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.
  - 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

Lab2: input files

sequence file

>seq1
atgaccgggatactgataaaaaaaggggggggggcgtacacattagataaacgtatgaagtacgttagactcggcgccgccg

score file

match=3
mismatch=-1
gap=-3

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

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