

Base-ic Genetics

Filename: genetics

The biology lab at UCF has recently been having problems transmitting genetic sequences between computers. Unfortunately, the current system represents the genetic sequences as a string of the characters: 'A', 'C', 'G' and 'T'. In order to speed up the data transfers you have been tasked with compressing the data. Luckily for you, your professor devised an easy way to do this, but he gave you the task of actually implementing it. He said that if you consider each of these letters as a number in base-4, such that 'A' = 0, 'C' = 1, 'G' = 2, and 'T' = 3, then any genetic sequence has a unique base-10 representation. He needs you to implement a program that will convert a string describing a genetic sequence to a base-10 number, or vice-versa (given a base-10 number, output the corresponding genetic sequence).

The Problem:

Given a genetic sequence, output the corresponding base-10 number. Likewise, given a number in base-10, output the corresponding genetic sequence.

The Input:

The first line of the input will contain a positive integer, q , representing the number of sequences to convert. The next q lines will contain either an integer, n ($1 \leq n \leq 2^{30}-1$), which represents a base-10 number and is guaranteed to have no leading zeroes, or a genetic sequence (represented by a string of the characters 'A','C','G' and/or 'T', and guaranteed to have no leading A's), between 1 and 15 characters in length.

The Output:

For each sequence, output the header "Sequence # j :" where j represents the sequence being processed (beginning with 1). Following the header, output either the corresponding genetic sequence for the integer given, or the corresponding base-10 number for the genetic sequence. The output for each sequence should each be on its own output line.

Sample Input:

```
3
CAACAGAT
16675
GAGGTATAC
```

Sample Output:

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Sequence #1: 16675
Sequence #2: CAACAGAT
Sequence #3: 142129
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