19 Become a professional bio-scientist

12 points

Introduction

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 line is the number of genes, followed by one gene each line. Last line is the full DNA to match against. Example:

```
3
TATCGTA
ATCGCA
AAAAAA
CATATCGTAACTGTGC
```

Output

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

```
3 0
4 1
0
```

Expect longer lengths though, for the genes instead of the 6 or 7 bp of the example, we will use up to 256 bp and for DNA we will use one very short, the DNA of a mitochondria less than 18 kbp.