

Problem D

Locating Conserved Genes in Multiple Species

Input file: *pd.in*
Time limit: 3 seconds

Problem Description

In the comparison of genomes of human, chimpanzee, and macaque, the order of genes in different species may be reshuffled by large rearrangement events. Using alignment algorithms, genes retained in all three species can be discovered. Genes reshuffled by rearrangement events may create lineage-specific features. On the other hand, genes in the same order and shared by three species are considered to have important functions among primates. Now, biologists would like to locate conserved genes in these three species. Suppose genes in the human genome are numbered in an increasing order (e.g., Genes 1, 2, 3, 4, 5). Genes in the other two species are numbered according to their matched genes in the human genome (e.g., Genes 2, 3, 1, 4, 5 in chimpanzee and Genes 5, 1, 2, 3, 4 in macaque). For each gene i , we also have a similarity score $S[i]$ obtained from the alignment results (e.g., $S[1] = 10$, $S[2] = 20$, $S[3] = 30$, $S[4] = 5$, $S[5] = 10$). Now you are asked to find a subset of genes having the same order in all species and having the largest total score. For example, Genes 2, 3, 4, and 5 are not a feasible solution, because this order is not consistent in macaque. On the other hand, Genes 2, 3, and 4 have the largest total score 55.

Technical Specification

1. The total number of genes N is an integer satisfying $1 \leq N \leq 5000$. Each gene appears only once in a genome.
2. Each gene is labeled with a distinct integer ranging from 1 to N .

3. The similarity score of each gene $S[i]$ is an integer satisfying $1 \leq S[i] \leq 100$, where $1 \leq i \leq N$.

Input Format

The first line of the input file contains an integer indicating the number of test cases to follow. Each test case starts with a positive integer N representing the number of genes, which is followed by one line of similarity score ($S[1]$, $S[2]$, ..., $S[N]$) and two lines of gene order in chimpanzee and macaque, separated by spaces.

Output Format

For each test case, output the maximum total score of conserved genes in each line.

Sample Input

```
2
3
4 5 6
1 2 3
1 3 2
6
2 3 10 2 4 5
1 5 6 2 4 3
1 6 5 2 3 4
```

Sample Output

```
10
15
```