

BIOL 5153, Practical Programming for Biologists
Assignment #6
Due Monday, 06 April 2020, by 5:00 PM.

Modify your script, 'parseGFF.py', to include the *argparse* and *csv* modules. Use the *csv* module to parse the tab-delimited GFF file. Use *argparse* so the user enters the names of two required inputs: the GFF file and the corresponding genome file. You should no longer have hard-coded filenames in your script. Your script should open and parse the GFF file, making sure that you can access the start and end coordinate of each feature. Your script should also be able to just open and close the FASTA file ('watermelon.fsa' in this case). Push your modified script to GitHub, being sure to use an informative message.