A DNA sequence is composed of a series of four possible nucleobases, namely Adenine, Guanine, Thymine and Cytosine; we will refer to each of these bases by their initial. For our purposes, nucleobases have an associated cyclic "order": `A` is followed by `G`, which in turn is followed by `T`, which is followed by `C`, which is followed by `A` again. State-of-the-art research in genomics has revealed the startling fact that many diseases are caused by certain subsequences of bases not forming a palindromic sequence! Your mission as a leading researcher at ICPC laboratories is to take a DNA string S and a series of subsets $P_1, \ldots, P_t$ of indices to characters (nucleobases) in S, and transform S so that each of the restrictions of the resulting string to $P_1, \ldots, P_t$ are palindromic. (The restriction of S to a subset $P = \{i_1, i_2, \ldots, i_k\}$ of indices, where $0 \leq i_1 < i_2 < \ldots < i_k < |S|$, is the string $S_{i_1} S_{i_2} \ldots S_{i_k}$). It is possible to inspect any base of S at will, but only three transformations can be applied to a base:

1. Leave it unaltered.
2. Increase it by 1 in the cyclic order of nucleobases (e.g. turn `C` into `A`).
3. Decrease it by 1 (e.g. turn `T` into `G`).

Moreover, owing to limitations of current technology, it is impossible to modify two bases in consecutive positions of the sequence. Is our goal achievable?

By way of example, consider DNA sequence `AGTAT`. Number positions starting from 0, and suppose we have the three subsets $P_1 = \{1, 4\}$, $P_2 = \{0, 1\}$ and $P_3 = \{0, 2, 4\}$. One solution is to increase the first character and decrease the last, yielding $S' =$ `GGTAG`. The restrictions of S' to P_1, P_2 and P_3 are `GG`, `GG` and `GTG`, respectively; all of them are palindromic.

One case where no solution is possible is when the string is `CATGC`, and we require the subsequences determined by positions $\{0, 3\}$ and $\{3, 4\}$ be palindromic. Here, characters 3, 0 and 4 would all need to become a `T`. But this entails modifying consecutive characters 3 and 4, which is not allowed.

Input

The first line of each test case has two integers N and T ($1 \leq N \leq 10\,000, 1 \leq T \leq 6\,000$), the sequence length and number of subsets to consider. The next line contains the DNA sequence of length N, all of whose characters are in `ACGT`. The subsets are described by the following T lines. Each line starts by "L:", where L ($0 \leq L \leq N$) is the number of positions in the subset, and is followed by L distinct integers between 0 and $N - 1$ in increasing order. Subsets may overlap partially or totally.

A blank line separates different test cases. The input file is terminated by a line containing '`0 0`'.

Output

In a single line per test case, print '`YES`' if the task is solvable and '`NO`' otherwise.

Sample Input

```
5 3
AGTAT
2: 1 4
2: 0 1
3: 0 2 4

5 3
CATGC
0:
2: 0 3
2: 3 4

0 0
```

Sample Output

```
YES
NO
```