Become a professional bio-scientist   P71311_en

DNA (deoxyribonucleic acid) is the molecule that encapsulates all the information of the life species. The encoding is done through four nucleotides: adenine, thymine, cytosine and guanine that are usually abbreviated by A, T, C, G. In each position of one DNA strand we can have just one of these nucleotides and the paired strand codifies the opposite base (A links with T, C with G) so the molecule encodes two bits per base pair.

Genes are segments of the DNA that code proteins. Finding genes in a DNA is a common and important task in bioinformatics. This is a complex task because there may be skips and mutations in the sequences and DNA molecules are very long. Human DNA contains, for instance, around 2900 million base pairs (Mbp) and is not the longest one, the one of an ameba is 200 times longer!

We are going to simplify a little bit this: the problem you need to solve is to find the first position of a gene coded as nucleotides in a full DNA coded in the same way. The gene may have a maximum of one mutation, so you need to find perfect matches or matches for all nucleotides except one.

Input

First word is the the full DNA to match against. Then follow each gene as a word.

Output

You need to output the first matching position (0 if it matches at first position) or a dash if there is no match. In case of a match, output the number of mutations as well (0 or 1).

Observation

This problem does not have private test cases. It's up to you to prepare them! In order to be sure you do that, please add one comment at the end of the program wich includes a valid input whose output is

```
-
0 0
1 0
2 0
3 0
0 1
1 1
2 1
3 1
```

Sample input

```
CATATCGTAACTGTGC
TATCGTA
ATCGCA
AAAAAA
CTGTGC
A AT
```

Sample output

```
2 0
3 1
-
10 0
0 1
1 0
```

Problem information

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Generation : 2024-05-08 12:12:59