Overview

The est2assembly platform is the only platform for standardising transcriptome projects: go from raw trace files to an annotated GBrowse interface driven by the Seqfeature database. It accepts both Sanger and 454 sequencing technology for a denovo assembly, annotation and data mining of EST data.

It is available from http://est2assembly.googlecode.com

 Dependencies

The platform makes use of a number of BioPerl and other tools such as prot4EST. Depending on what you want to use it for, not all of these need to be installed. Please see the manual.

Features

- Currently makes use of MIRA and Newbler cDNA assemblers (the only NGS assemblers currently designed for ESTs)
- Standardized methods for judging transcriptome quality
- In active development for more packages for transcriptome analysis (e.g. digital transcriptomics with edgeR, curation and others)

Demos and Screenshots

Screenshots are available from the project website.

License

This software is GPLv2+ licensed as part of the Drupal package. It is currently supported by Alexie Papanicolaou while at CSIRO, the Australian Commonwealth Scientific and Research Organization (http://www.csiro.au).