Biyoinformatiğe Giriş Proje 2:

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Example 1:

```python
import Bio
from Bio.Align import PairwiseAligner
aligner = PairwiseAligner()

#aligner.mode = 'local'
#'local' for local alignment
#aligner.match_score = 2
#aligner.mismatch_score = -1
#aligner.open_gap_score = -0.5
#aligner.extend_gap_score = -0.1

seq1 = 'ACCGT'
seq2 = 'ACG'
alignment = aligner.align(seq1, seq2)

#1. örnek aligment score 3
for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: 3.0
Sequence 1: [[0 2]
 [3 4]]
Sequence 2: [[0 2]
 [2 3]]
Alignment score: 3.0
Sequence 1: [[0 1]
 [2 4]]
Sequence 2: [[0 1]
 [1 3]]
```

Example 2:

```python
#2.örnek global aligment
aligner.mode = 'global'
seq1 = 'ACCGT'
seq2 = 'ACG'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: 3.0
Sequence 1: [[0 2]
 [3 4]]
Sequence 2: [[0 2]
 [2 3]]
Alignment score: 3.0
Sequence 1: [[0 1]
 [2 4]]
Sequence 2: [[0 1]
 [1 3]]
```

Example 3:

```python
#3. örnek local aligment
aligner.mode='local'
seq1 = 'ACCGT'
seq2 = 'ACG'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: 3.0
Sequence 1: [[0 2]
 [3 4]]
Sequence 2: [[0 2]
 [2 3]]
Alignment score: 3.0
Sequence 1: [[0 1]
 [2 4]]
Sequence 2: [[0 1]
 [1 3]]
```

Example 4:

```
#4. örnek global aligment
aligner.mode='global'
aligner.match_score = 2 # her match için 2 puan
aligner.mismatch_score = -1 # her mismatch için -1 puan
seq1 = 'ACCGT'
seq2 = 'ACG'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: 6.0
Sequence 1: [[0 2]
 [3 4]]
Sequence 2: [[0 2]
 [2 3]]
Alignment score: 6.0
Sequence 1: [[0 1]
 [2 4]]
Sequence 2: [[0 1]
 [1 3]]
```

Example 5:

```
#5. örnek
aligner.mode='global'
aligner.match_score = 2 # her match için 2 puan
aligner.mismatch_score = -1 # her mismatch için -1 puan
aligner.open_gap_score = -0.5 #açık boşluk cezası yeni bir boşluğun oluşturulması için bir cezadır
aligner.extend_gap_score = -0.1 #uzatma boşluğu cezası ise mevcut bir boşluğu uzatmak için cezadır

seq1 = 'ACCGT'
seq2 = 'ACG'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: 5.0
Sequence 1: [[0 1]
 [2 4]]
Sequence 2: [[0 1]
 [1 3]]
Alignment score: 5.0
Sequence 1: [[0 2]
 [3 4]]
Sequence 2: [[0 2]
 [2 3]]
```

Example 6:

```
#6. örnek
aligner.mode='global'
aligner.match_score = 5 # her match için 5 puan
aligner.mismatch_score = -4 # her mismatch için -4 puan
aligner.open_gap_score = -1 # açık boşluk için -1 puan
aligner.extend_gap_score = -0.1 # boşluk uzatma için -0.1 puan

seq1 = 'A'
seq2 = 'T'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: -2.0
Sequence 1: []
Sequence 2: []
Alignment score: -2.0
Sequence 1: []
Sequence 2: []
```

Example 7:

```
#7. örnek
aligner.mode='global'
aligner.match_score = 5 # her match için 5 puan
aligner.mismatch_score = -4 # her mismatch için -4 puan
aligner.open_gap_score = -3 # açık boşluk için -3 puan
aligner.extend_gap_score = -0.1 # boşluk uzatma için -0.1 puan

seq1 = 'A'
seq2 = 'T'
alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
    print('Sequence 1:', aln.aligned[0])
    print('Sequence 2:', aln.aligned[1])
```

```
Alignment score: -4.0
Sequence 1: [[0 1]]
Sequence 2: [[0 1]]
```

Example 8:

```
# 8. örnek
from Bio.Align import substitution_matrices
matrix = substitution_matrices.load("BLOSUM62")
aligner.mode = 'global'
aligner.substitution_matrix=matrix
seq1 = 'KEVLA'
seq2 = 'EVL'

alignment = aligner.align(seq1, seq2)

for aln in alignment:
    print('Alignment score:', aln.score)
```

```
Alignment score: 13.0
```

Example 9:

```
#9.örnek
from math import log
def gap_function(x, y):  # x is gap position in seq, y is gap length
    if y == 0:  # No gap
        return 0
    elif y == 1:  # Gap open penalty
        return -2
    return - (2 + y/4.0 + log(y)/2.0)
aligner.match_score = 5
aligner.mismatch_score = -4
aligner.open_gap_score = gap_function()
aligner.extend_gap_score = gap_function()
#globalmc fonksiyonu Align modülü içinde bulunmuyor
alignment = aligner.align.globalmc("ACCCCCGT", "ACG")

for aln in alignment:
    print('Alignment score:', aln.score)
```