

1608 - DNA Sorting

Description

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 specification

The input consists of several test cases. The first line of each test case 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 . After the last input set is a single line containing the text "0 0".

Output specification

Output the list of input strings arranged from *most sorted* to *least sorted*. Since two strings can be equally sorted, the inputs with the same number of inversions must be ordered lexicographically. You must output an empty line between test cases.

Sample input

```
10 6
AACATGAAGG
TTTTGGCCAA
TTTGGCCAAA
```

```
GATCAGATTT
CCCGGGGGGA
ATCGATGCAT
0 0
```

Sample output

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

Hint(s)

Source	University of Valladolid Online Judge
Added by	ymondelo20
Addition date	2011-11-15
Time limit (ms)	1000
Test limit (ms)	1000
Memory limit (kb)	130000
Output limit (mb)	64
Size limit (bytes)	30000
Enabled languages	C C# C++ Java Pascal Perl PHP Python Ruby Text