





Bear and Steady Gene ☆

195/563 challenges solved

Rank: **1320** | Points: **5072.26** (!)



Problem

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A gene is represented as a string of length n (where n is divisible by n), composed of the letters n, n, and n0. It is considered to be steady if each of the four letters occurs exactly n2 times. For example, n3 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 $m{s}$ is a subsequence made up of zero or more contiguous characters of $m{s}$.

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 d, that denotes the length of a string gene.

The second line contains a string gene of length n.

Constraints

- 4 < n < 500000
- **n** is divisible by **4**
- $gene[i] \in [CGAT]$

Subtask

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



