Lab2

- Perform a global and local alignment to measure sequence similarity

  - input: two sequence files and one score file

    - Each file consists of two lines.

    - The fist line starts with >.

    - The second line is a DNA sequence that consist of A, C, G, and T.
      100개 미만으로 주어짐

  - output: a file with the result of alignment

- Due on 2018.9.28 11:59 PM

- You should submit a code and a readme file including usages to portal

sequence file

>seq1
atgaccgggatactgataaaaaaagggggggggcgtacacattagataaacgtatgaagtacgttagactcggcgccgccg

score file

match=3
mismatch=-1
gap=-3

linear scoring scheme을 이용한 dynamic programming

```
matches: 8
mismatches: 2
gaps: 6
score: 4

A---ACTGAG---TCA
ACCCCCTGAGAGTTCT
```