

Module 4 - Loops

CMPT220L

Due on Oct 2, 2020 by 11:59PM

Points: 100

Problems

1. (*Math tutor*) Write a program that displays a menu as shown in the sample run. You can enter 1, 2, 3, or 4 for choosing an addition, subtraction, multiplication, or division test. After a test is finished, the menu is redisplayed. You may choose another test or enter 5 to exit the system. Each test generates two random single-digit numbers to form a question for addition, subtraction, multiplication, or division. For a subtraction such as `number1 - number2`, `number1` is greater than or equal to `number2`. For a division question such as `number1 / number2`, `number2` is not zero.

```
Main menu
1: Addition
2: Subtraction
3: Multiplication
4: Division
5: Exit
Enter a choice: 1
What is 1 + 7? 8
Correct
Main menu
1: Addition
2: Subtraction
3: Multiplication
4: Division
5: Exit
Enter a choice: 1
12
What is 4 + 0? 5
Your answer is wrong. The correct answer is 4
Main menu
1: Addition
2: Subtraction
3: Multiplication
4: Division
5: Exit
Enter a choice: 4
What is 4 / 5? 1
Your answer is wrong. The correct answer is 0
Main menu
1: Addition
2: Subtraction
3: Multiplication
4: Division
5: Exit
```

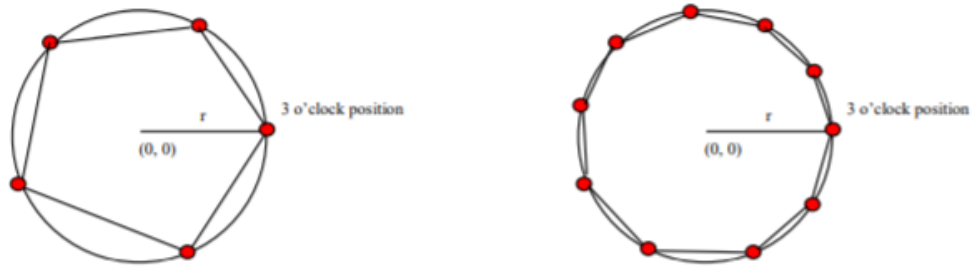


Figure 1: An n -sided polygon is centered at $(0,0)$ with one point at the 3 o'clock position

Enter a choice:

2. (*Corner point coordinates*) Suppose an n -sided regular polygon is centered at $(0,0)$ with one point at the 3 o'clock position, as shown in Figure 1. Write a program that prompts the user to enter the number of the sides, the radius of the bounding circle of a polygon, and displays the coordinates of the corner points on the polygon.

Here is a sample run:

```
Enter the number of the sides: 6
Enter the radius of the bounding circle: 100
The coordinates of the points on the polygon are
(100.0, 0.0)
(50.0, 86.6)
(-50.0, 86.6)
(-100.0, 1.22)
(-50.0, -86.6)
(50, -86.60)
```

3. (*Bioinformatics: find genes*) Biologists use a sequence of the letters A, C, G, and T to model a genome. A gene is a substring of a genome that starts after a triplet ATG and ends before a triplet TAG, TAA, or TGA. Furthermore, the length of a gene string is a multiple of 3, and the gene does not contain any of the triplets ATG, TAG, TAA, or TGA. Write a program that prompts the user to enter a genome and displays all genes in the genome. If no gene is found in the input sequence, display "no gene is found".

Here are the sample runs:

```
Enter a genome string: TTATGTTTTAAGGATGGGCGTTAGTT
TTT
GGGCGT
```

```
Enter a genome string: TGTGTGTATAT
no gene is found
```

4. (*Reduce square root*) Write a program that prompts the user to enter a positive integer and obtains its square root in simplest form. For example, the simplest form for $\sqrt{18}$ is $3\sqrt{2}$ is, for 28 is $2\sqrt{7}$, and for $3\sqrt{648}$ is $18\sqrt{2}$.

Here are some sample runs:

```
Enter a positive integer: 1300
sqrt(1300) is 10*sqrt(13)
```

```
Enter a positive integer: 31
sqrt(31) is sqrt(31)
```

```
Enter a positive integer: 64
sqrt(64) is 8
```

Submission

Make sure you create one Java file per project. Place your `.java` files under the corresponding folder in your local copy of the GitHub repository, commit and push it to the remote repository. Make sure that the professor has access to the repository (`jfac65-marist`).

```
cmpt220lastname\
  hw\
    4\
      Problem1.java
      Problem2.java
      Problem3.java
      Problem4.java
```