



# Longest Prefix

## IOI'96

The structure of some biological objects is represented by the sequence of their constituents, where each part is denoted by an uppercase letter. Biologists are interested in decomposing a long sequence into shorter sequences called *primitives*.

We say that a sequence **S** can be composed from a given set of primitives **P** if there is a some sequence of (possibly repeated) primitives from the set whose concatenation equals **S**. Not necessarily all primitives need be present. For instance the sequence **ABABACABAABC** can be composed from the set of primitives

**{A, AB, BA, CA, BBC}**

The first **K** characters of **S** are the *prefix of S with length K*. Write a program which accepts as input a set of primitives and a sequence of constituents and then computes the length of the longest prefix that can be composed from primitives.

**PROGRAM NAME: prefix**

### INPUT FORMAT

First, the input file contains the list (length 1..200) of primitives (length 1..10) expressed as a series of space-separated strings of upper-case characters on one or more lines. The list of primitives is terminated by a line that contains nothing more than a period ('.'). No primitive appears twice in the list. Then, the input file contains a sequence **S** (length 1..200,000) expressed as one or more lines, none of which exceeds 76 letters in length. The "newlines" (line terminators) are not part of the string **S**.

### SAMPLE INPUT (file prefix.in)

```
A AB BA CA BBC
.
ABABACABAABC
```

### OUTPUT FORMAT

A single line containing an integer that is the length of the longest prefix that can be composed from the set **P**.

### SAMPLE OUTPUT (file prefix.out)

```
11
```

Submit a solution:

Choose File No file chosen

Send it in!