

Epigenomic Marks 2

While having a constant nucleotide sequence, DNA molecules in a cell can be chemically modified in several different ways. For example, the DNA bases can be methylated, or histone proteins, around which DNA is wrapped, can be supplied with chemical tags such as acetylation. It is thought that such modifications (or epigenomic marks) define cell specialization or a cell state when a specific combination of marks regulates how genes are expressed.

In this problem, you are given genomic tracks describing the presence or absence of several epigenomic marks. Your task is to split the genomic positions into the smallest number of states so that each state corresponds to a particular combination of marks.

Input format

The first line of the input contains t — the number of tests.

Each test consists of multiple lines. The first line contains two integers n and l — the number of sequences and their length. The remaining n lines in the test include sequences of 0 and 1, describing the epigenomic marks. All sequences have the same length l .

Output format

Your output file should contain $2t$ lines with two lines per test. The first line of the answer on a test should contain the minimal number of used states s to distinguish all combinations of marks. The second line should contain l numbers separated by spaces — the states per each position, encoded as numbers from 1 to s .

Scoring

Scoring is described in the first step.

Sample input

```
2
4 10
0010001000
1001000001
```

```
00011100010100
00111000010001
```

Sample output

```
6
1 2 3 4 5 2 3 6 5 4
4
1 1 2 3 3 4 1 1 1 3 1 4 1 2
```

Notes

Let us consider the first sample test case. We have the following states (as read by positions): 0100, 0010, 1001, 0110, 0000, 0010, 1001, 0001, 0000, 0110. There are only 6 different states. Thus, we should map them to numbers from 1 to 6 as shown in the sample output.