Task: NIE
Nonchalance

XXVI OI, Stage I. Source file `nie.*` Available memory: 512 MB. *8.10 – 12.11.2018*

Mr Byteasar, the science teacher of the Byteotian High School no. $2^8 - 1$, is extremely unfair. He set Bytie and Bytie's friends the following genetics task: They are to determine the similarity of two genotypes. To this end, the pupils have to find the longest sequence of amino-acids that is a common subsequence (not necessarily consecutive) of both genotypes. The boys know all too well that this is a tedious task, and simply cannot believe that Mr Byteasar, known for his laziness, would check it thoroughly. Having asked older colleagues, they are nearly certain that the teacher is only going to check if the sequence found by the pupils can be extended by a single amino-acid, inserted at any position, so that the extended sequence is also a common subsequence of both genotypes. If such insertion is not possible, the teacher will give the solution the top grade.

We assume that genotypes are sequences composed of letters `A`, `C`, `G`, and `T`. Let $S = (s_1, \ldots, s_n)$ and $T = (t_1, \ldots, t_m)$ denote two genotypes of lengths n and m respectively. Reporting a sequence $W = (w_1, \ldots, w_k)$ as the homework solution is going to earn the top grade if W is a subsequence of both S and T and for every sequence W' which contains W as a subsequence, W' is *not* a common subsequence of S and T.

Help Bytie and his friends through the moral grey area to reach the top grade.

Input

In the first line of the standard input, the first genotype appears, represented as a string of n capital letters `A`, `T`, `C`, and `G`. The second line contains the other genotype, of length m, represented the same way.

Output

In the first and only line of the standard output, a single string should appear. It should consist of the letters `A`, `C`, `G` and `T`, and represent the non-extensible common subsequence of the input sequences. Should there be more than one correct answer, your program can output any of those.

You may assume that there is a non-empty common subsequence.

Example

For the following input data:

```
ACTAGG
GATCA
```

the correct answer is:

```
ACA
```

or:

```
ATA
```

or:

```
G
```

Sample grading tests:

`1ocen`: $n = m = 7$, only letters `A` and `T`;

`2ocen`: $n = 100$, $m = 10\,000$, the first genotype is a subsequence of the second;

`3ocen`: $n = m = 1\,000\,000$, amino-acids are alphabetically ordered in the first genotype.

Grading

The set of tests consists of the following subsets. Within each subset, there may be several unit tests.

Subset	Property	Score
1	$n, m \leq 12$	10
2	$n, m \leq 100$	10
3	$n, m \leq 1000$	10
4	$n, m \leq 50\,000$	20
5	$n, m \leq 1\,000\,000$, only amino-acids `A` and `T`	20
6	$n, m \leq 1\,000\,000$	30