## Problem #7 **MPDNA**

You are a forensic analyst working for the Milwaukee Police Department. You've recently been assigned to work on kidnapping cases involving multiple suspects. Fortunately, DNA evidence has been recovered from the crime scenes, and all suspects are currently being detained, pending the outcome of your analysis.

Your job is to compare the DNA sequences of each suspect to the DNA found at the crime scene, and determine which suspect's DNA is the closest match. In this case, the closest match is the suspect whose DNA has the longest sequence in common with that of the crime scene DNA. This is what is sometimes called "substring" matching. That is, we want a section of consecutive characters from one string matching a section of consecutive characters in the other string. For example, the longest common sequence between GCTGCA and AGCTCT is GCT of length 3. The longest common sequence between AAAAAA and AAAATAAAA is AAAA at either end of the second sequence, giving a common sequence of length 4.

The input DNA sequences will be represented by strings containing any combination of the letters G, A, T, and C and will be between lengths 5 and 30, inclusively.

The first line will contain an integer N representing the number of cases to be analyzed. N cases will follow. Each case will begin with a single line will containing the DNA sequence found at the crime scene. The next line will contain an integer S representing the number of sequences to be analyzed. This will be followed by S lines each containing one suspect's DNA sequence. A blank line will follow each case.

Your program should print a single integer between 1 and S for each case on its own line representing the suspect whose DNA was the closest match to the crime scene DNA. If more than one suspect DNA has the closest match, any one of the closest matches is acceptable.

## Sample Input

GCTGCA

AGCTCT

TAGATT

GCGATT

GTATAT

TAGCGA

GGATAC

**GTACGA** 

CCGATA

## Sample Output

1

[Quoted text hidden]