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HW 8.1 - Paying in Coins (25 pts)

You have a pocket full of coins (pennies, nickels, dimes, and quarters with values of 1, 5, 10, and 25 cents respectively) that you wish to get rid of. Each time you go to buy an item, you try to *pay with the most number of coins possible*.

Construct an algorithm that, given a cost and the number of coins you have available, pays the cost with as many coins as possible.

Your main will start with a pocket full of coins (loaded from stdin). Everytime an item is bought, the value of the item will be entered via stdin and your algorithm should be used to determine how you will pay for the item, and determine your remaining coins.

Input:

- starting number of each coin
- value of items to be bought

Output:

 for each item bought, the coins that were used, and the number of coins remaining in your pocket

Section 1: Successful compilation of program

```
[hardikkhare@Hardiks-MacBook-Pro AP HW 8 % javac -Xlint COINSQ1.java
[hardikkhare@Hardiks-MacBook-Pro AP HW 8 % java COINSQ1
```

Section 2: program running on the provided example from the assignment

HW 8.3 - DNA Sequence Alignment Part I (25 pts)

In DNA sequences, there are four types of repeating units (called bases) denoted as A, T, C, and G. Two opposite strands are aligned if All A's in one string are matched with T's in the opposing string, and all C's in one string are matched with G's in the opposing string.

An example of a valid alignment is:

```
A C C T C G
T G G A G C
```

...and an example of an invalid alignment is:

```
A G C T T G T G A A
```

Assume that given opposing strands that do not align, and that you are allowed to put spacers to align them. For example:

We could transform this:

```
A G C T T G
T G C G A A
...into this:
A _ G C T T G
T G C G A A _
```

Write a program that takes two opposing strands of DNA, and determines the best way to align the sequences by inserting the minimum number of spacers.

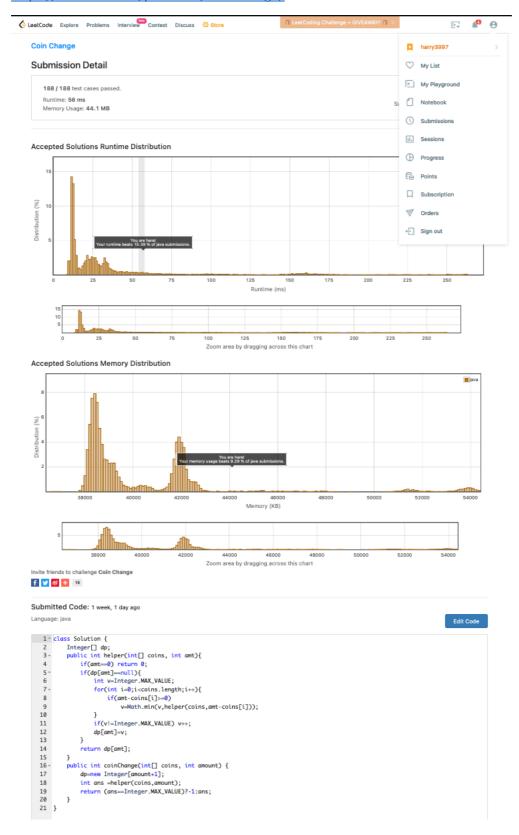
Section 1: Successful compilation of program

```
[hardikkhare@Hardiks-MacBook-Pro AP HW 8 % javac -Xlint DNAQ1.java
[hardikkhare@Hardiks-MacBook-Pro AP HW 8 % java DNAQ1
```

Section 2: program running on the provided example from the assignment

```
[hardikkhare@Hardiks-MacBook-Pro AP HW 8 % java DNAQ1
Enter DNA strand 1
AGCTTG
Enter DNA strand 2
TGCGAA
Aligned Strands are:
A_GCTTG
AGCTTG
hardikkhare@Hardiks-MacBook-Pro AP HW 8 % ■
```

https://leetcode.com/problems/coin-change/



https://leetcode.com/problems/coin-change-2/

