

More Exercise: Arrays

Problems for exercises and homework for the ["Programming Fundamentals" course @ SoftUni](#).

You can check your solutions in [Judge](#).

1. Encrypt, Sort and Print Array

Write a program that reads a **sequence of strings** from the console. Encrypt every string by summing:

- The code of **each vowel multiplied by the string length**.
- The code of **each consonant is divided by the string length**.

Sort the **number** sequence in ascending order and print it on the console.

On the first line, you will always receive the number of strings you must read.

Examples

Input	Output	Comments
4 Peter Maria Katya Todor	1032 1071 1168 1532	Peter = 1071 Maria = 1532 Katya = 1032 Todor = 1168
3 Sofia London Washington	1396 1601 3202	Sofia = 1601 London = 1396 Washington = 3202

2. Pascal Triangle

The triangle may be constructed in the following manner: In row 0 (the topmost row), there is a unique nonzero entry 1. Each entry of each subsequent row is constructed by adding the number above and to the left with the number above and to the right, treating blank entries as 0. For example, the initial number in the first (or any other) row is 1 (the sum of 0 and 1), whereas the numbers 1 and 3 in the third row are added to produce the number 4 in the fourth row.

If you want more info about it: https://en.wikipedia.org/wiki/Pascal's_triangle

Print each row element, separated with whitespace.

Examples

Input	Output
4	1 1 1 1 2 1 1 3 3 1
13	1 1 1 1 2 1 1 3 3 1 1 4 6 4 1

	1	5	10	10	5	1							
	1	6	15	20	15	6	1						
	1	7	21	35	35	21	7	1					
	1	8	28	56	70	56	28	8	1				
	1	9	36	84	126	126	84	36	9	1			
	1	10	45	120	210	252	210	120	45	10	1		
	1	11	55	165	330	462	462	330	165	55	11	1	
	1	12	66	220	495	792	924	792	495	220	66	12	1

Hints

- The input number **n** will be **1 <= n <= 60**.
- Think about the proper **type** for elements in an array.
- Don't be scared to use **more and more arrays**.

3. Recursive Fibonacci

The Fibonacci sequence is quite a famous sequence of numbers. Each sequence member is calculated from the sum of the two previous elements. The **first two** elements are 1, 1. Therefore the sequence goes like 1, 1, 2, 3, 5, 8, 13, 21, 34...

The following sequence can be generated with an array, but that's easy, so your task is to implement it recursively.

So if the function **GetFibonacci(n)** returns the n'th Fibonacci number we can express it using **GetFibonacci(n) = GetFibonacci(n-1) + GetFibonacci(n-2)**.

However, this will never end and in a few seconds, a StackOverflow Exception is thrown. For the recursion to stop, it has to have a "**bottom**". At the bottom of the recursion is **GetFibonacci(2)** should return 1, and **GetFibonacci(1)** should return 1.

Input

- The user should enter the wanted Fibonacci number on the only line in the input.

Output

- The output should be the n'th Fibonacci number counting from 1.

Constraints

- $1 \leq N \leq 50$

Examples

Input	Output
5	5
10	55
21	10946

For the Nth Fibonacci number, we calculate the N-1th and the N-2th number, but for the calculation of the N-1th number, we calculate the N-1-1th(N-2th) and the N-1-2th number, so we have a lot of repeated calculations.

5. Kamino Factory

The clone factory in Kamino got another order to clone troops. But this time, you are tasked to find **the best DNA** sequence to use in the production.

You will receive the **DNA length**, and until you receive the command **"Clone them!"** you will be receiving **DNA sequences of ones and zeroes, split by "!"** (one or several).

You should select the sequence with the **longest subsequence of ones**. If there are several sequences with the **same length of a subsequence of ones**, print the one with the **leftmost starting index**, if there are several sequences with the same **length and starting index**, select the sequence with the **greater sum** of its elements.

After you receive the last command **"Clone them!"**, you should print the collected information in the following format:

"Best DNA sample {bestSequenceIndex} with sum: {bestSequenceSum}."

"{DNA sequence, joined by space}"

Input / Constraints

- The **first line** holds the **length of the sequences – integer in the range [1...100]**.
- On the next lines, until you receive **"Clone them!"** you will be receiving sequences (at least one) of ones and zeroes, **split by "!"** (one or several).

Output

The output should be printed on the console and consists of two lines in the following format:

"Best DNA sample {bestSequenceIndex} with sum: {bestSequenceSum}."

"{DNA sequence, joined by space}"

Examples

Input	Output	Comments
5 1!0!1!1!0 0!1!1!0!0 Clone them!	Best DNA sample 2 with sum: 2. 0 1 1 0 0	We receive 2 sequences with the same length of a subsequence of ones , but the second is printed because its subsequence starts at index[1] .
4 1!1!0!1 1!0!0!1 1!1!0!0 Clone them!	Best DNA sample 1 with sum: 3. 1 1 0 1	We receive 3 sequences. Both 1 and 3 have the same length of a subsequence of ones -> 2, and both start from the index[0] , but the first is printed because its sum is greater .

6. LadyBugs

You are **given a field size** and the **indexes of ladybugs** inside the field. After that, on every new line, **until the "end" command** is given, a ladybug changes its position to its left or **right by a given fly length**.

A **command to a ladybug** looks like this: **"0 right 1"**. This means that the little insect placed on index 0 should fly one index to its right. If the ladybug **lands on a fellow ladybug**, it **continues to fly** in the same direction **by the same fly length**. If the ladybug **flies out of the field**, it is **gone**.

For example, imagine you are given a field with size 3 and ladybugs on indexes 0 and 1. If the ladybug on index 0 needs to fly to its right by the length of 1 (0 right 1) it will attempt to land on index 1, but as there is another ladybug there,

it will continue further to the right by an additional length of 1, landing on index 2. After that, if the same ladybug needs to fly to its right by the length of 1 (2 right 1), it will land somewhere outside of the field, so it flies away:



If you are given a ladybug index that does not have a ladybug there, nothing happens. If you are given a ladybug index that is outside the field, nothing happens.

Your job is to create the program, simulating the ladybugs flying around doing nothing. In the end, **print all cells in the field separated by blank spaces**. For each cell that has a ladybug on it print '1' and for each empty cell print '0'. For the example above, the output should be '0 1 0'.

Input

- On the first line, you will receive an integer - the size of the field.
- On the second line, you will receive the initial **indexes** of all ladybugs separated by a blank space. **The given indexes** may or may not be inside the field range.
- On the next lines, until you get the "end" command you will receive commands in the format: "{ladybug index} {direction} {fly length}".

Output

- Print the **all cells within the field in format**: "{cell} {cell} ... {cell}"
 - If a cell has a ladybug in it, print '1'.
 - If a cell is empty, print '0'.

Constraints

- The **size of the field** and **number of commands** will be in the range [0 ... 1000].
- The **ladybug indexes** and **fly length** will be in the range [-2,147,483,647 ... 2,147,483,647].

Examples

Input	Output	Comments
3 0 1 0 right 1 2 right 1 end	0 1 0	1 1 0 - Initial field 0 1 1 - field after "0 right 1" 0 1 0 - field after "2 right 1"
3 0 1 2 0 right 1 1 right 1 2 right 1 end	0 0 0	
5 3 3 left 2 1 left -2 end	0 0 0 1 0	