6303 Species Evolution

If a group of genes remain physically close to each other in multiple genomes, often called *gene clusters*, then the genes may be either historically or functionally related. Thus, the study of gene clusters is important for the understanding of evolution, since genomes evolved from a common ancestor tend to share the same varieties of gene clusters.

There are many gene cluster models. Dr. Lee uses the following approach to evaluate the quality of a given model. First, he finds a sequence of n species $(S_1, S_2, \ldots, S_n)$, where each S_i, $2 \leq i \leq n$, is evolved from S_{i-1}. Let k be a positive integer. Define $[0, k]$ to be an integer set ranging from 0 to k. Based upon the given gene cluster model, Dr. Lee computes a sequence of numbers $A = (a_1, a_2, \ldots, a_n)$, where each a_i, $1 \leq i \leq n$, is an integer in $[0, k]$ indicating the score of similarity between S_i and S_n. Of course, $a_n = k$. Dr. Lee believes that a perfect gene cluster model should satisfy the following two properties:

P1. The sequence A is digressing (i.e., $a_1 \leq a_2 \leq \ldots \leq a_n$). This property indicates that S_n is more similar to S_i than to S_{i-1} , $2 \leq i \leq n$.

P2. For $2 \leq i \leq n$, the difference between a_{i-1} and a_i is bounded by some threshold δ (i.e., $a_i - a_{i-1} \leq \delta$). This property indicates that S_i should not deviate far from S_{i-1}, since S_i is evolved from S_{i-1}.

In practice, the sequence A may not satisfy properties P1 and P2. Let R^n be the set of all possible sequences of n integers that satisfy properties P1 and P2. Dr. Lee defines the *distance* between A and a sequence $X = (x_1, x_2, \ldots, x_n) \in R^n$ to be $d(A, X) = \sum_{1 \leq i \leq n} (x_i - a_i)^2$. (You may consider $d(A, X)$ as the total cost of modifying each a_i to x_i , $1 \leq i \leq n$.) In addition, he defines the *inaccuracy* of the given gene cluster model to be $\varepsilon(A) = min_{X \in R^n}\{d(A, X)\}$. In other words, he defines the inaccuracy to be the minimum cost of modifying A into a sequence (of n integers) that satisfies properties P1 and P2.

Consider an example of $n = 4$, $k = 10000$, $\delta = 3000$, and $A = (5000, 2000, 6000, 10000)$. Let $B = (5000, 7000, 10000, 12000)$, $C = (3500, 3500, 6500, 9500)$, $D = (5000, 4000, 6000, 8000)$, and $E = (5000, 5500, 6000, 10000)$. Both B and C are in the set R^4. However, D and E are not, since they do not satisfy P1 and P2, respectively. We have $d(A, B) = (5000 - 5000)^2 + (7000 - 2000)^2 + (10000 - 6000)^2 + (12000 - 10000)^2 = 45000000$ and $d(A, C) = (3500 - 5000)^2 + (3500 - 2000)^2 + (6500 - 6000)^2 + (9500 - 10000)^2 = 5000000$. In this example, C has the minimum distance from A among all sequences in R^4. Thus, $\varepsilon(A) = 5000000$.

Please write a program to compute $\varepsilon(A)$.

Input

There are at most 10 test cases. Each case consists of two lines. The first line contains the integer n $(1 \leq n \leq 100)$, the integer k $(10000 \leq k \leq 50000)$, and the integer δ $(0 \leq \delta \leq 5000)$. The second line contains the sequence $A = (a_1, a_2, \ldots, a_n)$, where $a_i \in [0, k]$ for $1 \leq i \leq n - 1$ and $a_n = k$. The last test case will be followed by a line containing a single zero.

Output

For each test case, output one line for $\varepsilon(A)$.

Sample Input

```
4 10000 3000
5000 2000 6000 10000
3 10000 2000
8200 5900 10000
0
```

Sample Output

```
5000000
3246667
```