

## 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 a **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 **same length of subsequence of ones**, print the one with the **leftmost starting index**, if there are several sequences with 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 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 <b>same length of subsequence of ones</b> , but the second is printed, because its subsequence starts at <b>index[1]</b> .
Input	Output	Comments
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 <b>have same length</b> of subsequence of ones -> 2, <b>and both start from index[0]</b> , but the first is printed, because its <b>sum is greater</b> .