Problem 7: Genome Matching

Genes are DNA sequences that cause certain traits in living organisms. For example, a specific DNA sequence, called the sickle cell gene, manifests itself in Sickle Cell Anemia, a deadly disease of the blood. Similarly, other genes are responsible for traits like blue or brown eyes, blond or brunette hair, and so on[1]. The human DNA code, called the human genome, has already been extensively studied and fully mapped out to genes. Thus, it is possible to collect a DNA sample from a person and predict some of the traits in that individual, caused by genes found in the sample.

Your task is to locate and identify a number of pre-defined genes in several given DNA sequences. All DNA molecules, as well as any gene, are sequences composed from only four distinct chemicals, called nucleotides (Adenine, Cytosine, Guanine, and Thymine), which are labeled with the following letters: A, C, G, and T. From biology, we know a DNA molecule forms a right-handed double-helix structure where each base from one of the strands connects to exactly one corresponding base from the second strand. The bases always form A-T or C-G pairs (or, reflexively, T-A, and G-C) and thus, any gene sequence always has its complement in the pairing strand. Due to the method of collecting and examining DNA material, any given gene DNA sequence may be found in the DNA sample in either its original sequence, or in reverse, or in its complement image, or its reverse complement image. For example:

The gene ACTTAGAAGGT may be found as
- ACTTAGAAGGT (original)
- TGAATCTTCCA (original's complement)
- TGGAAGATTCA (original reversed)
- ACCTTCTAAGT (reversed complement)

Further, even though unlikely, some genes, or one of their alternative sequences, may be fragments of other, larger genes. Finally, the same gene may be found in the same DNA sample in multiple locations, either in its original, or one of its alternative sequences. You will be given a set of genes, one gene per input line, each labeled with a simple name. The name and the gene sequence will be separated by a colon (":"). For example:

```
Blue_eyes:ACTTAGAAGGT
Blond_hair:CTTAAGGGCGGGCTTCTTTA
...
```

The list of genes will be followed by one or more sample DNA sequences, which are submitted to you for your evaluation. Your program must display the list of genes present in each sample DNA sequence and the location (counting from 1) of the first base of the that gene, in the order in which those genes were encoded by the sequence. For example, the sequence

```
ACCTTACCCTTAAGGGCGGGCTTCTTTAGTGCTTGAGGACCTTCTAAGT
TTACGGAATAACGATTTCTTCGGGCGGGAATTCCAAGTCCCGGATCGA
```

encodes Blond_hair , Blue_eyes, and Blond_Hair at locations 9, 39, and 63, respectively. If the DNA sequence does not encode any of the known genes, simply output "none".

[1] *Admittedly, this is an oversimplification of the structure and function of genes, but it will do for this problem.*

Input

The first line of input will contain a single integer *NG* indicating the number of genes that are supplied. This number will be no larger than 20. *NG* lines will follow this line, each containing a simple name for a gene (1 to 18 characters), a colon, and the gene sequence (no more than 40 characters each of which is A, T, C, or G). There may be whitespace following the gene before the end of line.

Following the *NG* lines containing genes there will appear an arbitrary number of sample DNA sequences, none of which is longer than 5000 characters. These are numbered sequentially, starting with 1. Each sample sequence will begin on a new line, and will naturally be composed from the letters A, T, C, and G. There may be multiple lines required for a single sample sequence, and the last letter in the last line of the sample will be followed immediately by a period (“.”). There may be whitespace at the end of each line (including the last in a sample). The sample input illustrates this format.

A line containing only a single period in the first column follows the last sample.

Output

For each sample DNA sequence, display the sequence number (1, 2, …). If none of the NG genes appear in the sequence, then display the word “none” on the same line as the sequence number. Otherwise, display the names of the genes – in the order they appear – on separate lines following the sequence number. After the name of each gene encountered in the DNA sequence, output the index of the first matching nucleotide of the gene (counting from 1). If multiple genes match at the same index, they should be displayed in the same order they appear in the input. Each gene will match the DNA sequence at most once for a given index value. Your output should be very similar to that shown below, including the indentation of the names of the genes. Display a blank line after the output for each sample DNA sequence.

Sample Input

```
2
Blue_eyes:ACTTAGAAGGT
Blond_hair:CTTAAGGGCGGGCTTCTTTA
ACCTTACCCTTAAGGGCGGGCTTCTTTA
GTGCTTGAGGACCTTCTAAGT
TTACGGAATAACGATTTCTTCGGGCGGGAAT
TCCAAGTCCCGGATCGA.
.
```

Output for the Sample Input

```
Sequence 1:
    Blond_hair at 9
    Blue_eyes at 39
    Blond_hair at 63

Sequence 2: none
```