Aim: In this assignment, given two DNA sequences in fasta file format, we ask to implement 'Smith-Waterman algorithm that uses substitution matrix and linear gap penalty' and 'Smith-Waterman algorithm that uses substitution matrix and affine gap penalty'.

Same input file **"sequences.fasta"** will be used for both parts and two separate output files will be generated, named **"naiveGap.txt"** and **"affineGap.txt"**, respectively.

Below is the substitution matrix that will be used for scoring matches and mismatches in both parts:

Substitution Matrix:
```
    A   T   C   G
A   4  -2  -3  -1
T  -2   4  -1  -3
C  -3  -1   4  -2
G  -1  -3  -2   4
```

Input file format (sequences.fasta):
```
>Sequence1
TCGACCCAAGTAGGGAAAGAATATCAACACAAAGGCTCGAGAAGAGCCACC
CCATGAGCCACCGCATCTACCCCGTGCCCCAGCAAATTAAGAATAG
>Sequence2
GCCTGGATGTCTGTACCGAGCCACCCATCTACTGAGCCACCCATCTTTCAG
TTGAATTCGCTT
```

First Part (Smith-Waterman that uses substitution matrix and naive gap penalty):

In the output file, first line represents the maximum score in alignment matrix, the second line represents the first sequence after alignment, and the third line represents the second sequence after alignment. Substitution matrix will be used for matches and mismatches and **gap penalty** will be **-4**.

Output file format (naiveGap.txt):
```
85
AAGGCTCGAGAAGAGCCACCC--C-A-TGAGCCACCGCATCTACCCCGT
ATGTCT-GTACCGAGCCACCCATCTACTGAGCCACC-CATCT-TTCAGT
```

Second Part (Smith-Waterman that uses substitution matrix and affine gap penalty):

In the output file, first line represents the maximum score in alignment matrix, the second line represents the first sequence after alignment, and the third line represents the second sequence after alignment. Substitution matrix will be used for 'matches and mismatches', **gap opening penalty** will be **-16** and **gap extension penalty** will be **-4.**

Output file format (affineGap.txt):
```
53
GAGCCACCGCATCTACCCCGTGCCCCAGC
GAGCCACC-CATCTACTGAGCCACCCATC
```

Notes:

- Your code must be written by yourself. Sufficient evidence of plagiarism will be treated the same as for plagiarism or cheating.
- **Non-compiling submissions will not be evaluated.**
- Your code must be complete.
- **Do not submit the program binary.**
- You must submit the following items:
  - **For C & C++:** All of the header and source files (.h & .cpp) or (.h & .c) and a script to compile the source code and produce the binary (Makefile).
    For Java: All of the source files (.java)
    For Python: All of the source files (.py)
- Submit your answers to Fatma Kahveci at ' fatma.balci@bilkent.edu.tr '.
- Use ' **CS481 Assignment-3** ' in the subject line of your e-mail.
- Zip your files and send them **in only one zipped file**.
  File name format='**surname_name_hw3.zip**'
- Name your source and header files **properly**.
- **C / C++, Python, or Java** will be used as programming language.
- **Do not add input and output files.** You can assume that input file is found in the same directory with your header and/or sources files.
- All submissions must be made by **23:59**, **November ?, 2017**.
- Assignments that are sent after the deadline will not be accepted **in any reason**.
- **Bonus** will be given for the fastest code. The fastest wins.
- **Command format for C/C++(i.e.):**
  - gcc ${c_file(s)}.c -o ${executable_file_name}
  - g++ ${cpp_file(s)}.cpp -o ${executable_file_name}