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| :---: | :---: | :---: |
| Input: Standard Input |
| Output: Standard Output |$\quad$ acm

The whole world has become worried about the rapid spread of a virus. Scientists need to understand the folding of RNA of that virus so that they can have more information about its structure.

The basic RNA-folding problem is defined by a string $\mathbf{S}$ of length $\mathbf{n}$ over the four-letter alphabet $\{\mathbf{A}, \mathbf{U}, \mathbf{C}, \mathbf{G}\}$, and an integer $\mathbf{d}$ (distance parameter). Each letter in this alphabet represents an RNA nucleotide. Nucleotides $\mathbf{A}$ and $\mathbf{U}$ are called complimentary as are the nucleotides $\mathbf{C}$ and $\mathbf{G}$. A matching consists of a set $\mathbf{M}$ of disjoint pairs of positions of $\mathbf{S}$, i.e. in a set $\mathbf{M}$ no position $i$ can be paired with two different positions $\mathbf{j}$ and $\mathbf{j}^{\prime}$. If pair ( $\mathbf{i}, \mathbf{j}$ ) is in $\mathbf{M}$, then the nucleotide at $i$-th position is said to match the nucleotide at position $\mathbf{j}$. A match is a permitted match if the nucleotides at sites $\mathbf{i}$ and $\mathbf{j}$ are complimentary, $\mathbf{i}<\mathbf{j}$ and $|\mathbf{i}-\mathbf{j}|>\mathbf{d}$. A matching $\mathbf{M}$ is non-crossing if and only if it does not contain any four sites $\mathbf{i}<\mathbf{i}^{\prime}<\mathbf{j}<\mathbf{j}^{\prime}$ where $(\mathbf{i}, \mathbf{j})$ and $\left(\mathbf{i}^{\prime}, \mathbf{j}^{\prime}\right)$ are matches in $\mathbf{M}$. Finally, a permitted matching $\mathbf{M}$ is a matching that is non-crossing, where each match in $\mathbf{M}$ is a permitted match. The basic RNA-folding problem is to find a permitted matching of maximum cardinality.

In this problem, you need to find the maximum cardinality of a permitted matching and the number of different sets $\mathbf{M}$ of that maximum cardinality. A set $\mathbf{M}$ is different from another set $\mathbf{M}^{\prime}$ if there exists at least one pair (i, $\mathbf{j}$ ) in $\mathbf{M}$ and $\left(\mathbf{i}^{\prime}, \mathbf{j}^{\prime}\right)$ in $\mathbf{M}^{\prime}$ such that either $\mathbf{i}$ and $\mathbf{i}^{\prime}$ or $\mathbf{j}$ and $\mathbf{j}^{\prime}$ are different.

## Input

The first line of input file contains the number of test cases, $\mathbf{T}(\mathbf{1} \leq \mathbf{T} \leq \mathbf{8 0})$. Then $T$ cases follow:

Each case consists of two lines. The first line contains one integer: $\mathbf{d}(\mathbf{O} \leq \mathbf{d} \leq|\mathbf{S}|)$. Then the second line contains the string $\mathbf{S}(\mathbf{1} \leq|\mathbf{S}| \leq \mathbf{2 5 0})$. It will contain only the uppercase characters $\{\mathbf{A}, \mathbf{U}, \mathbf{C}, \mathbf{G}\}$.

## Output

For each case, print "Case $\langle\mathbf{x}>$ : $\langle\mathbf{y} \mathbf{z}>$ " in a separate line, where $\mathbf{x}$ is the case number, $\mathbf{y}$ is the maximum cardinality and $\mathbf{z}$ is the number of sets with maximum cardinality. As the value of $\mathbf{z}$ can be very large, print $\mathbf{z}$ modulo 10007.

## Sample Input

```
2
1
AUA
4
GGACCUUUUGGACGC
```


## Explanation of Sample cases

For $1^{\text {st }}$ case, there is no pair of positions which satisfies the conditions of permitted match, i.e. empty set is the only possible answer.
For $2^{\text {nd }}$ case, the matches are shown below where the first position of a pair is denoted by '(' and the other position is denoted by ')':
GGACCUUUUGGACGC
((.((....)).).)

This is the only possible set with 4 permitted matches: $\{(1,15),(2,13),(4,11),(5,10)\}$.

