**Name: Ayush S. Tiwari**

**Class- MSc CS – I**

**Roll No.- 511**

**Subject – Bioinformatics**

**Topic – Identity of Two Protein Sequence**

## Practical No: 2

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

### Code:

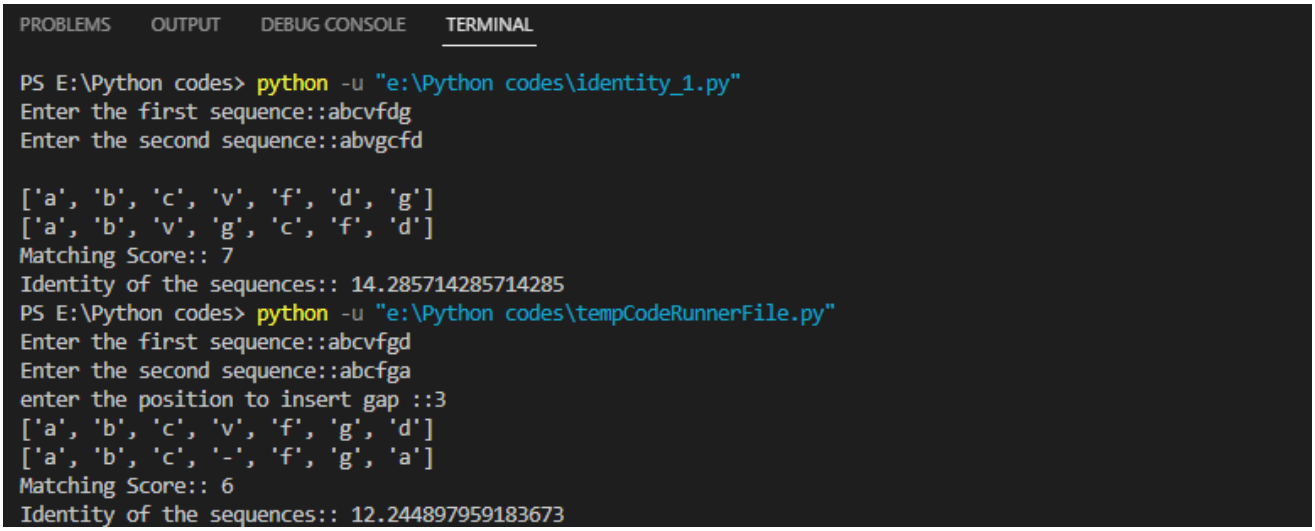
```
se1=input("Enter the first sequence::")
se2=input("Enter the second sequence::")
seq1=list(se1)
seq2=list(se2)

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:


PROBLEMS
OUTPUT
DEBUG CONSOLE
TERMINAL
PS E:\Python codes> python -u "e:\Python codes\identity_1.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
PS E:\Python codes> python -u "e:\Python codes\tempCodeRunnerFile.py"
Enter the first sequence::abcvfgd
Enter the second sequence::abcfga
enter the position to insert gap ::3
['a', 'b', 'c', 'v', 'f', 'g', 'd']
['a', 'b', 'c', '-', 'f', 'g', 'a']
Matching Score:: 6
Identity of the sequences:: 12.244897959183673