DNA Sorting

One measure of ``unsortedness'' in a sequence is the number of pairs of entries that are out of order with respect to each other. For instance, in the letter sequence ``DAABEC'', this measure is 5, since D is greater than four letters to its right and E is greater than one letter to its right. This measure is called the number of inversions in the sequence. The sequence ``AACEDGG'' has only one inversion (E and D)--it is nearly sorted--while the sequence ``ZWQM'' has 6 inversions (it is as unsorted as can be--exactly the reverse of sorted).

You are responsible for cataloguing a sequence of DNA strings (sequences containing only the four letters A, C, G, and T). However, you want to catalog them, not in alphabetical order, but rather in order of ``sortedness'', from ``most sorted'' to ``least sorted''. All the strings are of the same length.

Input

The first line of the input is an integer M, then a blank line followed by M datasets. There is a blank line between datasets.

The first line of each dataset contains two integers: a positive integer n ($0 < n \leq 50$) giving the length of the strings; and a positive integer m ($0 < m \leq 100$) giving the number of strings. These are followed by m lines, each containing a string of length n.

Output

For each dataset, output the list of input strings, arranged from ``most sorted'' to ``least sorted''. If two or more strings are equally sorted, list them in the same order they are in the input file.

Print a blank line between consecutive test cases.

Sample Input

```
1

10 6
AACATGAAGG
TTTTGGCCAA
TTTGGCCAAA
GATCAGATTT
CCCGGGGGGA
ATCGATGCAT
```

Sample Output

```
CCCGGGGGGA
AACATGAAGG
GATCAGATTT
ATCGATGCAT
TTTTGGCCAA
TTTGGCCAAA
```

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1999-03-24