## Rajalakshmi Engineering College

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## NeoColab\_REC\_CS23221\_Python Programming

REC\_Python\_Week 5\_CY

Attempt : 1 Total Mark : 40 Marks Obtained : 40

Section 1: Coding

### 1. Problem Statement

Riya owns a store and keeps track of item prices from two different suppliers using two separate dictionaries. He wants to compare these prices to identify any differences. Your task is to write a program that calculates the absolute difference in prices for items that are present in both dictionaries. For items that are unique to one dictionary (i.e., not present in the other), include them in the output dictionary with their original prices.

Help Riya to implement the above task using a dictionary.

## Input Format

The first line of input consists of an integer n1, representing the number of items in the first dictionary.

## The next n1 lines contain two integers

- 1. The first line contains the item (key), and
- 2. The second line contains the price (value).

The following line consists of an integer n2, representing the number of items in the second dictionary

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The next n2 lines contain two integers

- 1. The first line contains the item (key), and
- 2. The second line contains the price (value).

## **Output Format**

The output should display a dictionary that includes:

- 1. For items common to both dictionaries, the absolute difference between their prices.
- 2. For items that are unique to one dictionary, the original price from that dictionary.

Refer to the sample output for formatting specifications.

## Sample Test Case

```
Input: 1
4
4
1
8
7
Output: {4: 4, 8: 7}

Answer

n1 = int(input())
dict1 = {}
order = []
for _ in range(n1):
    key = int(input())
```

```
value = int(input())
   dict1[key] = value
   if key not in order:
      order.append(key)
 n2 = int(input())
 dict2 = {}
 for _ in range(n2):
    key = int(input())
   value = int(input())
   dict2[key] = value
    if key not in dict1 and key not in order:
      order.append(key)
 result = {}
for key in order:
    if key in dict1 and key in dict2:
      result[key] = abs(dict1[key] - dict2[key])
    elif key in dict1:
      result[key] = dict1[key]
    else:
      result[key] = dict2[key]
 print(result)
```

Status: Correct Marks: 10/10

# 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()
set_w1=set(w1)
set_w2=set(w2)
common=sorted(set_w1.intersection(set_w2))
```

```
unique=sorted(set_w1.symmetric_difference(set_w2))
superset=set_w1.issuperset(set_w2)
no_common=len(common)==0
print(common)
print(unique)
print(superset)
print(no_common)
```

Status: Correct Marks: 10/10

#### 3. Problem Statement

James is an engineer working on designing a new rocket propulsion system. He needs to solve a quadratic equation to determine the optimal launch trajectory. The equation is of the form ax2 +bx+c=0.

Your task is to help James find the roots of this quadratic equation. Depending on the discriminant, the roots might be real and distinct, real and equal, or complex. Implement a program to determine and display the roots of the equation based on the given coefficients.

#### **Input Format**

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

The second line contains three space-separated integers a,b, and c representing the coefficients of the quadratic equation.

### **Output Format**

The output displays:

- 1. If the discriminant is positive, display the two real roots.
- 2. If the discriminant is zero, display the repeated real root.
- 3. If the discriminant is negative, display the complex roots as a tuple with real and imaginary parts.

Refer to the sample output for formatting specifications.

```
Sample Test Case
```

Input: 3

```
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    Output: (-2.0, -3.0)
    Answer
    import math
    n = int(input())
    a, b, c = map(int, input().split())
    d = b**2 - 4*a*c
    if d > 0:
      root1 = (-b + math.sqrt(d)) / (2*a)
      root2 = (-b - math.sqrt(d)) / (2*a)
      print((round(root1, 1), round(root2, 1)))
elif d == 0:
      root = -b / (2*a)
      print((round(root, 1), round(root, 1)))
    else:
      real = -b / (2*a)
      imag = math.sgrt(-d) / (2*a)
      print(((round(real, 1), round(imag, 1)), (round(real, 1), round(-imag, 1))))
```

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

#### Answer

```
n=int(input())
s1=tuple(map(int,input().split()))
m=int(input())
s2=tuple(map(int,input().split()))
l=min(n,m)
matched=[str(s1[i]) for i in range(l) if s1[i]==s2[i]]
print(''.join(matched))
```

Status: Correct Marks: 10/10

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