



≡ Item Navigation

Programming Exercise: Finding Many Genes

You can find a PDF of this programming exercise in the **Resources** tab.

For files related to this assignment, visit the DukeLearnToProgram Project Resources page for this course: <http://www.dukelearntoprogram.com/course2/files.php> (also linked in the **Resources** tab).

You can also find the frequently asked questions page for this course's assignments on DukeLearnToProgram: <http://www.dukelearntoprogram.com/course2/faq.php> (also linked in the **Resources** tab).

Part 1: Finding many Genes

This assignment is to write the code from the lesson to make the following improvements to your algorithm:

- A. Find a gene in a strand of DNA where the stop codon could be any of the three stop codons "TAA", "TAG", or "TGA".
- B. Find all the genes (where the stop codon could be any of the three stop codons) in a strand of DNA.

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 StringsSecondAssignments. You can put all the classes for this programming exercise in this project.
2. Create a new Java Class named Part1. The following methods go in this class.
3. Write the method findStopCodon that has three parameters, a String parameter named dna, an integer parameter named startIndex that represents where the first occurrence of ATG occurs in dna, and a String parameter named stopCodon. This method returns the index of the first occurrence of stopCodon that appears past startIndex and is a multiple of 3 away from startIndex. If there is no such stopCodon, this method returns the length of the dna strand