J', 'G', 'E', 'K', 'Z', 'S', 'T', 'X', 'M', '
C', 'S', 'I', 'R', 'E', 'Y', 'Z', 'J', 'O', 'J', 'E', 'R', 'L']
Sequence 2 is>
 ['C', 'Y', 'D', 'O', 'X', 'T', 'O', 'G', 'E', 'P', 'W', 'O', 'T', 'C', 'C', 'Q', 'X', 'C', 'Q', 'Z', '
F', 'K', 'D', 'J', 'L', 'B', 'H', 'G', 'R', 'D', 'B', 'P', 'N']


Enter the number of similar protein sets>       5
Enter similar protein set 1>    QPBRY
Enter similar protein set 2>    WYT
Enter similar protein set 3>    PX
Enter similar protein set 4>    SBEXC
Enter similar protein set 5>    GA
Similar protein sets are>
 [['Q', 'P', 'B', 'R', 'Y'], ['W', 'Y', 'T'], ['P', 'X'], ['S', 'B', 'E', 'X', 'C'], ['G', 'A']]


Similarity list is>
 [1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 1, 0]
Similarity is 21.21%
```

Practical 4

Aim: Write a Python3/Java program to calculate percentage of matching of two sequences.

Code:

```
from random import choice, randint

from string import ascii_uppercase

from operator import eq


sequence_list = []


def get_sequences() → tuple[list[str]]:


    sequence_1 = [choice(ascii_uppercase) for i in
range(randint(8, 50))]

    sequence_2 = [choice(ascii_uppercase) for i in
range(randint(8, 50))]


    return sequence_1, sequence_2
```

```
def insert_gap(sequence : list[str]) → list[str]:
    sequence.insert(randint(0, len(sequence) - 1), '-')

    return sequence



def insert_gaps(sequence_1 : list[str], sequence_2 :
list[str]) → tuple[list[str]]:
    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 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 : list[str], sequence_2 :
list[str]) → int:
    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
```

```
def identity(sequence_1 : list[str], sequence_2 :
list[str]) → int:


    return sum(map(eq, sequence_1, sequence_2))



def count_gaps(sequence_1 : list[str], sequence_2 :
list[str]) → int:
    return sequence_1.count("-") +
sequence_2.count("-")



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")


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


    similarity_value = similarity(sequence_1,
sequence_2)
    identity_value = identity(sequence_1, sequence_2)
    gap_count = count_gaps(sequence_1, sequence_2)


    print("Similarity value is>\t", similarity_value)
    print("Identity value is>\t", identity_value)
    print("Gap count is>\t", gap_count)
    print("\n")
```

```
    print(f"Percentage of matching is
{round(((similarity_value + identity_value) /
(len(sequence_1) - gap_count)) * 100, 2)}%")
```

Output:

```
C:\Temp\Bioinformatics>python percent_matching.py
Sequence 1 is>
 ['H', 'B', 'Z', 'E', 'N', 'M', 'E', 'O', 'N', 'R', 'E', 'J', 'F', 'C', 'N', 'R', 'F', 'A']
Sequence 2 is>
 ['B', 'B', 'Q', 'F', 'G', 'X', 'J', 'X', 'S', 'P', 'B', 'Z', 'D', 'W', 'N', 'X', 'Z', 'E', 'T', 'Y', '
C', 'U']


Sequence 1 after adding gaps is>
 ['H', 'B', 'Z', 'E', 'N', 'M', 'E', 'O', 'N', 'R', 'E', 'J', '-', '-', 'F', '-', 'C', 'N', '-', 'R', '
F', 'A']
Sequence 2 after adding gaps is>
 ['B', 'B', 'Q', 'F', 'G', 'X', 'J', 'X', 'S', 'P', 'B', 'Z', 'D', 'W', 'N', 'X', 'Z', 'E', 'T', 'Y', '
C', 'U']


Enter the number of similar protein sets>       5
Enter similar protein set 1>    PX
Enter similar protein set 2>    GA
Enter similar protein set 3>    WYT
Enter similar protein set 4>    SBEXC
Enter similar protein set 5>    QPBRY

Similar protein sets are>
 [['P', 'X'], ['G', 'A'], ['W', 'Y', 'T'], ['S', 'B', 'E', 'X', 'C'], ['Q', 'P', 'B', 'R', 'Y']]
```

```
Similarity value is>     3
Identity value is>       1
Gap count is>    4


Percentage of matching is 22.22%
```

Practical 5

Aim: Write a Python3/Java program to generate a scoring matrix for global alignment of a pair of sequences.

Code:

```
from random import randint, choice

from math import inf


def generate_sequences() → tuple[list[str]]:

    sequence_1 = [choice(('A', 'C', 'T', 'G')) for i in
range(randint(6, 7))]

    sequence_2 = [choice(('A', 'C', 'T', 'G')) for i in
range(randint(6, 7))]


    return sequence_1, sequence_2



class GlobalAlignment:


    @staticmethod
```

```
    def generate_scoring_matrix(sequence_1:list[str],
sequence_2:list[str]) → list[list[list[int,
list[str]]]]:
        sequence_1.insert(0, '-')
        sequence_2.insert(0, '-')
        result_matrix = [[[0] for i in
range(len(sequence_2))] for j in
range(len(sequence_1))]


        for i in range(1, len(sequence_1)):
            result_matrix[i][0][0] = result_matrix[i -
1][0][0] - 2
            result_matrix[i][0].append(["up"])


        for j in range(1, len(sequence_2)):
            result_matrix[0][j][0] = result_matrix[0]
[j - 1][0] - 2
            result_matrix[0][j].append(["besides"])


        for i in range(1, len(sequence_1)):
            for j in range(1, len(sequence_2)):
                besides_value = result_matrix[i][j -
1][0] - 2
```

```
                up_value = result_matrix[i - 1][j][0]
- 2
                diagonal_value = result_matrix[i - 1]
[j - 1][0]

                additive_value = None
                direction = []

                if(sequence_1[i] == '-') or
(sequence_2[j] == '-'):
                    additive_value = - 2
                elif (sequence_1[i] != sequence_2[j]):
                    additive_value = - 1
                elif (sequence_1[i] == sequence_2[j]):
                    additive_value = 1

                diagonal_value += additive_value

                largest_value = besides_value
                direction.append("besides")

                if (largest_value < up_value):
```

```
                    largest_value = up_value
                    direction[0] = "up"

                elif (largest_value == up_value):
                    direction.append("up")

                if (largest_value < diagonal_value):
                    largest_value = diagonal_value
                    direction[0] = "diagonal"
                    if len(direction) > 1:
                        direction.pop()

                elif (largest_value ==
diagonal_value):
                    largest_value = diagonal_value
                    direction.append("diagonal")



                result_matrix[i][j][0] = largest_value
                result_matrix[i][j].append(direction)

        return result_matrix
```

```
    @staticmethod
    def
print_scoring_matrix(result_matrix:list[list[list[int,
list[str]]]]):
        for i in range(len(result_matrix)):
            print(result_matrix[i])
            print("\n")



if __name__ == "__main__":
    sequence_1, sequence_2 = generate_sequences()

    print("Sequence 1 is:\t", sequence_1)
    print("Sequence 2 is:\t", sequence_2)

    result_matrix =
GlobalAlignment.generate_scoring_matrix(sequence_1,
sequence_2)
    print("Scoring matrix is:")
    GlobalAlignment.print_scoring_matrix(result_matrix)
```

Output:

```
C:\Temp\Bioinformatics>python global_alignment.py
Sequence 1 is:   ['A', 'C', 'C', 'C', 'T', 'T']
Sequence 2 is:   ['C', 'A', 'T', 'G', 'G', 'C']
Scoring matrix is:
[[0], [-2, ['besides']], [-4, ['besides']], [-6, ['besides']], [-8, ['besides']], [-10, ['besides']], [
-12, ['besides']]]


[[-2, ['up']], [-1, ['diagonal']], [-1, ['diagonal']], [-3, ['besides']], [-5, ['besides']], [-7, ['bes
ides']], [-9, ['besides']]]


[[-4, ['up']], [-1, ['diagonal']], [-2, ['diagonal']], [-2, ['diagonal']], [-4, ['besides', 'diagonal']
], [-6, ['besides', 'diagonal']], [-6, ['diagonal']]]


[[-6, ['up']], [-3, ['up', 'diagonal']], [-2, ['diagonal']], [-3, ['diagonal']], [-3, ['diagonal']], [-
5, ['besides', 'diagonal']], [-5, ['diagonal']]]


[[-8, ['up']], [-5, ['up', 'diagonal']], [-4, ['up', 'diagonal']], [-3, ['diagonal']], [-4, ['diagonal'
]], [-4, ['diagonal']], [-4, ['diagonal']]]


[[-10, ['up']], [-7, ['up']], [-6, ['up', 'diagonal']], [-3, ['diagonal']], [-4, ['diagonal']], [-5, ['
diagonal']], [-5, ['diagonal']]]
```

```
[[-12, ['up']], [-9, ['up']], [-8, ['up', 'diagonal']], [-5, ['up', 'diagonal']], [-4, ['diagonal']], [
-5, ['diagonal']], [-6, ['diagonal']]]
```

Practical 6

Aim: Write a Python3/Java program to perform multiple sequence alignment.

Code:

```
from random import choice, randint


def get_sequences(no_of_sequences : int) →
list[list[str]]:
    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) →
list[list[str]]:
```

```
    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 :
list[list[str]]) → list[str]:
    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:

```
C:\Temp\Bioinformatics>python multiple_sequence_alignment.py
Multiple sequence alignment in Python 3.6+
Enter the number of input sequences>    6
Do you want the sequences to be randomly generated? [Yes]/No>
Sequences are as follows:
Sequence 1>     ['D', 'B', 'D', 'C', 'E', 'E', 'D', 'B', 'E', 'A', 'C']
Sequence 2>     ['C', 'D', 'B', 'A', 'D', 'A', 'D', 'B', 'E', 'B', 'E']
Sequence 3>     ['E', 'A', 'D', 'D', 'D', 'E', 'C', 'C', 'D', 'D', 'E']
Sequence 4>     ['D', 'D', 'C', 'D', 'C', 'D', 'D', 'B', 'C', 'B', 'B']
Sequence 5>     ['B', 'D', 'C', 'C', 'B', 'D', 'C', 'C', 'A', 'D', 'A']
Sequence 6>     ['A', 'A', 'E', 'B', 'B', 'B', 'D', 'E', 'B', 'C', 'B']
Multiple sequence alignment for given sequences is:     ['d', 'B/A/D', 'd', 'd', 'd', 'd', 'C/D', 'B/C
/E', 'e', 'd', 'e']
```

Practical 7

Aim: Write a Python3/Java program to find the regular expression from a set of sequences.

Code:

```
from random import choice, randint

from string import ascii_uppercase


def get_sequences(no_of_sequences : int) →
list[list[str]]:

    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) →
list[list[str]]:
    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 :
list[list[str]]) → list[str]:
    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:

```
C:\Temp\Bioinformatics>python regular_expression.py
Regular Expression in Python 3.6+
Enter the number of input sequences>    6
Do you want the sequences to be randomly generated? [Yes]/No>
Sequences are as follows:
Sequence 1>     ['C', 'A', 'C', 'D', 'D', 'F', 'A', 'B', 'B', 'B', 'C', 'B', 'A', 'E', 'B', 'F', 'A',
'F', 'C']
Sequence 2>     ['F', 'B', 'F', 'B', 'A', 'B', 'E', 'B', 'F', 'B', 'A', 'F', 'F', 'D', 'F', 'C', 'C',
'D', 'A']
Sequence 3>     ['F', 'A', 'F', 'E', 'F', 'D', 'B', 'B', 'B', 'B', 'D', 'B', 'A', 'E', 'D', 'B', 'F',
'E', 'D']
Sequence 4>     ['A', 'E', 'D', 'A', 'B', 'B', 'F', 'E', 'F', 'F', 'A', 'F', 'C', 'B', 'D', 'E', 'B',
'C', 'E']
Sequence 5>     ['A', 'A', 'E', 'D', 'D', 'F', 'C', 'D', 'D', 'C', 'F', 'C', 'E', 'A', 'F', 'E', 'C',
'A', 'D']
Sequence 6>     ['B', 'B', 'E', 'F', 'E', 'E', 'C', 'A', 'C', 'D', 'C', 'E', 'A', 'D', 'F', 'A', 'E',
'B', 'B']
Regular expression for given sequences is:      ['[BCAF]', '[BEA]', '[DECF]', '[FDEAB]', '[DAEFB]', '[
DBEF]', '[AECFB]', '[ABED]', '[DBCF]', '[DBCF]', '[DFCA]', '[BCEF]', '[EFCA]', '[BEAD]', '[DBF]', '[FEC
AB]', '[AECFB]', 'X', '[DECAB]']
```

Practical 8

Aim: Write a Python3/Java program to find the fingerprint of the sequence.

Code:

```
from random import choice, randint

import sys


def generate_sequences() → list[list[str]]:

    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:list[list[str]]) →
list[dict[str, int]]:

    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:list[dict[str,
int]]):

    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:

```
C:\Temp\Bioinformatics>python fingerprint.py
Sequence 1 is>
 ['T', 'T', 'A', 'G', 'A', 'G', 'A', 'C', 'G', 'A', 'C', 'C', 'T', 'A']

Sequence 2 is>
 ['C', 'C', 'C', 'A', 'C', 'G', 'T', 'C', 'A', 'T', 'T', 'A', 'C', 'G']

Sequence 3 is>
 ['G', 'C', 'G', 'A', 'C', 'C', 'A', 'T', 'A', 'T', 'G', 'A', 'T', 'T']

Sequence 4 is>
 ['T', 'G', 'G', 'C', 'G', 'C', 'C', 'C', 'G', 'G', 'G', 'T', 'C', 'T']

Sequence 5 is>
 ['A', 'A', 'T', 'C', 'C', 'C', 'T', 'G', 'A', 'T', 'C', 'T', 'G', 'A']

Sequence 6 is>
 ['G', 'T', 'C', 'G', 'G', 'G', 'C', 'T', 'C', 'T', 'A', 'T', 'C', 'T']

Sequence 7 is>
 ['C', 'A', 'A', 'A', 'G', 'A', 'T', 'C', 'A', 'T', 'T', 'G', 'T', 'C']

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

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

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

Sequence 11 is>
 ['G', 'A', 'T', 'G', 'C', 'C', 'G', 'C', 'C', 'T', 'C', 'G', 'G', 'T']

Sequence 12 is>
 ['A', 'T', 'G', 'G', 'C', 'C', 'A', 'A', 'C', 'G', 'G', 'C', 'T', 'G']

Sequence 13 is>
 ['T', 'G', 'G', 'A', 'C', 'T', 'T', 'A', 'T', 'G', 'C', 'C', 'C', 'G']

Sequence 14 is>
 ['T', 'A', 'G', 'A', 'G', 'C', 'A', 'G', 'T', 'C', 'A', 'A', 'G', 'G']

Sequence 15 is>
 ['A', 'G', 'T', 'A', 'C', 'T', 'G', 'C', 'C', 'A', 'G', 'G', 'A', 'G']

Sequence 16 is>
 ['G', 'C', 'A', 'C', 'A', 'G', 'C', 'C', 'C', 'A', 'T', 'T', 'G', 'G']

Sequence 17 is>
 ['G', 'G', 'T', 'C', 'T', 'A', 'A', 'A', 'T', 'G', 'C', 'G', 'G', 'A']

Sequence 18 is>
 ['T', 'A', 'C', 'C', 'T', 'A', 'A', 'C', 'A', 'C', 'T', 'G', 'A', 'G']
```

Col	A	C	G	T
1	4	2	6	6
2	6	3	6	3
3	3	4	6	5
4	6	6	4	2
5	3	8	5	2
6	3	7	5	3
7	7	5	2	4
8	5	8	2	3
9	7	5	2	4
10	3	2	7	6
11	4	5	5	4
12	5	4	5	4
13	3	5	6	4
14	4	1	7	6

Practical 9

Aim: Write a Python3/Java program to find the motif of the sequence.

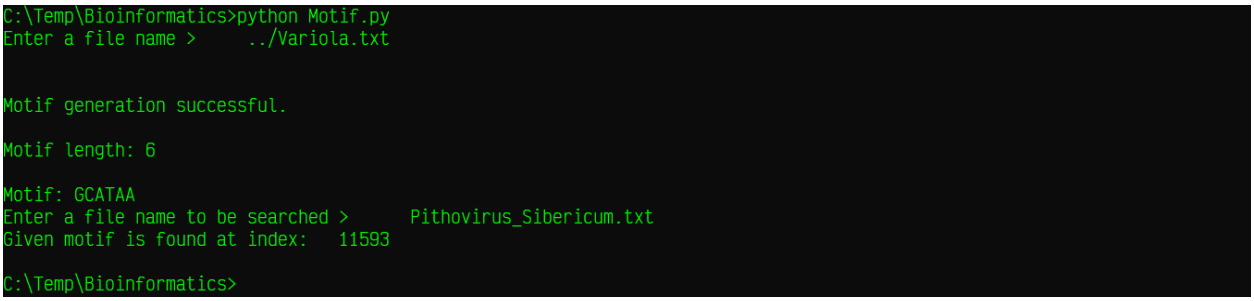
Code:

```
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)
    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:



Practical 10

Aim: Write a Python3/Java program to perform BLAST search and find the no of repetition of each nucleotide in the sequence.

Code:

```
if __name__ == "__main__":
    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}")
    print(f"Genome length:\t{sum(base_dict.values())}")
    print(f"Nucleotide count:")
```

```
    for i in "ACGT":
        print(f"\t{i} : {base_dict[i]}")
```

Output:

- Absolute filepath:

```
C:\Temp\Bioinformatics>python BLAST.py
Enter a filename.>      C:/Temp/Salmonella_Enterica.txt

BLAST search successful.
Test results:
File name:       C:/Temp/Salmonella_Enterica.txt
Genome length:  4791950
Nucleotide count:
        A : 1146820
        C : 1243619
        G : 1250672
        T : 1150839
```

- Relative filepath:

```
C:\Temp\Bioinformatics>python BLAST.py
Enter a filename.>      ../Variola.txt

BLAST search successful.
Test results:
File name:       ../Variola.txt
Genome length:  185578
Nucleotide count:
        A : 62782
        C : 30524
        G : 30223
        T : 62049
```

- Current working directory:

```
C:\Temp\Bioinformatics>python BLAST.py
Enter a filename.>      Pithovirus_Sibericum.txt

BLAST search successful.
Test results:
File name:       Pithovirus_Sibericum.txt
Genome length:  610033
Nucleotide count:
        A : 196380
        C : 109028
        G : 109354
        T : 195271
```