Problem I.
Protein Structures

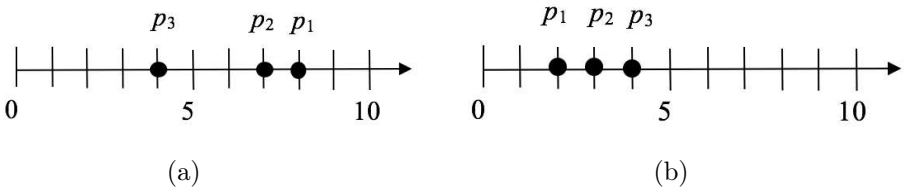
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A protein is a compound made of amino acids, which are linked into a chain. The determination of the amino acid sequence of a protein is an important step toward quantifying this protein and solving its structure and function. However, such a determination is difficult.

Recently, one scientist found that the amino acid sequence of a given protein can be determined by firstly performing a number of experiments on an (expensive) equipment to obtain some useful information and then solving an optimization problem as follows.

The input of the problem consists of a positive integer t and two sets of integers $A = \{a_1, a_2, ..., a_m\}$ and $X = \{x_1, x_2, ..., x_{n-1}\}$, where $0 < a_i < t$ for each $a_i \in A$ and $0 < x_i < t/2$ for $x_i \in X$. Image that we want to place $n-1$ points $p_1, p_2, ..., p_{n-1}$ on a number line. A placement is *valid* if the position of each p_i is either x_i or $t - x_i$.

For example, let $t = 10$, $n = 4$, and $X = \{2, 3, 4\}$. In this example, p_1 can be placed at either 2 or 8; p_2 can be placed at either 3 or 7; and p_3 can be placed at either 4 or 6. Figure 1 shows two valid placements for this example.



(a) (b)

Figure 1: Two valid placements for $t = 10$ and $X = \{2, 3, 4\}$.

Consider a valid placement P. Let $(s_1, s_2, ..., s_{n-1})$ be the sorted sequence of the positions of the $n-1$ points and let $D(P) = (d_1, d_2, ..., d_n)$ be the sequence in which $d_k = s_k - s_{k-1}$ for $1 \le k \le n$, where $s_0 = 0$ and $s_n = t$. For example, in Figure 1(a), we have $(s_1, s_2, s_3) = (4, 7, 8)$ and $(d_1, d_2, d_3, d_4) = (4,$

3, 1, 2); and in Figure 1(b), we have $(s_1, s_2, s_3) = (2, 3, 4)$ and $(d_1, d_2, d_3, d_4) = (2, 1, 1, 6)$.

Different amino acids have different weights. In our application, A represents the set of weights of various known amino acids, n is the number of amino acids in the given protein, and t is the weight of the protein. The set X is produced at the experimental stage. Ideally, there are no errors at the experimental stage and there exists a valid placement P such that the k-th number in $D(P)$, d_k, is just the weight of the k-th amino acid of P; and our problem is to find a valid placement such that all numbers in $D(P)$ are weights in A.

However, in practice, since there may be errors at the experimental stage, our problem is to find a valid placement P such that for each d_k in $D(P)$ there is a number in A that is close to d_k. More formally, define the error of each d_k, $1 \le k \le n$, to be

$$e(d_k) = \min_{1 \le i \le m} |d_k - a_i|$$

and define the error of P to be

$$E(P) = \sum_{1 \le k \le n} e(d_k)$$

For example, let $m = 3$ and $A = \{1, 4, 7\}$. Then, in Figure 1(a), we have $e(d_1) = e(4) = |4 - 4| = 0$, $e(d_2) = e(3) = |3 - 4| = 1$, $e(d_3) = e(1) = |1 - 1| = 0$, and $e(d_4) = e(2) = |2 - 1| = 1$. Thus, for the placement in Figure 1(a), we have $E(P) = 2$. Similarly, it can be seen that for the placement in Figure 1(b), we have $E(P) = 1 + 0 + 0 + 1 = 2$. The number of valid placements is 2^{n-1}. Our problem is to find a valid placement P that minimizes $E(P)$.

Input

The first line contains an integer T indicating the number of test cases.

Each test case begins with a line containing the three integers t, m, and n. Then, two lines follow, where the first line gives the m integers of A and the second line gives the $n - 1$ integers of X.

- $1 \leq T \leq 10$
- $2 \leq t \leq 10^7$
- $2 \leq m \leq 10^6$
- $2 \leq n \leq 3000$
- All numbers in A are (distinct) integers between 1 and t.
- All numbers in X are (distinct) integers between 1 and $t/2 - 1$.

Output

For each test case, print a line containing the minimum error $E(P)$.

Sample Input	Sample Output
2 10 3 4 1 7 4 2 3 4 20 4 5 1 3 4 9 8 1 5 9	2 0

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