P25. Bond

(Time Limit: 8 seconds)

Once again, James Bond is on his way to saving the world. Bond's latest mission requires him to travel between several pairs of cities in a certain country.

The country has N cities (numbered by 1, 2, . . . , N), connected by M bidirectional roads. Bond is going to steal a vehicle, and drive along the roads from city s to city t. The country's police will be patrolling the roads, looking for Bond, however, not all roads get the same degree of attention from the police.

More formally, for each road MI6 has estimated its dangerousness, the higher it is, the more likely Bond is going to be caught while driving on this road. Dangerousness of a path from s to t is defined as the maximum dangerousness of any road on this path.

Now, it's your job to help Bond succeed in saving the world by finding the least dangerous paths for his mission.

Input

There will be at most 5 cases in the input file.

The first line of each case contains two integers N, M ($2 \le N \le 50000$, $1 \le M \le 100000$) – number of cities and roads. The next M lines describe the roads. The i-th of these lines contains three integers: x_i, y_i, d_i ($1 \le x_i$, $y_i \le N$, $0 \le d_i \le 10^9$) – the numbers of the cities connected by the i-th road and its dangerousness.

Description of the roads is followed by a line containing an integer Q ($1 \le Q \le 50000$), followed by Q lines, the i-th of which contains two integers s_i and t_i ($1 \le s_i$, $t_i \le N$, $s_i \ne t_i$).

Consecutive input sets are separated by a blank line.

Output

For each case, output Q lines, the i-th of which contains the minimum dangerousness of a path between cities s_i and t_i.

Consecutive output blocks are separated by a blank line.

The input file will be such that there will always be at least one valid path.

Sample Input

4 5

1 2 10

1 3 20

1 4 100

2 4 30

3 4 10

2

1 4

4 1

2 1

1 2 100

1

1 2

Sample Input

20

20

100

P26. GATTACA

The Institute of Bioinformatics and Medicine (IBM) of your country has been studying the DNA sequences of several organisms, including the human one. Before analyzing the DNA of an organism, the investigators must extract the DNA from the cells of the organism and decode it with a process called "sequencing".

A technique used to decode a DNA sequence is the "shotgun sequencing". This technique is a method applied to decode long DNA strands by cutting randomly many copies of the same strand to generate smaller fragments, which are sequenced reading the DNA bases (A, C, G and T) with a special machine, and re-assembled together using a special algorithm to build the entire sequence.

Normally, a DNA strand has many segments that repeat two or more times over the sequence (these segments are called "repetitions"). The repetitions are not completely identified by the shotgun method because the re-assembling process is not able to differentiate two identical fragments that are substrings of two distinct repetitions.

The scientists of the institute decoded successfully the DNA sequences of numerous bacterias from the same family, with other method of sequencing (much more expensive than the shotgun process) that avoids the problem of repetitions. The biologists wonder if it was a waste of money the application of the other method because they believe there is not any large repeated fragment in the DNA of the bacterias of the family studied.

The biologists contacted you to write a program that, given a DNA strand, finds the largest substring that is repeated two or more times in the sequence.

Input

The first line of the input contains an integer T specifying the number of test cases ($1 \leq T \leq 100$). Each test case consists of a single line of text that represents a DNA sequence S of length n ($1 \leq n \leq 1000$).

You can suppose that each sequence S only contains the letters 'A', 'C', 'G' and 'T'.

Output

For each sequence in the input, print a single line specifying the largest substring of S that appears two or more times repeated in S, followed by a space, and the number of ocurrences of the substring in S.

If there are two or more substrings of maximal length that are repeated, you must choose the least according to the lexicographic order.

If there is no repetition in S, print 'No repetitions found!'.

Sample Input

6

GATTACA

GAGAGAG

GATTACAGATTACA

TGAC

TGTAC

TTGGAACC

Sample Output

A 3

GAGAG 2

GATTACA 2

No repetitions found!

T 2

A 2