Task 6: RNA

RNA is an important molecule in our body. The structure of an RNA molecule can be described by a pair (S, P) where

1. $S = s_1 s_2 \cdots s_n$ and $P = p_1 p_2 \cdots p_n$ for some positive integer $n \leq 450$.
2. Each element s_i of S is one of the letters A, C, G, U.
3. Each element p_i of P is an asterisk, a left parenthesis, or a right parenthesis.
4. Furthermore, the sequence P is a sequence of balanced parentheses. This means, after ignoring the asterisks (if any), each left parenthesis can be matched by a unique succeeding right parenthesis and each right parenthesis can be matched by a unique preceding left parenthesis.

For example, below shows two RNA structures: $A_1 = (S_1, P_1)$ (on the left) and $A_2 = (S_2, P_2)$ (on the right).

```
ACCCGAACUU          AAUAUCCCGAAU
((**)*(*))          *(**)(**)*()
```

Given two RNA structures $A = (S, P)$ and $A' = (S', P')$, A' is called a substructure of A if there exist integers $i \leq j$ such that $S' = s_i \cdots s_j$ and $P' = p_i \cdots p_j$. (Note that the parentheses of P' should be balanced since $A' = (S', P')$ is an RNA structure.) For example, $A_3 = (S_3, P_3)$ which is

```
CCCG
(**)
```

is a substructure of A_1 but $A_4 = (S_4, P_4)$ which is

```
ACCCGAACU
((**)*(*)
```

is **not** a substructure of A_1 because P_4 is not a sequence of balanced parentheses.

For two RNA structures X and Y, if Z is a substructure of both of them, Z is called a common substructure of X and Y. A longest common substructure is a common substructure with maximum length among all common substructures.

For example, for the above A_1 and A_2, their longest common substructure has length 5 and is

```
CCCGA
(**)*
```

Note that the following example is not a common substructure of A_1 and A_2 because the parentheses are not balanced.

```
CCCGAA
(**)*(
```

In this task, given two RNA structures of length at most 450, you are required to report the length of a longest common substructure.

Input

The input file `RNA.IN` consists of 4 lines. The first two lines are the RNA sequence (first line) and the parenthesis sequence (second line) for the first RNA. The last two lines are the RNA sequence (third line) and the parenthesis sequence (fourth line) for the second RNA. Remember the length of each sequence is at most 450.

Output

The output file `RNA.OUT` contains a single integer which represents the length of a longest common substructure.

Input/Output Example

For the above example, the input and output files contain

Sample Input

```
ACCCGAACUU
((**)*(*))
AAUAUCCCGAAU
*(**)(**)*()
```

Sample Output

```
5
```