# **Bear and Steady Gene**



A gene is represented as a string of length n (where n is divisible by 4), composed of the letters A, C, T, and G. It is considered to be *steady* if each of the four letters occurs exactly  $\frac{n}{4}$  times. For example, GACT and AAGTGCCT are both steady genes.

Bear Limak is a famous biotechnology scientist who specializes in modifying bear DNA to make it steady. Right now, he is examining a gene represented as a string *gene*. It is not necessarily steady. Fortunately, Limak can choose one (maybe empty) substring of *gene* and replace it with any string of the same length.

Modifying a large substring of bear genes can be dangerous. Given a string *gene*, can you help Limak find the length of the smallest possible substring that he can replace to make *gene* a steady gene?

Note: A substring of a string s is a subsequence made up of zero or more contiguous characters of s.

As an example, consider gene = ACTGAAAG. The substring AA just before or after G can be replaced with CT or TC. One selection would create ACTGACTG.

#### **Function Description**

Complete the **steadyGene** function in the editor below. It should return an integer that represents the length of the smallest substring to replace.

steadyGene has the following parameter:

· gene: a string

#### **Input Format**

The first line contains an interger n divisible by 4, that denotes the length of a string gene. The second line contains a string gene of length n.

#### **Constraints**

- $4 \le n \le 500\,000$
- n is divisible by 4
- $gene[i] \in [CGAT]$

#### Subtask

•  $4 \le n \le 2000$  in tests worth 30% points.

## **Output Format**

Print the length of the minimum length substring that can be replaced to make *gene* stable.

#### Sample Input

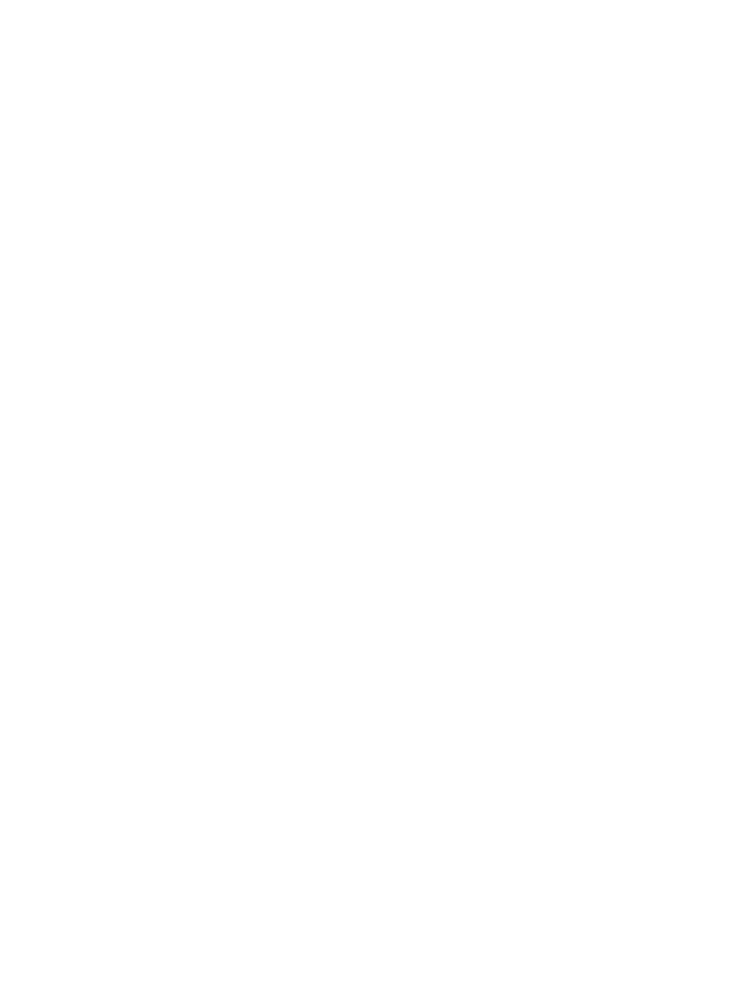


### **Sample Output**

5

## **Explanation**

One optimal solution is to replace **AAATA** with **TTCCG** resulting in **GTTCCGAA**.



The replaced substring has length  ${\bf 5}$ .