11 Monsters on Mars

Time Limit: 1 Second
Memory Limit: 2 MB

You have been deputized by the Doom Guy. He is tired of endless monsters spawning in the deserted Mars Research Facility. He would prefer to get to the root of the problem. The geneticists back on Earth have developed a serum that will "neutralize" the monsters when shot through the BFG. However, the serum is calibrated to the base genome sent to Earth. Doom Guy needs to recalibrate the machine by reconstructing the phylogenetic relationship among the all of the monsters, identifying the position of the current monster on the phylogenetic tree and turning the handy dial attached to the New and Improved BFG^{TM} left and right based on the branching of the tree from the base monster to the current monster.

Your job is to read the genomes and create the phylogenetic tree of the monsters. Monster DNA is not regular DNA. In the Monster DNA phylogenetic tree, every DNA sequence mutates at most twice. Each of those can mutate twice, and so on. And the two mutations are closer (differing in fewer base pairs) to their parent than all the other mutations in the tree.

Once the phylogenetic tree is available, Doom Guy can use it locate the genome of the target monster on it and move the dial appropriately left and right as he proceeds down the tree from the base DNA to the target DNA. Unfortunately, monsters do not stand around waiting as their DNA is sequenced, so Doom Guy would have to match a fragment of the whole DNA to find the closest match from the base to the DNA on the tree that contains the whole fragment.

11.1 Input

The first line of input is a string that holds the base DNA for the whole group of monsters. This is followed by an integer 'N', 0 <N $\leq$ 10000. The following N lines will be the mutations of the DNA that will be used to generate the phylogenetic tree. The base genomes and mutated genomes will be of equal length 'S'. The next line will be the DNA fragment of the target monster, of length 'K', 3 $\leq$ K $\leq$ S.

11.2 Output

The output will be the space separated series of directions (Left or Right) from the base genome to the first genome that contains the entire target fragment. The test cases guarantee unique output.

11.3 Sample Input/Output

Sample Input	Sample Output
ACGTACT 5 ACGATCT CCGGACT ACGATAT ACGGTCT ACGGACT CGGT	Left Right