DNA ALIGNMENT

CHALLENGE DESCRIPTION:

In this challenge, you have to deal with biological code: DNA sequences. DNA sequences are made up of four bases: A, C, T, and G. New DNA sequences are formed by copying the existing ones. However, sometimes, this process is accompanied by errors: one base may be replaced with another; fragments may be deleted or inserted.

Your task is to compare two related sequences that parted from one another million years ago and changed during this time.

To do this, bioinformaticians use sequence alignment: they present them in the form of a matrix, indicating gaps with a minus sign (-), so that the maximum number of identical bases (symbols) are under each other.

For example, for GAAAAAAT and GAAT sequences, one of the possible alignments will be the following:

```
GAAAAAAT
G--A—A—T
```

Scoring systems are used to assess the alignment. These are rules, according to which the alignment receives:

- positive points — for each match (when the symbols in two lines match)
- negative points — for mismatch (different symbols in two lines)
- negative points — for indel (an insertion or deletion, i.e. a gap in one of the lines)

In some scoring systems, indel start "costs" more than indel extension, because one big gap is biologically more likely to appear than two or more smaller gaps.

In this challenge, we use the following scoring system:

```
Match: +3
Mismatch: -3
Indel start: -8
Indel extension: -1
```

Thus, the score for the above sequence is calculated as follows:

```
 G  A  A  A  A  A  A  T
 G  -  -  A  —  A  —  T
+3 -8 -1 +3 -8 +3 -8 +3 = -13
```

Another version of the same sequences alignment:

```
 G  A  A  A  A  A  A  T
 G  A  A  -  -  -  -  T
+3 +3 +3 -8 -1 -1 -1 +3 = 1
```

For most pairs of sequences, there is more than one optimal alignment. Your task is to find the highest possible score of such alignments.

INPUT SAMPLE:

Your program should accept a path to a file as its first argument. Each line of the file is a pair of DNA sequences separated by vertical bar (|).

```
GAAAAAAT | GAAT
GCATGCT | GATTACA
```

OUTPUT SAMPLE:

Print to stdout the score of the best possible alignment taking into account the above scoring system.

```
1
-3
```

CONSTRAINTS:

1. The length of each sequence does not exceed 400 symbols.