

User Manual

Description

Genome Assembly Viewer is a java based program that parses assembled .fasta and relevant .gff files from the user to display various statistics and properties about the files.

Usage

Program is ran by executing the GenomeAssemblyViewer.jar or the source code can be compiled to produce an executable.

Any fasta file can be uploaded and used, but three example files, namely dbg27, dbg50 and masurca is in the main folder. GFF file that is used should be the matching one for the uploaded fasta file. An example gff file for masurca.fasta is in the main folder. (You can use Blast2Go augustus geneFinding to get .gff files for any fasta file)

Upload Fasta button creates a file chooser and asks for a .fasta file input from the user. If the upload is successful, information such as general statistics, the contig list and the graph containing contig sizes (sorted by largest to smallest) are displayed on the interface.

Upload GFF button creates a file chooser and asks for a .gff file input from the user. If the upload is successful, a list is created at the bottom showing all contig hits for region/gene or CDS in the file.

If the user selects a specific contig from the Contig List, the sequence of the contig is displayed in Contig Sequence along with Contig Length and GC% content. In addition, the Contig Hits list are filtered down to the selected contig, showing only the hits for that specific contig.

The N50 contig is highlighted with red on the graph.

Example output from masurca.fasta and masurca.gff which is an assembled genome from Illumina PE 101x2 reads and pacbio long reads:

