Local and global alignment scoring Due Mon Jan 24

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 optimal global and local alignments and alignment scores for these 2 sequences. Assume gap opening and extension penalties apply to end gaps.

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
TAGTTCACGGCTA
```

Global alignment:

Global alignment score:

Local alignment

Local alignment score: