Problem E. Ants

Input file:	e.in
Output file:	e.out
Time limit:	2 seconds
Memory limit:	256 megabytes

There are K ants running along coordinate grid lines inside the field. A field of size $W \times H$ centimeters has one corner at (0,0) and another one at (W, H). Each ant can run in one of 4 directions with speed 1 centimeter per second.

Since ants are very proude creatures, they never give way. Thus, if several ants face head-on, they immediately turn around and run in the opposite direction. When two ants run perpendicular they will not pay attention to each other. If an ant reaches the boundary of the field it also turns around and runs back.

You are given positions and directions of movement of all the ants in initial moment of time. Find their positions and directions of movement after T seconds.

Input

The first line of input contains 4 integers: W, H, K, T ($1 \le W, H, K \le 100$, $1 \le T \le 10^9$).

Each of the following K lines contains 3 integers: X_i, Y_i, D_i, where (X_i, Y_i) — coordinates the i—th ant, D_i — direction of his movement ($0 < X_i < W$, $0 < Y_i < H$, $1 \le D_i \le 4$). $D_i = 1$ if ant moves in direction of increasing X, $D_i = 2$ — in direction of increasing Y, $D_i = 3$ — in direction of decreasing X, $D_i = 4$ — in direction of decreasing Y.

All of the numbers in lines are separated by single spaces. All ants are located in different points.

Output

Output file consists of exactly K lines — one line for each ant in the same order as they are given in the input. Each line contains 3 integers separated by single spaces — coordinates of the ant and direction of his movement.

Examples

e.in	e.out
4 4 2 3 1 1 1 3 3 4	4 1 3 3 0 2
4 4 2 4 1 1 1 3 3 4	3 1 3 3 1 2
4 4 2 2 1 1 1 3 1 3	1 1 3 3 1 1
4 4 2 2 2 1 1 3 1 3	1 1 3 4 1 3

Note

In 60% testcases $1 \le T \le 1000$.

Problem F. Monkey and Apple-trees

Input file:	`f.in`
Output file:	`f.out`
Time limit:	2 seconds
Memory limit:	256 megabytes

Everyone knows that the yummiest fruit in the world is an apple. Even the monkey Chris knows that. There are many apple-trees in the a forest located along the river and numerated consecutively starting from 1. Sometimes Chris comes to the forest, chooses a group of apple-trees growing consecutively (selected interval) and counts the amount of apple-trees with red-ripen apples among them. Sometimes apples on a few consequtive apple-trees have red-ripen before his next arrival.

You have to answer how many apple-trees in the selected interval have red-ripen apples at each Chris's arrival. At the beginning all the apples are unripen.

Input

In the first line of input file an integer M is given — number of events ($1 \le M \le 100000$). The following M lines contain description of events — each contains three integers D_i, X_i, Y_i ($1 \le D_i \le 2$, $X_i \le Y_i$). If the $D_i = 1$, then the event is Chris's arrival, if the $D_i = 2$ — red-ripening of all apples in the selected interval of the apple-trees. Other two numbers X_i and Y_i, describe the interval for the event.

For calculating the limits of the interval there is an additional number C. At the beginning $C = 0$. An interval for the event is interval from X_i+C to Y_i+C inclusively. It's guaranteed that $1 \le X_i+C, Y_i+C \le 10^9$. If the event is apples red-ripening then C doesn't change. If the event is Chris's arrival, then as the result C becomes equal to the amount of red-ripen apple-trees he has counted.

Output

For each of Chris's arrival output one line with one number in it — the task answer.

Examples

f.in	f.out
3 2 5 8 2 7 10 1 1 10	6
4 2 2 3 1 1 3 2 2 3 1 -1 3	2 4
6 2 1 7 2 10 12 1 7 11 2 11 13 1 8 10 1 15 17	3 2 0

Note

In 35% testcases $M \le 10\,000$, $1 \le X_i + C, Y_i + C \le 10^6$.

In 60% testcases $1 \le X_i + C, Y_i + C \le 10^7$.

Problem G. Mountain Trek Route

Input file:	`g.in`
Output file:	`g.out`
Time limit:	2 seconds
Memory limit:	64 megabytes

In Almaty countryside a mountain cycle trek route (a route with a start and finish at one point) has been constructed. We will simulate the route in a way of stairs (not hills) of one and the same width each, each step i is horizontal and is marked by the sea level a_i meters. Hegths of neighbor stairs may be equal. The $difficulty$ of the route is a sum of *ups* and *downs*. More formaly,

$difficulty = |a_1 - a_2| + |a_2 - a_3| + \cdots + |a_{n-1} - a_n| + |a_n - a_1|$.

The first constructed trek route appeared to be too challenging for tourists. To decrease the route difficulty we can use k blocks. The block's wigth equals stair's width and the block's height equals one meter. We may put any block on any stair or on another block or does't use it at all.

Define the maximum possible decrease of the trek route difficulty.

Input

In the first input file line there are the following numbers N ($2 \le N \le 10^6$) and k ($1 \le k \le 10^9$). In the next line there are n non-negative integers which are the height of each of the stairs.

Output

Output one number, which is maximum possible decrease of the trek route difficulty.

Examples

g.in	g.out
4 5 4 3 2 1	4
3 2 1 2 1	2
7 1000 4 3 3 2 3 2 1	8

Note

In the first test case the difficulty of the trek was equal to 6 (3 *downs* at height one and one *up* at height 3 taking into account the cycle feature of the trek). If we put one block on the third stair and two blocks on the last stair we will decrease the difficulty of the trek at 4. We can use all 5 blocks to produce the same answer, but it's impossible to make any changes to simplify the route more.

In 30% of testcases $N \le 100$, $k \le 1000$.

In 60% of testcases $N \le 100\,000$.

Problem H. Substrings

Input file:	h.in
Output file:	h.out
Time limit:	2 seconds
Memory limit:	256 megabytes

[http://en.wikipedia.org/wiki/Bioinformatics] Since the Phage F-X174 was sequenced in 1977, the DNA sequences of thousands of organisms have been decoded and stored in databases. This sequence information is analyzed to determine genes that encode polypeptides (proteins), RNA genes, regulatory sequences, structural motifs, and repetitive sequences. A comparison of genes within a species or between different species can show similarities between protein functions, or relations between species (the use of molecular systematics to construct phylogenetic trees). With the growing amount of data, it long ago became impractical to analyze DNA sequences manually. Today, computer programs such as BLAST are used daily to search sequences from more than 260 000 organisms, containing over 190 billion nucleotides. These programs can compensate for mutations (exchanged, deleted or inserted bases) in the DNA sequence, to identify sequences that are related, but not identical. A variant of this sequence alignment is used in the sequencing process itself. The so-called shotgun sequencing technique (which was used, for example, by The Institute for Genomic Research to sequence the first bacterial genome, Haemophilus influenzae) does not produce entire chromosomes, but instead generates the sequences of many thousands of small DNA fragments (ranging from 35 to 900 nucleotides long, depending on the sequencing technology). The ends of these fragments overlap and, when aligned properly by a genome assembly program, can be used to reconstruct the complete genome. Shotgun sequencing yields sequence data quickly, but the task of assembling the fragments can be quite complicated for larger genomes. For a genome as large as the human genome, it may take many days of CPU time on large-memory, multiprocessor computers to assemble the fragments, and the resulting assembly will usually contain numerous gaps that have to be filled in later. Shotgun sequencing is the method of choice for virtually all genomes sequenced today, and genome assembly algorithms are a critical area of bioinformatics research.

Input

N lines of input file contain N strings of the length L each. Given strings consists of only English alphabet letters $[A-Za-z]$. $2 \le N \le 100\,000$, $2 \le L \le 100\,000$. Note, letters are case sensitive. In the test cases $N \times L \le 5 \times 1\,024 \times 1\,024$ to reduce input/output.

Output

Output the string of the length $L + N - 1$ that all strings in the input file are its substrings, starting from different positions. It is guaranteed that the correct answer exists. In case of several possible answers output any of them.

Examples

h.in	h.out
abb bba	abba

Note

In about 20% of testcases all letters in answer are different.