Goal

Your mission is to evaluate the genetic potential of the candidates of a new space center. For this, you have developed a method of sequencing their DNA. The candidate is a 1-chromosome double-stranded species. That is to say that its DNA can be seen as two strings of characters **a** and **b** composed exclusively of the letters A, C, G and T. Moreover, these two chains are complementary, they are therefore of the same length and verify:

- $a[i] = A \Leftrightarrow b[i] = T$
- $a[i] = T \Leftrightarrow b[i] = A$
- $a[i] = C \Leftrightarrow b[i] = G$
- $a[i] = G \Leftrightarrow b[i] = C$

During sequencing, the two chains break into several small fragments that are mixed together. Your method is not that bad, you know that the order of characters in a fragment has not been reversed. However, you need to write a program to pick up the pieces in a plausible order to reconstitute the 2 strands. To make sure that you have not forgotten any fragments, your program will return the two strings **a** and **b** separating the different fragments by spaces.

Tip: the DNA of a candidate is not very complex, there will never be more than 8 fragments, so you can proceed by exhaustive enumeration (brute force).

Example

If you have the following fragments:
```
AT
G
CC
TAG
```

A possible solution would be:

Brin 1	T A G G
Brin 2	A T C C

That would give the following output (the output format is described in the Data section) :
```
TAG G#AT CC
```
Swapping strands *1* and *2* would also lead to a possible solution.

Data

<u>Input</u>

Row *1*: an integer number **N** comprised between *2* and *8*, representing the number of fragments.
Row *2* to **N+1**: a string comprising between 1 and 16 characters made only of the following letters A, T, C and G representing a fragment.

<u>Output</u>

A string representing the 2 strands. The 2 strands are separated by the # character and within a given strand the used fragments are separated by spaces.

You can download sample input and output data files to work locally by clicking on the link at the bottom of the French version of the question

⬇ Téléchargez des fichiers d'exemple ainsi qu'un modèle de code pour travailler localement.