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, indel (insertion or deletion) in order. These scores were separated 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 2020.9.26 11:59 PM
- You can ask questions during the lab session
- You should submit a code and a readme with a usage to portal

Lab1: input and output files

input file

3 -1 -3
atgaccgggatactgataaaaaaaaggggggggggcgtacacattagataaacgtatgaagtacgttagactcggcgccgccg
atgacggggatactgataaaaaggaggcgggcgtacacattagaacgtatgaacgatgtacgttagactcggcgccgccg

output file

73

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