

Germ Genealogy

Purpose: Storing Graphs, Topological Sort, Priority Queues

Due: March 27th

Description

Scientists are currently studying how germs are produced. Specifically they are looking at specific genes. A specific germ can be thought of as getting its genes from 1 ancestor cell or from a group of ancestor cells. You are to write a program to sort the germs by their genes. Given a set of germs you are sort them by order of inheritance. The germs that have no ancestors in the group come first and the germs that have no offspring germs come last.

Input

The first line of the standard input contains the single number n , $1 \leq n \leq 100$ —a number germs to be sorted. Germs will be identified with an integer from 1 up to n . This is followed by n lines; where the i^{th} line contains a list of i^{th} germ's children. The list of children is a sequence of serial numbers of children in an arbitrary order separated by spaces. The list of children may be empty. Each list ends with 0.

Output

The output consists of one line containing sequence of germ numbers. Each number is separated by a single space. If several sequences satisfy the conditions of the problem, you are to write the one that comes first lexicographically.

Sample Input

```
5
0
4 5 1 0
1 0
5 3 0
3 0
```

Corresponding Sample Output

2 4 5 3 1

How the program will be graded

Memo

What	pts	March 27 th
Name	1	
Justify your choices of all data structures/implementation Give at least 1 alternative for each , why it was rejected	10	
Time/Space analysis of all functions	10	

Source Code Document

What	pts	March 27 th
Name	1	
Description	4	
Style	10	
pre/post conditions	10	
Number of test cases passed by the autograder	30	
Implementation of a priority queue with updateKey	24	

Hint

A directed graph is used to represent the system of germ relationships, where germs are represented as vertices, and edges are from parents to children. The sequence of germs is a topological sort for the directed graph.