

Assignment 3 v2 Local and global alignment scoring Due 2021 01 18

Note: in the scoring matrix, the mismatch score is -4 (not -5, which was in a previous version of the assignment)

Consider the following nucleotide **global** alignment between a sequence of length 23 and a sequence of length 21

```
1 GTGATGTCTCCTCCGCCGACAAC      23
   |||.|||||||  |||||.
2 GTGCTGTCTCCT--GCCGACAAG      21
```

Assuming the matches are scored as 5, mismatches are scored as -4, gap openings are scored at -10, and gap extensions are scored at -0.5, the total score of this alignment is $19 * 5 - (2 * 4 + 10 + 0.5) = 76$

The **local** alignment with the same scoring matrix is:

```
1 GTGATGTCTCCTCCGCCGACAA      22
   |||.|||||||  |||||.
1 GTGCTGTCTCCT--GCCGACAA      20
```

With a score of $19 * 5 - (4 + 10 + 0.5) = 80.5$ (we don't have to include the final mismatch between C and G).

Using the same scoring matrix, what are the global and local alignments and alignment scores for these 2 sequences.

Hint, it will be easier to start the alignment from the right (the global alignment has 2 gaps in the upper sequence on the far left).

```
TCTCAGGGCTA
TATTCACGGCTA
```

Global alignment:

Global alignment score:

Local alignment

Local alignment score: