

SapFeederHub

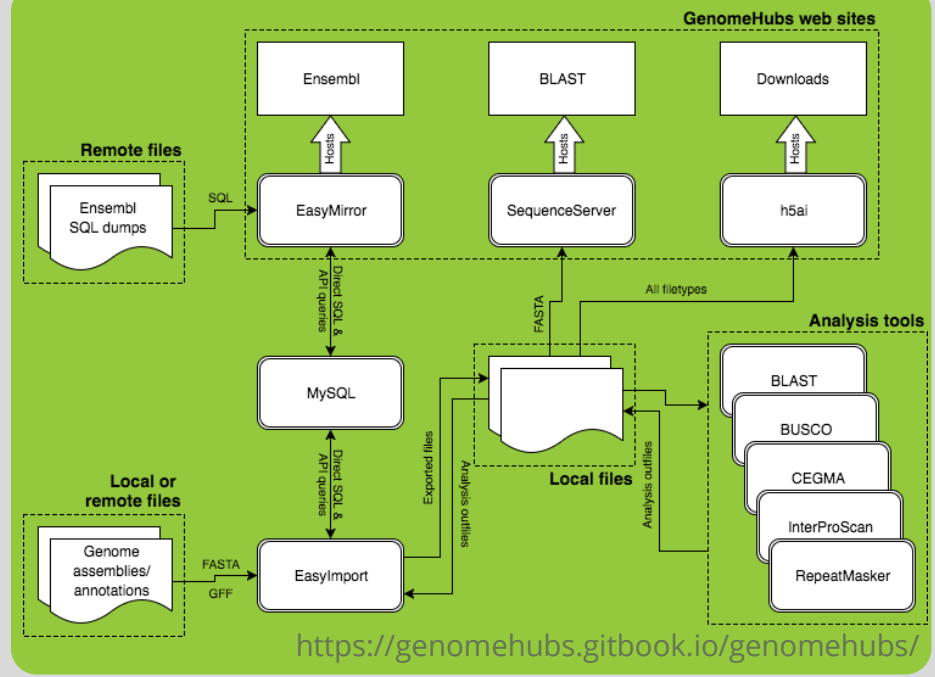
The Insect Vector Genome Sequence Database

matthew.couchman@jic.ac.uk

tjelvar.olsson@jic.ac.uk

SapFeederHub interface showing a grid of insect assemblies categorized by order: Aphid, Planthopper, Froghopper, and Heteroptera. The top navigation bar includes links for BLAST, Download, genomehubs.org, and Help, along with a search bar. The main content area lists various species and their assembly identifiers.

Screenshot of the SapFeederHub website showing a detailed view of the Aphid glycyces Aggly biotype4 v2.1 genome assembly. The page displays the location-based displays, chromosome summary, region overview, and a detailed view of a region on chromosome scaffold.3 (57,580-69,243). The detailed view shows a genomic map with gene models, exons, and introns, along with a gene legend and navigation controls.



<https://genomehubs.gitbook.io/genomehubs/>

Introduction

SapFeederHub is the database of the insect vector genomes that are being assembled for BRIGIT and also acts as a mirror site for related databases such as AphidBase (<https://bipaa.genouest.org/is/aphidbase/>).

Summary

We have established and documented an assembly data input and analysis pipeline which we have used to make 12 assembly data sets publicly available via the SapFeederHub website.

GenomeHubs

SapFeederHub has been built on the GenomeHubs software framework which provides a simplified interface to the Ensembl genome browser and database management tools. There are import and visualisation tools for assembly analysis tools such as Busco, download links for all inputs and outputs for transparency and an integrated BLAST server.

Acknowledgements

- John Innes Centre
 - Saskia Hogenhout
 - Roberto Biello
 - Thomas Mathers
- University of Edinburgh
 - Richard Challis

<http://sapfeederhub.jic.ac.uk>

