Problem C
Exon Chaining

Input File: *testdata.in*
Time Limit: 5 seconds

Problem Description

It is known that most human genes are broken into pieces called *exons* that
are separated by junk DNA, called *introns*. A DNA string is called *putative*
exon if it might be an exon. A putative exon can be modeled as a weighted
interval in the genomic sequence, which is described by three parameters
(l, r, w). Here, l is the left-hand position, r is the right-hand position, and
w is the weight of the putative exon. Of course, $l < r$. Two putative exons
$p_i = (l_i, r_i, w_i)$ and $p_j = (l_j, r_j, w_j)$ are *compatible* if $r_i \leq l_j$ or $r_j \leq l_i$. A
chain is a set of mutually compatible putative exons. A *maximum chain* is
a chain with maximum total weight among all possible chains. Given a set
of putative exons, the exon chaining problem is to find the total weight of a
maximum chain.

Technical Specifications

1. The number of test cases would be smaller than or equal to 10.

2. For any putative exon (l, r, w), $1 \leq l, r, w \leq 10000$.

Input Format

The first line of the input file contains an integer indicating the number of
test cases to follow. Each test case contains $n + 1$ lines. The first line is the
number n, *i.e.*, the number of putative exons. For the remaining lines, each
line contains three integers l, r, and w separated by spaces.

Output Format

For each test case, output the total weight of a maximum chain on a line.

Sample Input

```
2
4
1 3 2
2 5 4
6 9 7
4 8 5
5
2 3 3
1 5 6
4 8 5
6 10 9
7 12 7
```

Sample Output

```
11
15
```