

Alien DNA

In 2017, the mankind began exploring other planets in the universe. At the first planet where the spaceship landed, a new extra-terrestrial organism was found and further research showed that it inherits DNA information in a totally new way.

The steps of its DNA inheritance are as follows.

1. Initially, (generation 0) there are two kinds of DNA sequences T_1 and T_2 . T_1 is a male DNA sequence and T_2 is a female one. Note that their lengths may be different.
2. Both T_1 and T_2 are made up with four letters, A, G, C, and T.
3. The DNA sequences of their children is determined as follows. T_2 is attached at the end of T_1 , then one more copy of T_2 follows it. Finally, a copy of T_1 is attached to its end.
4. Each character of the result of step 2 is separated first, then all the characters at even positions are merged into one sequence following the original order. Similarly, all the characters at odd positions are merged into one sequence following the original order. Note that the first position of a DNA sequence is index 1.
5. The sequence made up with characters at odd positions becomes the male DNA sequence of generation 1. The one with characters at even positions becomes the female DNA sequence of generation 1.
6. Note that all the male in generation 1 will have the same DNA sequence. The same applies to all the females in generation 1.
7. To get the DNA sequences of generation 2, we go back to step 2. That is, let T_1 be the male DNA sequence of generation 1 and let T_2 be the female DNA sequence of generation 1 and follow steps 2-6.
8. The DNA sequences of generation 3, 4, ..., k can be obtained by following the above steps.

For example, $T_1=AGCTTCGA$ and $T_2=GGCCTA$ at generation 0. Then, the following table shows the male and female DNA sequences for generation 1 and 2. Boldfaces and underlines were used to highlight odd positions.

generation	male	female	note
0	AGCTTCGA	GGCCTA	
1	ACTGGCTGCTACTG	GTCAGCAGCAGTCA	AGCTTCGA + GGCCTA + GGCCTA + AGCTTCGA = <u>AGCTTCGAGGCCTAGGCCTAAGCTTCGA</u>
2	ATGTCATGCGACGC GCGACGCATGTCAT	CGCGTCGTACGATA TACGATACGCGTCG	ACTGGCTGCTACTG + GTCAGCAGCAGTCA + GTCAGCAGCAGTCA +

			ACTGGCTGCTACTG = <u>A</u> CTGGCTGCT <u>A</u> CTGGT <u>C</u> AG <u>C</u> AG <u>C</u> A GTCAGTCAGCAGCAGTCA <u>A</u> CTGGC TGCT <u>A</u> CTG
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Scientists wanted to model these steps but soon found out the steps were rather complicated. Instead of repeating these steps, is there any way that we just know one character at position j of male/female DNA at generation i ?

[Input]

The number of cases T is given in the first line of the input file. Here, $T \leq 100$. In the first line of each case, five integers n_1 , n_2 , i , s , and j are given. n_1 is the length of T_1 and n_2 is that of T_2 . $1 \leq n_1, n_2 \leq 1,000$. i is the generation you are interested in and $1 \leq i \leq 21$. If you are interested in the male DNA sequence, $s=0$. Otherwise, $s=1$. j is the position of the DNA sequence you want to know. It is guaranteed that j is positive and can be represented as a C/C++/Java int variable. Note that the first character of a sequence has index 1. The second line contains a string T_1 , and the third line contains a string T_2 . Both T_1 and T_2 are made up with A, G, C, and T. Their maximum length is 1,000.

The input is given from the following two sets.

- Set 1: $i \leq 10$
- Set 2: no additional constraint.

[Output]

In the first line, print one character which satisfies the input. If the length of the DNA sequence of generation i is smaller than j and no such character exists, print X.

[I/O example]

Input

3
8 6 2 0 1
AGCTTCGA
GGCCTA
4 4 2 1 100
ACTG
GTCA
3 3 3 0 2

AAA

TTT

Output

A

X

T