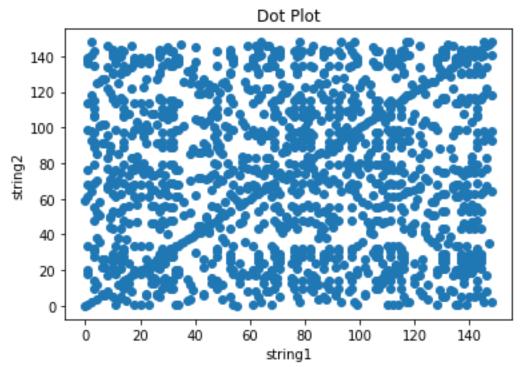
## Assignment 4

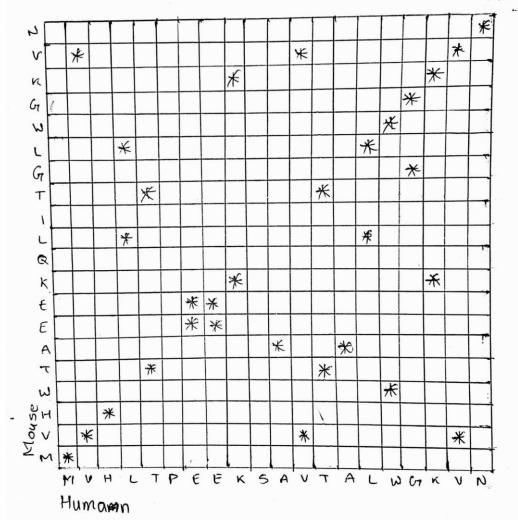
1. a. Write a program to construct a dot plot for the alignment of human and chicken hemoglobin β chain. Identify the segments, which are same in both sequences.

```
import matplotlib.pyplot as plt
def matchstr(s1, s2):
    seq=[]
    segrev=[]
    tempstr=''
    for i in range(len(s1)):
        if s1[i] == s2[i]:
            tempstr+=s1[i]
        else:
            seq.append(tempstr)
            tempstr=''
    return seq
def plot(s1, s2):
    x=[]
    y=[]
    for i in range(len(s1)):
        for j in range(len(s2)):
            if s1[i] == s2[j]:
                x.append(i)
                y.append(j)
    plt.scatter(x, y)
    plt.xlabel("string1")
    plt.ylabel("string2")
    plt.title("Dot Plot")
    plt.show()
if name ==" main ":
string1='''MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLST
PDAVMGNPK
VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG
KEFTPPVQAAYQKVVAGVANALAHKYH'''
string2='''MVHWTAEEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRFFASFGNLSS
PTAILGNPM
VRAHGKKVLTSFGDAVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFS
KDFTPECQAAWQKLVRVVAHALARKYH'''
    plot(string1, string2)
match=matchstr(string1, string2)
print(match)
Output:
```



['MVH', 'T', 'EEK', '', '', 'T', 'LWGKVNV', 'E', 'G', 'EAL', 'RLL', 'VYPWTQRFF', 'SFG', 'LS', 'P', 'A', '', 'GNP', '\nV', 'AHGKKVL', '', 'F', 'D', '', '', 'LDN', 'K', 'TF', '', 'LSELHCDKLHVDPENFRLLG', '', 'L', 'VLA', 'HF', '\nK', 'FTP', '', 'QAA', 'QK', 'V', '', 'VA', 'ALA']

b. Construct the dot plot manually for the residues 1-20 and verify with the plot obtained using program



2. Calculate the score for the following alignments using code:

Assume that the match score is 1, mismatch score is 0, origination penalty is -2, and length penalty is -1.

```
Output:
```

1

3. Verify the Q2 manually

```
String1=AATCTATA
String2=AAG--ATA
Starting from first character of two strings:
1. A - A = Match score=+1 (0+1)
2. A - A = Match
                       score=+2 (1+1)
3. T - G = mismatch
                      score = +2 (0+2)
4. C - - = OP + LP
                      score = -1 (-3 + 2)
5. T - - = LP
                      score=-2 (-1-1)
6. A - A = Match
                      score = -1 (1-2)
7. T - T = Match
                       score= 0 (1-1)
8. A - A = Match
                      score = +1 (1+1)
```

4. Using the Needleman and Wunsch dynamic programming method, construct the partial alignment score table and align the following two sequences (using code):

ACAGTCGAACG and ACCGTCCG

```
use the scoring parameters: match score: +2; mismatch score: -1 and gap penalty: -2
```

```
import numpy as np
import pandas as pd
def NnWa(s1, s2):
    arr=np.zeros((len(s1)+1, len(s2)+1))
    arr[:,0] = np.arange(0,2*(-len(s1)-1), -2)
    arr[0,:]=np.arange(0,2*(-len(s2)-1), -2)
    temp=[0, 0, 0]
    for i in range(len(s1)):
        for j in range(len(s2)):
            if (s1[i] == s2[j]):
                temp[0]=arr[i,j]+2
            else:
                 temp[0]=arr[i,j]-1
            temp[1] = arr[i, j+1] - 2
            temp[2] = arr[i+1, j] - 2
            arr[i+1,j+1] = max(temp)
    str1=" "+s1
    str2=" "+s2
    panda df=pd.DataFrame(data=arr.astype(int), index=[i for
i in str1], columns=[i for i in str2])
    print(panda_df)
    x=[]
    y=[]
    i=len(s1)
    j=len(s2)
    x.append(s1[i-1])
    y.append(s2[j-1])
    i-=1
    j−=1
    while i>0 or j>0:
```

```
if max(arr[i][j],
arr[i][j+1],arr[i+1][j]) == arr[i][j]:
           x.append(s1[i-1])
           y.append(s2[j-1])
           i-=1
           j-=1
       elif max(arr[i][j],
arr[i][j+1], arr[i+1][j]) == arr[i][j+1]:
           x.append(s1[i-1])
           y.append('-')
           i-=1
       elif max(arr[i][j],
arr[i][j+1],arr[i+1][j]) == arr[i+1][j]:
           x.append('-')
           y.append(s1[j-1])
           j-=1
   x=''.join(x[::-1])
   y=''.join(y[::-1])
   print(x)
   print(y)
#----MAIN PROGRAM-----
string1='ACAGTCGAACG'
string2='ACCGTCCG'
NnWa(string1, string2)
Output:
             C G T C C
       Α
          С
   0
          -4
             -6 -8 -10 -12 -14 -16
  -2
         0 -2 -4 -6 -8 -10 -12
Α
         4 2 0 -2 -4
C - 4
      0
                           -6 -8
A -6 -2
         2 3 1 -1 -3 -5 -7
                    3
G - 8 - 4
         0
              1 5
                           -1
                               -3
                        1
T -10 -6 -2 -1 3 7
                       5
                           3 1
C -12 -8 -4 0 1
                    5 9
                            7
                              5
G -14 -10
         -6 -2 2
                       7
                   3
                               9
                              7
A -16 -12 -8 -4 0 1 5 6
A -18 -14 -10
             -6 -2 -1
                        3
                              5
C -20 -16 -12 -8 -4 -3 1
                              3
G -22 -18 -14 -10 -6 -5 -1
                              7
ACAGTCGAACG
ACCGTC---CG
```

## 5. Verify Q4 manually

