

Problem GENOM: Genom Search

The human genom consists of a sequence of many genes. If the genom of a patient has to be checked for various hereditary diseases this is done by creating a diff between the genom of the patient and the genom of an unformed psycho human. If that diff is too big there is a mutation (deletion or duplication). Your task is to find all interesting regions in the genom. An interesting region is characterized as follows:

It starts and ends with one type of mutation (either deletion or duplication). Between start and end there is an arbitrary number of genes, at least *occ* which show the other type of mutation (either duplication or deletion, other than the beginning and ending mutation). There are no mutations of the first type within the interesting region. The sequence is allowed to include an arbitrary number of no mutated genes.

Note that interesting regions may overlap.

Input

The input contains a single test case. Genes are characterized by their size. The first line of the input contains a double value *deletion*. All genes that are smaller than this value must be treated as a deletions. The second line of the input contains another double value *duplication*. All genes that are larger than this value must be treated as a duplications. The third line contains the integer *occurrence* that determines the number of mutated genes (deletion or duplication) for a genom region to be interesting. The fourth line holds an integer *length* that is the number of genes in the genom we to be analyzed. You may assume that this number is never bigger than 1,000,000. After an empty line, *length* double values follow. These doubles represent the sizes of the genes of the genom.

Output

Each interesting genom region that was found in the given genom must be written to a single line. Sort the output by the beginning index of the interesting region.

If the gene value is below the *deletion* value an 'a' shall be written, If the value is above *duplication* a 'b' shall be written. And if the value is between *deletion* and *duplication* an 'X' for an unmutated gene shall be written.

(Sample Input and Output are provided on the next page)

Sample Input 1

0.2
0.5
2
13

0.3
0.1
0.4
0.7
0.8
0.3
0.4
0.7
0.1
0.1
0.3
0.1
0.7

Sample Output 1

aXbbXXba
baaXab