Task Description   **Day-2**
IOI 2004
Athens   **Version 1.2**
Greece   **empodia**

Empodia

PROBLEM

The ancient mathematician and philosopher Pythagoras believed that reality is mathematical in nature. Present-day biologists study properties of biosequences. A biosequence is a sequence of M integers, which

- contains each of the numbers $0,1,\ldots,M-1$,
- starts with 0 and ends with $M-1$, and
- has no two elements $E,E+1$ in adjacent positions in this order.

A subsequence consisting of adjacent elements of a biosequence is called a *segment.*.

A segment of a biosequence is called a *framed interval* if it includes all integers whose values are between the value of the first element, which must be the smallest element in the segment, and the last element, which must be the largest and different from the first. A framed interval is called an *empodio* if it does not contain any shorter framed intervals.

As an example, consider the biosequence (0,3,5,4,6,2,1,7). The whole biosequence is a framed interval. However, it contains another framed interval (3,5,4,6) and therefore it is not an empodio. The framed interval (3,5,4,6) does not contain a shorter framed interval, so it is an empodio. Furthermore, it is the only empodio in that biosequence.

You are to write a program that, given a biosequence, finds all empodia (plural for empodio) in that biosequence.

INPUT

The input file name is `empodia.in`. The first line contains a single integer M: the number of integers in the input biosequence. The following M lines contain the integers of the biosequence in the order of the sequence. Each of these M lines contains a single integer.

OUTPUT

The output file name is `empodia.out`. The first line in this file is to contain one integer H: the number of empodia in the input biosequence. The following H lines describe all empodia of the input biosequence in the order of appearance of the starting point in the biosequence. Each of these lines is to contain two integers A and B (in that order) separated by a space, where the Ath element of the input biosequence is the first element of the empodio and the Bth element of the input biosequence is the last element of the empodio.

EXAMPLE INPUTS AND OUTPUTS

`empodia.in`   `empodia.out`

```
8
0
3
5
4
6
2
1
7
```

```
1
2 5
```

CONSTRAINTS

In one input, $1000000 \leq M \leq 1100000$. In all other inputs, $1 \leq M \leq 60000$.
Additionally, in 50% of the inputs, $M \leq 2600$.