

Reviewer Report

Title: Genome Annotation Generator: A simple tool for generating and correcting WGS annotation tables for NCBI submission

Version: Original Submission **Date:** 08 Mar 2017

Reviewer name: Juan Oliveros

Reviewer Comments to Author:

The authors describe a command-line-based tool, "Genome Annotation Generator" (GAG) that simplify the task of annotating and formatting new genomes to be submitted to NCBI database. This tool is written in python, it is easy to install and has no external dependencies. Finally, as it uses standard python functions, it is compatible across platforms, provided that python language is previously installed.

The idea of creating a single command-line simplifying a number of tedious tasks is great. However, as more and more options and parameters are added, less simple becomes the tool.

For example, in its current implementation, GAG not only requires a FASTA and a GFF file. In addition, a tab-delimited annotation file (not standard) and a BED file with additional information about regions to be excluded are needed. Although these files are not mandatory, they are usually necessary for fulfilling a proper genome submission procedure. Furthermore, other 18 parameters, related to minimum and maximum genomic feature sizes to be excluded, must be defined by the user with no clear default values provided.

Even when it is true that GAG tool facilitates the task of submitting new genomes to NCBI, it still requires some knowledge of writing command-lines and managing their associated parameters. Including a graphical user interface (GUI) that allows point-and-click events to manage file selections and parameters settings, would be desirable to reach more potential users, not necessarily familiarized with the unix-like console. This GUI would be also helpful to show the user the multiple output files (stats reports, discarded features, session documentation, etc.) that GAG generates and that are very important to check the final quality of the new annotated genome.

Finally, a better explanation of example FASTA and GFF files available at "walkthrough/" folder would be desirable. To test the application, this reviewer used the files included in "basic/" subfolder, but other example folders are available (not described).

Found some typos:

Page 4. Line 18: "If she..." ---> "If the user..."

Page 4. Line 32: "The to add this level of..." ----> "To add this level of..."

Page 4. Line 60 "teh..." ----> "the..."

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