

CSCE 300 Assignment 1

Due: February 14, 2019 by class time on BeachBoard

In this assignment, you will develop a Python program that reads a chromosome file and reports some basic statistics about it. The output reports the following information

- 1- The count of each nucleotide
- 2- The total count of all nucleotide
- 3- The percentage of each nucleotide
- 4- The count of gaps
- 5- The percentage of gaps

Your program reports the above information for two human chromosomes, chromosom1 and 19.

We will discuss details of programing in the lab!

After finishing the code you need to submit the following:

- 1- Your source code (gene_stat.py).
- 2- A text file that contains your program output for the given input (output.txt).
- 3- A Readme file (Readme.txt) that contains the following information
 - a. The program authors name
 - b. Your interpretation of the result generated by your program

The submission format and rules (Some coding guideline):

- 1- For this assignment, send only one .py file.
- 2- On top of your code, you need to have proper description header (comments).
- 3- In the code if needed add inline description as comments.
- 4- All function requires comments before the function name describing the functionality of the function.

Resources:

- To read a file in python: <https://www.pythonforbeginners.com/files/reading-and-writing-files-in-python>
- NCBI human genome browser: <https://www.ncbi.nlm.nih.gov/genome/gdv/browser/?context=gene&acc=4524>
- You can download human genome from here: <http://hgdownload.cse.ucsc.edu/goldenPath/hg38/chromosomes/>