

# Determining DNA Health

**DNA** is a nucleic acid present in the bodies of living things. Each piece of DNA contains a number of *genes*, some of which are beneficial and increase the DNA's *total health*. Each gene has a *health value*, and the *total health* of a DNA is the sum of the health values of all the beneficial genes that occur as a substring in the DNA. We represent genes and DNA as non-empty strings of lowercase English alphabetic letters, and the same gene may appear multiple times as a substring of a DNA.

Given the following:

- An array of beneficial gene strings,  $genes = [g_0, g_1, \dots, g_{n-1}]$ . Note that these gene sequences are *not* guaranteed to be distinct.
- An array of gene health values,  $health = [h_0, h_1, \dots, h_{n-1}]$ , where each  $h_i$  is the health value for gene  $g_i$ .
- A set of  $s$  DNA strands where the definition of each strand has three components, *start*, *end*, and *d*, where string *d* is a DNA for which genes  $g_{start}, \dots, g_{end}$  are healthy.

Find and print the respective total healths of the *unhealthiest* (minimum total health) and *healthiest* (maximum total health) strands of DNA as two space-separated values on a single line.

## Input Format

The first line contains an integer,  $n$ , denoting the total number of genes.

The second line contains  $n$  space-separated strings describing the respective values of  $g_0, g_1, \dots, g_{n-1}$  (i.e., the elements of *genes*).

The third line contains  $n$  space-separated integers describing the respective values of  $h_0, h_1, \dots, h_{n-1}$  (i.e., the elements of *health*).

The fourth line contains an integer,  $s$ , denoting the number of strands of DNA to process.

Each of the  $s$  subsequent lines describes a DNA strand in the form `start end d`, denoting that the healthy genes for DNA strand *d* are  $g_{start}, \dots, g_{end}$  and their respective correlated health values are  $h_{start}, \dots, h_{end}$ .

## Constraints

- $1 \leq n, s \leq 10^5$
- $0 \leq h_i \leq 10^7$
- $0 \leq first \leq last < n$
- $1 \leq \text{the sum of the lengths of all genes and DNA strands} \leq 2 \times 10^6$
- It is guaranteed that each  $g_i$  consists of lowercase English alphabetic letters only (i.e., `a` to `z`).

## Output Format

Print two space-separated integers describing the respective total health of the *unhealthiest* and the *healthiest* strands of DNA.

Sample Input 0

```
6
a b c aa d b
1 2 3 4 5 6
3
1 5 caaab
0 4 xyz
2 4 bcdybc
```

Sample Output 0

```
0 19
```

Explanation 0

In the diagrams below, the ranges of beneficial genes for a specific DNA on the left are highlighted in *green* and individual instances of beneficial genes on the right are bolded. The total healths of the  $s = 3$  strands are:

$d = \text{caaab}, \text{first} = 1, \text{last} = 5$

indices	0	1	2	3	4	5
genes	a	b	c	aa	d	b
health	1	2	3	4	5	6

gene	caaab	caaab	caaab	caaab	caaab
value	3	4	4	2	6

1. The total health of caaab is  $3 + 4 + 4 + 2 + 6 = 19$ .

$d = \text{xyz}, \text{first} = 0, \text{last} = 4$

indices	0	1	2	3	4	5
genes	a	b	c	aa	d	b
health	1	2	3	4	5	6

gene	xyz
value	0

2. The total health of xyz is 0, because it contains no beneficial genes.

$d = \text{bcdybc}, \text{first} = 2, \text{last} = 4$

indices	0	1	2	3	4	5
genes	a	b	c	aa	d	b
health	1	2	3	4	5	6

gene	bcdybc	bcdybc	bcdybc
value	3	5	3

3. The total health of bcdybc is  $3 + 5 + 3 = 11$ .

The unhealthiest DNA strand is xyz with a total health of 0, and the healthiest DNA strand is caaab with a total health of 19. Thus, we print 0 19 as our answer.