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Class- MSc CS – I

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Subject – Bioinformatics

Topic – Pairwise Alignment

Practical No: 1

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

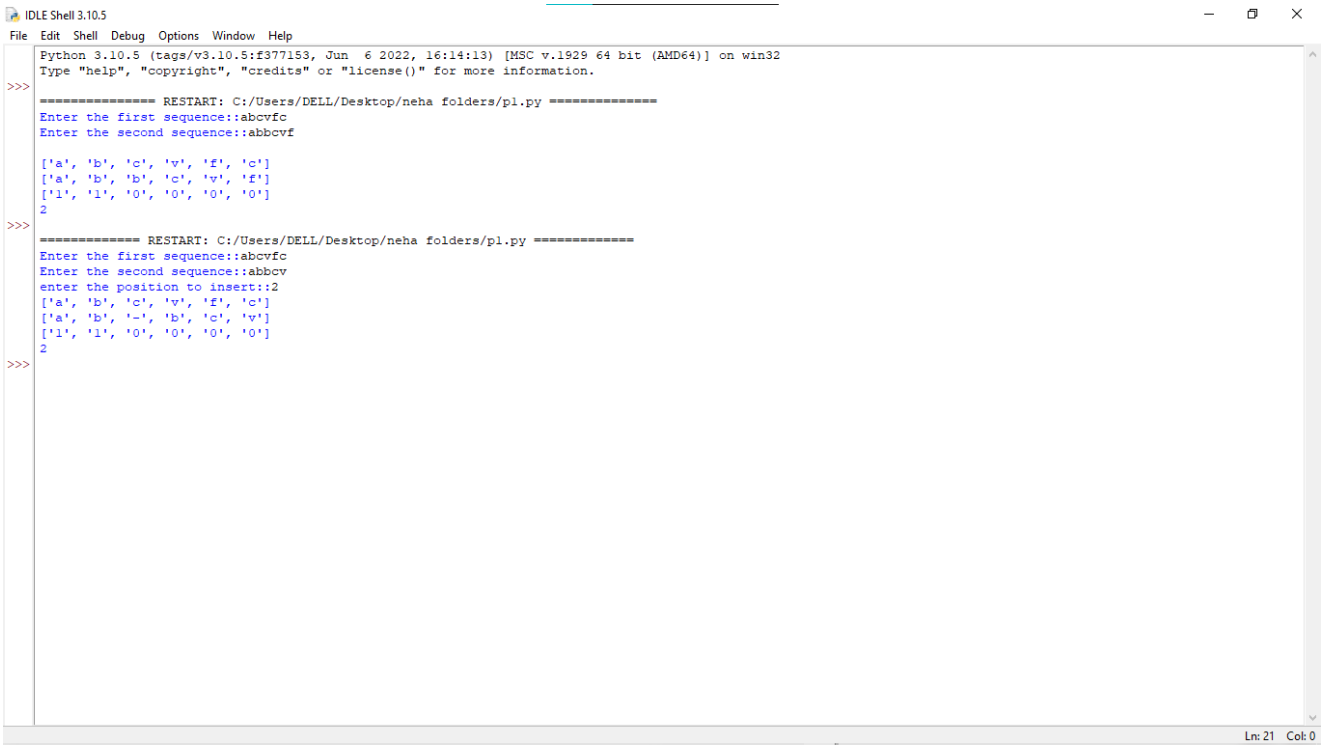
Code:

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

def Pairwise_alignment(a,b):
   gap(a,b)
   print(a)
   print(b)
   value=0
   length=len(a)
   for i in range(0,length):
      if(a[i]==b[i]):
         score.append('1')
         value=value+1
      else:
         score.append('0')
   print(score)
   print(value)

def gap(a,b):
   if(len(a)==len(b)):
       print()
   else:
      k=int(input("enter the position to insert::"))
      if (len(a)<len(b)):
         a.insert(k,'-')
      else:
         b.insert(k,'-')
   return(a,b)
Pairwise_alignment(seq1,seq2)
```

Output:


IDLE Shell 3.10.5
File Edit Shell Debug Options Window Help
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/p1.py ==========
Enter the first sequence::abcvfc
Enter the second sequence::abbcvf
['a', 'b', 'c', 'v', 'f', 'c']
['a', 'b', 'b', 'c', 'v', 'f']
['1', '1', '0', '0', '0', '0']
2
>>>
========== RESTART: C:/Users/DELL/Desktop/neha folders/p1.py ==========
Enter the first sequence::abcvfc
Enter the second sequence::abbcv
enter the position to insert::2
['a', 'b', 'c', 'v', 'f', 'c']
['a', 'b', '-', 'b', 'c', 'v']
['1', '1', '0', '0', '0', '0']
2
>>>
Ln: 21 Col: 0