Part 1

This assignment is to write the code from the lesson to use a StorageResource to store the genes you find instead of printing them out. This will help you see if you really understood how to put the code together, and might identify a part that you did not fully understand. If you get stuck, then you can go back and watch the coding videos that go with this lesson again.

Specifically, you should do the following:

1. Create a new Java project named StringsThirdAssignments. You can put all the classes for this programming exercise in this project.

2. Create a new Java Class named Part1. Copy and paste the code from your Part1 class in your StringsSecondAssignments project into this class.

3. Make a copy of the printAllGenes method called getAllGenes. Instead of printing the genes found, this method should create and return a StorageResource containing the genes found. Remember to import the edu.duke libraries otherwise you will get an error message cannot find the class StorageResource.

4. Make sure you test your getAllGenes method.

Part 2

Write the method cgRatio that has one String parameter dna, and returns the ratio of C's and G's in dna as a fraction of the entire strand of DNA. For example if the String were "ATGCCATAG," then cgRatio would return 4/9 or .4444444.

Hint: 9/2 uses integer division because you are dividing an integer by an integer and thus Java thinks you want the result to be an integer. If you want the result to be a decimal number, then make sure you convert one of the integers to a decimal number by changing it to a float. For example, (float) 9/2 is interpreted by Java as 9.0/2 and if one of the numbers is a decimal, then Java assumes you want the result to be a decimal number. Thus (float) 9/2 is 4.5.

Write a method countCTG that has one String parameter dna, and returns the number of times the codon CTG appears in dna.

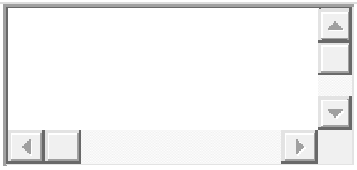
Part 3

Write the void method processGenes that has one parameter sr, which is a StorageResource of strings. This method processes all the strings in sr to find out information about them. Specifically, it should:

- print all the Strings in sr that are longer than 9 characters
- print the number of Strings in sr that are longer than 9 characters
- print the Strings in sr whose C-G-ratio is higher than 0.35
- print the number of strings in sr whose C-G-ratio is higher than 0.35
- print the length of the longest gene in sr

Write a method testProcessGenes. This method will call your processGenes method on different test cases. Think of five DNA strings to use as test cases. These should include: one DNA string that has some genes longer than 9 characters, one DNA string that has no genes longer than 9 characters, one DNA string that has some genes whose C-G-ratio is higher than 0.35, and one DNA string that has some genes whose C-G-ratio is lower than 0.35. Write code in testProcessGenes to call processGenes five times with StorageResources made from each of your five DNA string test cases.

We have some real DNA for you to test your code on. Download the file brca1line.fa from the DukeLearnToProgram Project Resources page. Make sure you save it in your BlueJ project so that your code can access it. You can use a FileResource to open the file and the FileResource method asString to convert the contents of the file to a single string so that you can use it like the other DNA strings you have been using. Here is an example:



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1
2
FileResource fr = new FileResource("brca1line.fa");

String dna = fr.asString();
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Modify your processGenes method so that it prints all the Strings that are longer than 60 characters and prints the number of Strings that are longer than 60 characters (you do not need to make changes to the rest of the method).

Modify the method testProcessGenes to call processGenes with a StorageResource of the genes found in the file brca1line.fa.