

RNA secondary structure

1 second, 256 MB

An RNA is a string consisting of 4 alphabets **A C G** and **U**. Formally, an RNA is a string of length $\mathbf{B}=\mathbf{b}_1\mathbf{b}_2...\mathbf{b}_N$ of length \mathbf{N} , where each character \mathbf{b}_i can be one of **A C G** or **U** ($1\leq\mathbf{N}\leq 200$). A secondary structure on \mathbf{B} is a matching \mathbf{S} of positions of characters in \mathbf{B} satisfying the following conditions

- (1) (No sharp turn.) For each pair (\mathbf{i}, \mathbf{j}) in \mathbf{S} , the indices are separated by at least four bases, i.e., $i < j - 4$.
 - (2) There are two ways to match characters: **A** with **U**, or **C** with **G**.
 - (3) Each character appears in only one pair in the matching.
 - (4) (Non-crossing) If (\mathbf{i}, \mathbf{j}) and (\mathbf{k}, \mathbf{l}) are two pairs in \mathbf{S} , we cannot have $\mathbf{i} < \mathbf{k} < \mathbf{j} < \mathbf{l}$.
- (See more description from the book.)

Given a string \mathbf{B} representing an RNA, you want to find the largest matching that satisfies the above 4 conditions.

Input

The first and only line of the input consists of a string \mathbf{B} , of length \mathbf{N} ($\mathbf{N}\leq 200$).

Output

You program should print the size of the largest matching.

Example 1

Input	Output
GCGAUGCGCAUAACG	4

Explanation:



Example 2

Input	Output
GCGAUGCGCAUAACGCGCAAAAAGCGU	7

Explanation:

