DNA Damage (5pts)

Aishwariya ma'am is teaching her students about the nucleotide sequences in DNA. These sequences consist of two strands: the primary strand and the complementary strand. Each strand is composed of four distinct nucleotides represented by letters – **A** (adenine), **C** (cytosine), **G** (guanine), and **T** (thymine). The pairing of nucleotides of the main and complementary strand follows a specific rule: **A** pairs with **T**, and **G** pairs with **C**. Seems like there is a mutation in this sequence, Aishwariya ma'am needs your help determining which nucleotide is wrongly paired.

Example

ATGA

TACG

The first and second strands are separated by newlines. The pairs are the **n**th letter in each strand - **AT**, **TA**, **GC**, and **AG**. Since **AG** is not a valid pair, the output is **AG-4**, (**4** since it's the 4th pair starting from 1).

Additional Info

1. The input only consists of the letters **A**, **T**, **C**, **G** and the newline characters separating the strands.
2. There is only one invalid pair of nucleotides in the sequence.
3. The pairs are numbered beginning from **1**.
4. You can disregard the direction of the strands (if you know what that is).

Resources

DNA base pairing — YouTube

Base pairs — NHGRI

Get Input Answer Submit