

Programming Exercise: Storing All Genes

Assignment

This assignment is to find all the genes in a DNA string and then store them using the `StorageResource` class. You will modify the program you wrote to find and print all genes, storing them instead of printing. You should write and test each method on small data before moving on to the next step. Then you will look for all the genes in a file and answer questions about them.

Specifically, you should do the following.

1. Make a copy of the `printAll` method called `storeAll`. Instead of printing the genes found, this method should create and return a `StorageResource` containing the genes found.
2. Write the void method named `testStorageFinder` that has one parameter `dna`, a `String` of DNA. This method reads in the file `brca1line.fa`, which is a large string of DNA and calls `storeAll` to find and store all the genes in this large strand of DNA. It then prints the number of genes found. Note: You should first make sure this method works by using one of the small DNA strands above, and then replacing that with the DNA string from the file.
3. 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.
4. Write the void method `printGenes` that has one parameter `sr`, which is a `StorageResource` of strings. This method processes all the strings in `sr` and does the following:
 - prints all the `Strings` that are longer than 60 characters
 - prints **the number** of `Strings` that are longer than 60 characters
 - prints the `Strings` whose C-G-ratio is higher than 0.35
 - prints **the number** of strings whose C-G-ratio is higher than 0.35

5. In the method `testStorageFinder`, call `printGenes` with a `StorageResource` of the genes found from the file `brca1line.fa`.