

Mutations

Statement

The recent viral pandemic has sparked Fluffy the Hamster's interest in computational biology. Now, he is studying the chromosome of a fast-mutating DNA-based virus ABC-21.

DNA can be represented as sequence of base pairs, which are pairs of adenine (**A**), cytosine (**C**), guanine (**G**) and thymine (**T**). In DNA, **A** pairs with **T**, and **G** pairs with **C**. Hence, knowing one strand of the chromosome is enough to determine the other strand's sequence.

The virus' chromosome is made of exactly 2 genes. The two genes may be of different lengths. If the chromosome is N base pairs long, and the length of the first gene is K , the first gene spans the base pairs in positions $[1 \dots K]$, while the second gene covers the remainder $[K + 1 \dots N]$.

Throughout the mutations, the lengths of each gene, and the total length of the chromosome remains the same. However, he finds that mutations **either exchange the order of the two genes, or swap two individual base pairs.**

Can you help him track the virus genome throughout all the mutations?

Input

The first line of the input contains 3 integers $N K Q$. N is the length of the whole chromosome, K is the length of the first gene. Q is the number of operations described later.

The second line of the input is the base pairs of the chromosome, given as a length- N string consisting of the letters A, C, G, T .

There will be Q operations given on the next Q lines. The type of operation is identified by the first letter T_i on the line, which is either B (corresponding to a base pair swap), G (corresponding to a whole-gene swap), or P (outputting a certain base pair). The format of the operation line is as:

- $B X_i Y_i$: There are 2 more integers X_i, Y_i on the line.
Swap the base pairs at the positions X_i and Y_i of the chromosome.
- G : There are no more integers on the line.
Exchange the positions of the two genes. The chromosome will now start with the previously second gene, followed by the previously first gene.
- $P X_i$: There is 1 more integer X_i on the line.
Print the current value of the base pair at position X_i of the chromosome. No change happens to the chromosome.

Constraints

- $1 \leq N \leq 10^5$
- $1 \leq K \leq N - 1$
- $1 \leq Q \leq 10^6$
- $1 \leq X_i, Y_i \leq N$
- It is guaranteed that the string representing the chromosome consists only of A,C,G,T characters.

NOTE: The input size is potentially large, usage of fast I/O routines is recommended.

Output

For each print operation, print the correct base pair at the requested position, **each on a new line**.

Finally, at the end of the program, print the **entire chromosome** after all mutations.

Examples

Sample Input	Expected Output
<pre> 10 5 6 ACGTACGTAC B 1 2 B 2 10 P 2 G P 2 B 8 3 </pre>	<pre> C G CGGAACCTTA </pre>
<pre> 5 1 3 CGTAC G P 1 G </pre>	<pre> G CGTAC </pre>

Notes

1. A skeleton file has been given to help you. You should not create a new file or rename the file provided. You should develop your program using this skeleton file.
2. You are free to define your own helper methods and classes (or remove existing ones) if it is suitable but you must put all the new classes, if any, in the same skeleton file provided.

Skeleton File

You are given the skeleton file `Mutations.java`. You should see the following contents when you open the file:

```
/**
 * Name      :
 * Matric. No :
 */

import java.util.*;

public class Mutations {
    private void run() {

    }

    public static void main(String args[]) {
        Mutations runner = new Mutations();
        runner.run();
    }
}
```