

# Rajalakshmi Engineering College

Name: ANIRUDH R  
Email: 240701039@rajalakshmi.edu.in  
Roll no: 240701039  
Phone: 9363540767  
Branch: REC  
Department: I CSE FA  
Batch: 2028  
Degree: B.E - CSE

Scan to verify results



## NeoColab\_REC\_CS23221\_Python Programming

### REC\_Python\_Week 5\_CY

Attempt : 1  
Total Mark : 40  
Marks Obtained : 36.5

### Section 1 : Coding

#### 1. Problem Statement

Alex is tasked with managing the membership lists of several exclusive clubs. Each club has its own list of members, and Alex needs to determine the unique members who are part of exactly one club when considering all clubs together.

Your goal is to help Alex by writing a program that calculates the symmetric difference of membership lists from multiple clubs and then finds the total number of unique members.

#### ***Input Format***

The first line of input consists of an integer  $k$ , representing the number of clubs.

The next  $k$  lines each contain a space-separated list of integers, where each

integer represents a member's ID.

### **Output Format**

The first line of output displays the symmetric difference of the membership lists as a set.

The second line displays the sum of the elements in this symmetric difference.

Refer to the sample output for the formatting specifications.

### **Sample Test Case**

Input: 3

1 2 3

2 3 4

5 6 7

Output: {1, 4, 5, 6, 7}

23

### **Answer**

```
k = int(input())
```

```
clubs = []
```

```
for _ in range(k):
```

```
    members = set(map(int, input().split()))
```

```
    clubs.append(members)
```

```
symmetric_difference = clubs[0]
```

```
for club in clubs[1:]:
```

```
    symmetric_difference = symmetric_difference.symmetric_difference(club)
```

```
symmetric_difference = sorted(symmetric_difference)
```

```
print(set(symmetric_difference))
```

```
print(sum(symmetric_difference))
```

**Status :** Partially correct

**Marks :** 6.5/10

## **2. Problem Statement**

Samantha is working on a text analysis tool that compares two words to find common and unique letters. She wants a program that reads two words, w1, and w2, and performs the following operations:

Print the letters common to both words, in alphabetical order. Print the letters that are unique to each word, in alphabetical order. Determine if the set of letters in the first word is a superset of the letters in the second word. Check if there are no common letters between the two words and print the result as a Boolean value.

Ensure the program ignores case differences and leading/trailing spaces in the input words.

Your task is to help Samantha in implementing the same.

#### ***Input Format***

The first line of input consists of a string representing the first word, w1.

The second line consists of a string representing the second word, w2.

#### ***Output Format***

The first line of output should display the sorted letters common to both words, printed as a list.

The second line should display the sorted letters that are unique to each word, printed as a list.

The third line should display a Boolean value indicating if the set of letters in w1 is a superset of the set of letters in w2.

The fourth line should display a Boolean value indicating if there are no common letters between w1 and w2.

Refer to the sample output for the formatting specifications.

#### ***Sample Test Case***

Input: program

Peace

Output: ['a', 'p']  
['c', 'e', 'g', 'm', 'o', 'r']  
False  
False

**Answer**

```
w1 = input().strip().lower()
w2 = input().strip().lower()
set1 = set(w1)
set2 = set(w2)
common_letters = sorted(set1.intersection(set2))
unique_letters = sorted((set1 - set2).union(set2 - set1))
is_superset = set1.issuperset(set2)
no_common_letters = len(common_letters) == 0
print(common_letters)
print(unique_letters)
print(is_superset)
print(no_common_letters)
```

**Status :** Correct

**Marks :** 10/10

### 3. Problem Statement

Noah, a global analyst at a demographic research firm, has been tasked with identifying which country experienced the largest population growth over a two-year period. He has a dataset where each entry consists of a country code and its population figures for two consecutive years. Noah needs to determine which country had the highest increase in population and present the result in a specific format.

Help Noah by writing a program that outputs the country code with the largest population increase, along with the increase itself.

**Input Format**

The first line of input consists of an integer  $N$ , representing the number of countries.

Each of the following  $N$  blocks contains three lines:

1. The first line is a country code.
2. The second line is an integer representing the population of the country in the first year.
3. The third line is an integer representing the population of the country in the second year.

### **Output Format**

The output displays the country code and the population increase in the format {code: difference}, where code is the country code and difference is the increase in population.

Refer to the sample output for formatting specifications.

### **Sample Test Case**

Input: 3

01

1000

1500

02

2000

2430

03

1500

3000

Output: {03:1500}

### **Answer**

```
N = int(input())
```

```
max_increase = 0
```

```
country_code_with_max_increase = ""
```

```
for _ in range(N):
```

```
    country_code = input().strip()
```

```
    population_year_1 = int(input().strip())
```

```
    population_year_2 = int(input().strip())
```

```
    increase = population_year_2 - population_year_1
```

```
    if increase > max_increase:
```

```
        max_increase = increase
```

```
    country_code_with_max_increase = country_code
```

```
print(f"{{{country_code_with_max_increase}:{max_increase}}}")
```

**Status :** Correct

**Marks :** 10/10

#### 4. Problem Statement

Riley is analyzing DNA sequences and needs to determine which bases match at the same positions in two given DNA sequences. Each DNA sequence is represented as a tuple of integers, where each integer corresponds to a DNA base.

Your task is to write a program that compares these two sequences and identifies the bases that match at the same positions and print it.

##### **Input Format**

The first line of input consists of an integer  $n$ , representing the size of the first tuple.

The second line contains  $n$  space-separated integers, representing the elements of the first DNA sequence tuple.

The third line of input consists of an integer  $m$ , representing the size of the second tuple.

The fourth line contains  $m$  space-separated integers, representing the elements of the second DNA sequence tuple.

##### **Output Format**

The output is a space-separated integer of the matching bases at the same positions in both sequences.

Refer to the sample output for format specifications.

##### **Sample Test Case**

Input: 4

5 1 8 4

4

4 1 8 2

Output: 1 8

**Answer**

```
n = int(input())
dna_sequence_1 = tuple(map(int, input().strip().split()))
m = int(input())
dna_sequence_2 = tuple(map(int, input().strip().split()))
matching_bases = []
for i in range(min(n, m)):
    if dna_sequence_1[i] == dna_sequence_2[i]:
        matching_bases.append(dna_sequence_1[i])
print(" ".join(map(str, matching_bases)))
```

**Status :** Correct

**Marks :** 10/10