

Do the same as in Part 1 of Programming Assignment #1, except experiment with setting the `penalize_extend_when_opening` and `penalize_end_gaps` alignment parameters to see if you can get a better global alignment score than you achieved in Part 1 of Programming Assignment #1.

Need to beat: 142

```

Global alignment starting=====
M--A---ALSGGGG-----GG-AE---P-GQALFNQDM-E----P--EAGAGAGAA-AS--SAA--DP--AIPE--EVWNIQM--I-KLTQEHI EAL--LDKFGG
| | | .          || | | | .   | . | | | | | .   | | .   | | | . || |   | |
MEVAVEKA-A-----AAAAPAGGPA-AAAPSGE---N-E-AESRQGP DSE--SG-G--EASRLN--LLD-TCAV--CHQ--NI-Q-SRPVKL-----LPCL-----
Score=142

```

penalize\_extend\_when\_opening: 2

penalize\_end\_gaps: -1

```
51 # Global alignment using BLOSUM62 matrix
52 # and print the results to the console (using format_alignment function)
53 print("Global alignment starting=====")
54 for a in pairwise2.align.globalmx(seq1, seq2, 2, -1):
55     print(pairwise2.format_alignment(*a))
56 print("Print global successful=====")
57
```

PROBLEMS OUTPUT DEBUG CONSOLE TERMINAL PORTS ... powershell + ▢ ▢ ... ^ ×

```
Global alignment starting=====
M--A--ALSGGGGGGAEPGQALFNQDMEPEAGAGAG--A--AASSADP---AI-----P--E---E-----VW---NIK
|MI---KLTQEHEIAL--LDKFGG                ||||| ||||| | | | | | | | | | | | |
MEVAVEKA-----A---A-----A-A-A-PAGGPAA--AA-PSGENEA-ESRQGPDSSESGEASRLNLDTCAV-CHQNI-
Q--SRVPKL-----LPCL-----
Score=52
```

penalize\_extend\_when\_opening: 4

```
penalize_end_gaps: -1
```

```
51 # Global alignment using BLOSUM62 matrix
52 # and print the results to the console (using format_alignment function)
53 print("Global alignment starting=====")
54 for a in pairwise2.align.globalmx(seq1, seq2, 4, -1):
55     print(pairwise2.format_alignment(*a))
56 print("Print global successful=====")
```

PROBLEMS OUTPUT DEBUG CONSOLE TERMINAL PORTS ... powershell + ▢ ▣ ... ^ X

```
Imports successful
Matrix created
Global alignment starting=====
M--A---ALSGGGGGAEPGQALFNCDMEPEAGAG-A---AASSADP----AI-----P-E---E-----VW---NIK
QMI----KLTQEHEIAL--LDKFEGG                ||| | |||| |   | | | |   | ||
|  |  |      |    |           |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
MEVAVEKA-----A---A-----A-A-A-PAGGPAA--AA-PSGENEA-ESRQGPDSSESGGEASRLNLLDTCAV-CHQNI-
Q--SRVPKL-----LPCL-----
Score=104
```

penalize extend when opening: 6

penalize\_end\_gaps: -1

```
51 # Global alignment using BLOSUM62 matrix
52 # and print the results to the console (using format_alignment function)
53 print("Global alignment starting=====")
54 for a in pairwise2.align.globalmx(seq1, seq2, 6, -1):
55     print(pairwise2.format_alignment(*a))
56 print("Print global successful=====")
57
```

PROBLEMS OUTPUT DEBUG CONSOLE TERMINAL PORTS ... powershell + v [ ] [ ] ... ^ x

```
Imports successful
Matrix created
Global alignment starting=====
M-A--A--ALSGGGGGGAGPGQALFNGDMEPEAGAGAG-A--AASSAADP-----AI-----P-E---VW---NIK
QMI-----KLTQEHIIEAL--LDKFGG                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
MEVAVEKA-----A-----A-----A-A-A-PAGGPAA--AA-PSGENEA-ESRQGPDS ESGGEASRLNLLDTC AV-CHQNI-
Q--SRVPKL-----LPCL-----
Score=156
```

Submit your code and this worksheet. NOTE: do not use absolute paths in your code. If you use absolute paths, your code will be deemed not working. Your submission should work “relative” to any Python working directory that your code is placed and run

As long as seq1.txt and seq2.txt are in same directory as file, this should allow the read and saving of the sequences.

```
# Read in the sequences from the files: seq1.txt and seq2.txt
# and store them in variables
with open("seq1.txt", "r") as seq1_file:
    lines = seq1_file.readlines()
    seq1 = lines[1].strip()

with open("seq2.txt", "r") as seq2_file:
    lines = seq2_file.readlines()
    seq2 = lines[1].strip()
```