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

- $4 \leq n \leq 500\,000$

- n is divisible by 4

- $gene[i] \in [CGAT]$

Subtask

- $4 \leq n \leq 2000$ 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

```
8
GAAATAAA
```

Sample Output

```
5
```

Explanation

One optimal solution is to replace AAATA with TTCCG resulting in $\mathrm{GTTCCGAA}$.
The replaced substring has length 5.