

3952 Rabbit detector

You work in a population genetics lab, studying the effects of applying cosmetics to furry animals (on their health, not on their social lives). One day when you try to open a database of results, you realise that a power glitch has corrupted your files.

After looking at the raw data, you realise that the effect of the data corruption was that your experiment labels have been shuffled. In other words, you no longer know whether a set of results belong to experiments conducted on rabbits, rats, or an experiment which included both rats and rabbits.

Fortunately, one of the fields in each set of results is the monthly population size of the experimental group. You begin to ponder if it may be possible to identify what the experimental label should be, given the population numbers.

You recall that rabbits multiply at a fixed rate. In other words, if you start with two rabbits, they will produce one little rabbit every month. The baby rabbits take one month to mature, after which they start reproducing at the same rate. A sequence of rabbit population number would thus look as follows:

1, 1, 2, 3, 5, 8, 13, ...

In general, the rabbit population size in month n (for $n \geq 2$) can be expressed using the following recurrence relation:

$$L_n = L_{n-1} + L_{n-2}$$

where

$$L_0 = 1, \text{ and } L_1 = 1.$$

For the specific type of lab rat that you use in your experiments, a similar sequence describes the population numbers, namely:

1, 1, 3, 5, 11, 21, 43, ...

The recurrence relation describing the rat population size in month n (for $n \geq 2$) can be expressed using the following recurrence relation:

$$R_n = R_{n-1} + 2R_{n-2}$$

where

$$R_0 = 1, \text{ and } R_1 = 1.$$

Lastly, in experiments that involved both rabbits and rats, the population size field in your result set represent the sum of the rabbit and rat population sizes. This means for such mixed experiments, the population size in month n can be expressed as

$$P_n = L_n + R_n$$

You decide to write a program to process the corrupted file, and guess what the appropriate label should be for each record, based on the population size field.

Sometimes it will not be possible to uniquely identify what the appropriate label should be; in those cases you would be happy with multiple labels for now.

Input

Your input will be a list of positive integers, with each integer representing the population size field of an experiment. The input will be terminated by a negative integer.

The integers will always be smaller than 2^{32} .

Output

Your output must be of the format

`< value > < space > : < space > < id > [, < space > < id >] [, < space > < id >]`

where square brackets '[' and ']' denote optional strings, and `< value >` is the input population size value. The `< id >` tag denotes one of the strings 'rat', 'rabbit', or 'rat+rabbit'. Each output record must be separated with a newline character.

It is possible that a given population size value (for example, the value 4) does not correspond to any valid rat, rabbit, or rat-and-rabbit experiment. These numbers should be ignored, and no output should be produced for such numbers.

When more than one label is applicable to a given input value, the labels must be output in the order 'rat', 'rabbit', and then 'rat+rabbit'.

Sample Input

```
1
2
4
5
13
11
7
-1
```

Sample Output

```
1 : rat, rabbit
2 : rabbit, rat+rabbit
5 : rat, rabbit, rat+rabbit
13 : rabbit
11 : rat
```