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Class- MSc CS – I

Roll No.- 536

Subject – Bioinformatics

Topic – Identity of Sequences

Practical No: 2

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

Code:

```
se1=input("Enter the first sequence::")
se2=input("Enter the second sequence::")
seq1=list(se1)
seq2=list(se2)

def find_identity(a,b):
    gap(a,b)
    print(a)
    print(b)
    score=0
    length=len(a)
    total_elements=len(a)*len(b)
    for i in range(0,length):
        for j in range(0,length):
            if(a[i]==b[j]):
                score=score+1
    identity=(score/total_elements)*100
    print("Matching Score::",score)
    print("Identity of the sequences::",identity)

def gap(a,b):
    if(len(a)==len(b)):
        print()
    else:
        k=int(input("enter the position to insert gap ::"))
        if (len(a)<len(b)):
            a.insert(k,'-')
        else:
            b.insert(k,'-')
    return(a,b)

find_identity(seq1,seq2)
```

Output:

```
Python 3.10.5 (tags/v3.10.5:f377153, Jun 6 2022, 16:14:13) [MSC v.1929 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
===== RESTART: C:/Users/DELL/Desktop/neha folders/p2.py =====
Enter the first sequence::abcvfdg
Enter the second sequence::abvgcfd

['a', 'b', 'c', 'v', 'f', 'd', 'g']
['a', 'b', 'v', 'g', 'c', 'f', 'd']
Matching Score:: 7
Identity of the sequences:: 14.285714285714285
>>> |
```

Ln: 12 Col: 0