Mehmet Beraat SAĞIN

URL : https://www.spoj.com/problems/MUTDNA/

MUTDNA - DNA

no tags

Biologists have discovered a strange DNA molecule, best described as a sequence of N characters from

the set {A, B}. An unlikely sequence of mutations has resulted in a DNA strand consisting only of A"s.

Biologists found that very odd, so they began studying the mutations in greater detail.

They discovered two types of mutations. One type results in changing a single character of the sequence (A \rightarrow B or B \rightarrow A). The second type changes a whole prefix of the sequence, specifically

replacing all characters in positions from 1 to K (for some K between 1 and N, inclusive) with the other

character (A with B, B with A).

Compute the least possible number of mutations that could convert the starting molecule to its end

state (containing only A characters). Mutations can occur in any order

Biologists have discovered a strange DNA molecule, best described as a sequence of N characters from

the set {A, B}. An unlikely sequence of mutations has resulted in a DNA strand consisting only of A's.

Biologists found that very odd, so they began studying the mutations in greater detail.

They discovered two types of mutations. One type results in changing a single character of the sequence (A \rightarrow B or B \rightarrow A). The second type changes a whole prefix of the sequence, specifically

replacing all characters in positions from 1 to K (for some K between 1 and N, inclusive) with the other

character (A with B, B with A).

Compute the least possible number of mutations that could convert the starting molecule to its end

state (containing only A characters). Mutations can occur in any order

Input

The first line of input contains the positive integer N (1 \leq N \leq 1 000 000), the length of the molecule.

The second line of input contains a string with N characters, with each character being either A or B

This string represents the starting state of the molecule.

Output

The first and only line of output must contain the required minimum number of mutations.

Example

```
Input 1:
ABBA
Output 1:
Input 2:
BBABB
Output 2:
Input 3:
12
AAABBBAAABBB
Output 3:
```

```
SOURCE CODE:
#include <iostream>
using namespace std;
main() {
 char DNA[1000001];
 int size;
  cin >> size;
  cin >> DNA;
  char x='A';
  int count=0;
 for(int i=size-1; i>0; i--) {
  if(x!=DNA[i]) {
                      // IF LAST ELEMENT IS B -> ENTER
     if(x!=DNA[i-1]) { // IF NEXT TO LAST ELEMENT IS B -> ENTER
      x=DNA[i];
     i--;
     count++;
 if(DNA[0]!=x) {
    count++;
  cout << count << endl;
 return 0;
}
```

