

Problem: DNA

DNA

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The Limonian scientists specialize in genetic engineering that they carry out at local flora. Lately, they have tried to cross-breed orange and lime to get the perfect fruit for juice production. (Limonian traders can't wait to sell it in bottles whose lids have definitions of difficult words on them and that programmers are so keen to collect.) To achieve this, the scientist induce different mutations in fruit DNA chains and create new DNA chains. However, not all of them turn out to be stable. Your task is help in marking the stability of DNA chains.

In DNA chains there are purines (adenine and guanine) and pyrimidines (cytosine and thymine). According to Limonian scientists, pyrimidines are susceptible to changes only if there are many purines in their neighbourhood. For every consecutive fragment of the DNA chain we define its *volatility measure*. If such a fragment does not include any pyrimidines, it is fully stable, which means its volatility measure is 0. Otherwise, the volatility measure of the DNA chain fragment is defined as ratio of the number of purines in it (denoted shortly by letters **A** and **G**) to the number of pyrimidines in it (denoted by letters **C** and **T**). The volatility measure of the DNA chain is the highest possible volatility measure of any of its coherent fragments.

The scientists want you to tell them how many purines and how many pyrimidines there are in the most volatile DNA chain fragment. If there are many of such fragments, scientists are interested in the longest one.

Input

In the first line of the input file there is one integer t ($1 \leq t \leq 10$) specifying the number of test cases. In every of t further lines there is n -letter word ($1 \leq n \leq 1\,000\,000$) consisting of letters **A**, **C**, **G** and **T**. The word stands for the DNA chain given to you by Limonian scientists for analysis

Output

The output file should consist of t lines containing answers to consecutive input test cases. The answers to the test case is a pair of numbers meaning, respectively, the number of purines and the number of pyrimidines in the longest of the most volatile DNA chain fragments.

Scoring

Scoring of this problem is binary; in case of the correct answer, the score for a test is 1. Percentage of guaranteed points is 50%.

Example

For the input data:

```
2
ATAG
TATA
```

the correct result is:

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3 1
2 1
```

Explanation of the example: The most volatile fragment in the first DNA chain is the whole chain (with volatility measure of 3), and in the second one it is the **ATA** fragment (volatility measure of 2).