# Lab1: Sequence alignment

- Perform a global alignment between two sequences

  - input: a file with three lines.

    - The first line shows a score for match, mismatch, insertion, and deletion in order. These scores were seperated by space.

    - The second and third lines are two sequences.

    - The sequence consists of A, C, G, and T.

  - output: a file with the number of matches in the first line and the result of alignment

- Due on 2020.9.24 11:59 PM

- You should submit a code and a readme with a usage to portal

# Lab1: input and output files

## input file

```
3 -1 -3 -3
atgaccgggatactgataaaaaaaaggggggggggcgtacacattagataaacgtatgaagtacgttagactcggcgccgccg
atgacggggatactgataaaaaggaggcgggcgtacacattagaacgtatgaacgatgtacgttagactcggcgccgccg
```

## output file

```
73

atgaccgggatactgataaaaaaaaggggggggggcgtacacattagataaacgtatgaa----gtacgttagactcggcgccgccg
|||||| |||||||||||         ||||||| ||  ||||||||||||||         ||||||||||          |||||||||||||||||||||||||||
atgacggggatactgat---aaaaaggaggcgggcgtacacattag---aacgtatgaacgatgtacgttagactcggcgccgccg
```