DNA Matcher

The Problem

You are investigating the possible common ancestors of different species. One of the techniques you use is to search for common substrings of DNA between species. The longer the common substring, the more closely the species are related. In this case you will be looking for substrings of DNA which appear in the DNA of each of two different species. Each DNA sample is represented by a sequence of any of the letters "ACGT" in any order.

Given two strings representing DNA from two species find the length of the longest string which is a substring of both of the input strings.

In this problem "substring" has the usual definition. A string X is a substring of a string Y if and only if string X can be created from string Y by deleting zero or more consecutive characters from the start of string Y, and deleting zero or more consecutive characters from the end of string Y.

The Input

The first line contains the number of test cases T (T <= 50).

Each test case consists of two lines. On each line is a string of characters with length between 1 and 1000 inclusive.

The Output

For each test case, output the message "Test x: y-string", where x is the test case number, y is the length of the longest common substring and *string* is the lexicographically least common string of length y. Test case numbers start at 1.

Sample Input

```
2
CAT
AT
AAAAAAAAAAAAAAAAAAAAACCCGGGGGGGGGGGGGG
AAAACCCGGGGGGGGGGGGGGGGGTTTTTTTTTGGGGGGGGGGGGG
```

Sample Output

```
Test 1: 2-AT
Test 2: 20-AAAACCCGGGGGGGGGGGGG
```