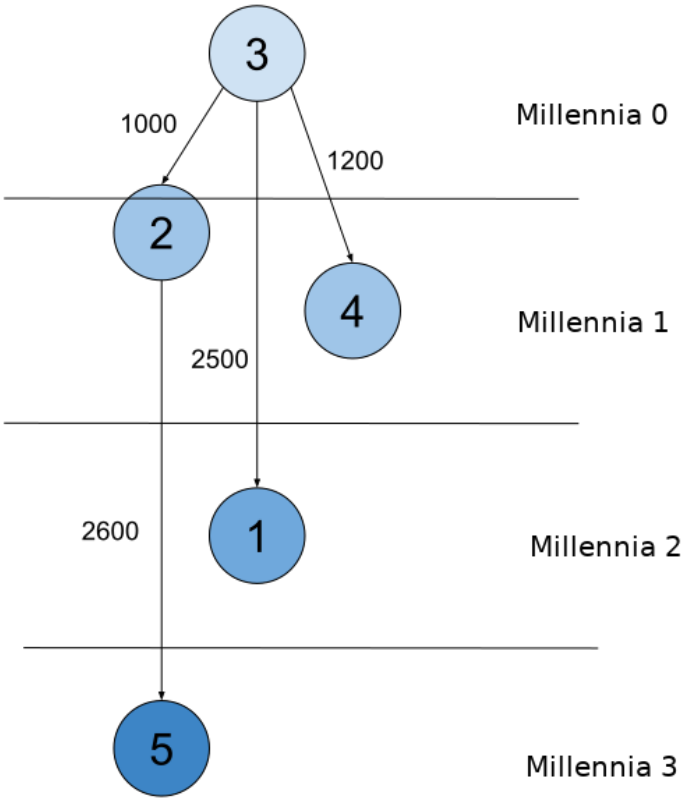
Famtree

SEASON 9 – FOURTH ROUND

Because of recent advances in paleontology and discoveries of new connections between species, a need for better processing of that data has arisen. You will be given a list of discoveries, every record of which containing: species **A**, which evolved from species **B** and after how many years that happened. Your task is to find millennia (period of 1000 years) where more species appeared than the millennia before and after it.

It is guaranteed that there is only one species that doesn't evolve from any other. We can presume that happened in year 0 and thus in millennia 0. There is no millennia before it. As you can see in the picture below, this is species №3. Species №2 and №4 evolve from it after 1000 and 1200 years, in millennia 1. Species №1 comes 2500 years after №3 (millennia 2). Finally, species №5 appears 2600 years after №2, which puts it in year 3600 and millennia 3.



Famtree

SEASON 9 – FOURTH ROUND

Input

From the first line of the input file `famtree.in` single integer **N** is entered - the number of known species. On each of the next **N-1** lines 3 integers are entered - $\mathbf{A_i}$, $\mathbf{B_i}$, $\mathbf{Y_i}$ - species $\mathbf{A_i}$ evolved from species $\mathbf{B_i}$ after $\mathbf{Y_i}$ years.

Output

In the output file `famtree.out` print on a **single line** the millennias in which more species appeared than the millennia before and after it, separated with spaces, in ascending order.

Constraints

$1 \leq N \leq 10\ 000$

$1 \leq Ai,\ Bi \leq N$

$1 \leq Yi \leq 10\ 000$

Time limit: 0.3 seconds
Memory limit: 256 MB

Example

Input (famtree.in)	Output (famtree.out)
5 5 2 2600 4 3 1200 2 3 1000 1 3 2500	1

The test matches the picture above. Millennia 1 has two species and millennias 0 and 2 have one.