Integrative Services for Genomic Analysis (ISGA)
An Intuitive Web Server for Prokaryotic Genome Annotation and Other Analyses

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ISGA is an intuitive web application designed for biologists to run and customize bioinformatics pipelines built using the Ergatis workflow system. ISGA addresses the gap between prokaryotic annotation services such as JCVI's Annotation Service that are easy to use but provide few customization options and workflow systems such as Ergatis which are powerful but prohibitively complex for most biologists to use.

Sequencing facilities can use a local installation of ISGA to offer data analysis services in conjunction with NGS operations. ISGA allows biologists to initiate and customize pipelines themselves rather than involving bioinformaticians. ISGA is open source software and freely available under the Apache License, Version 2.0 .
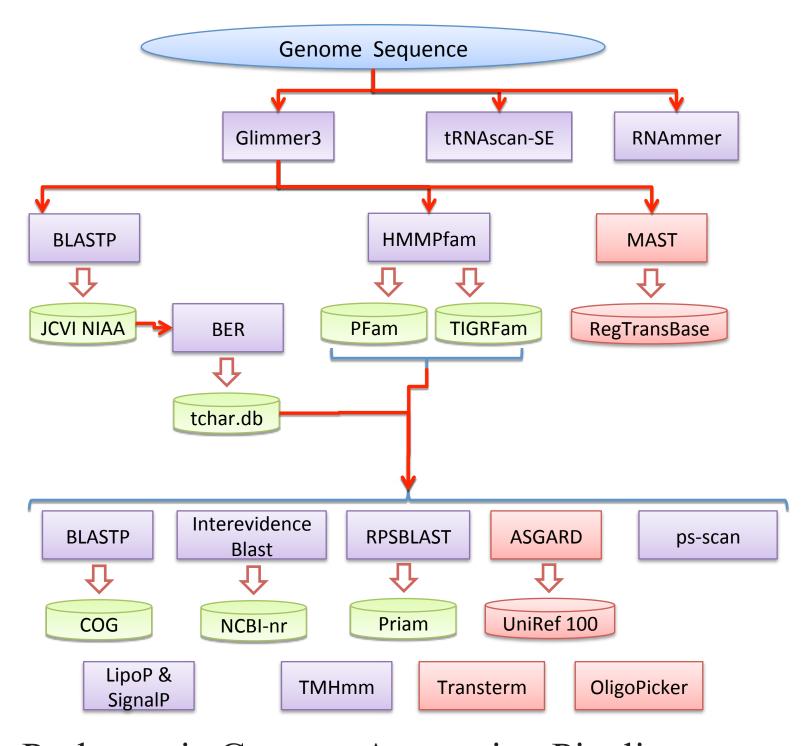
We are active members of the Ergatis community and ISGA pipelines can be run directly in Ergatis and converting new Ergatis pipelines to ISGA is straightforward.

The CGB hosts a local instance of ISGA for our collaborators and public evaluation. ISGA is open source and available for download and local installation at:
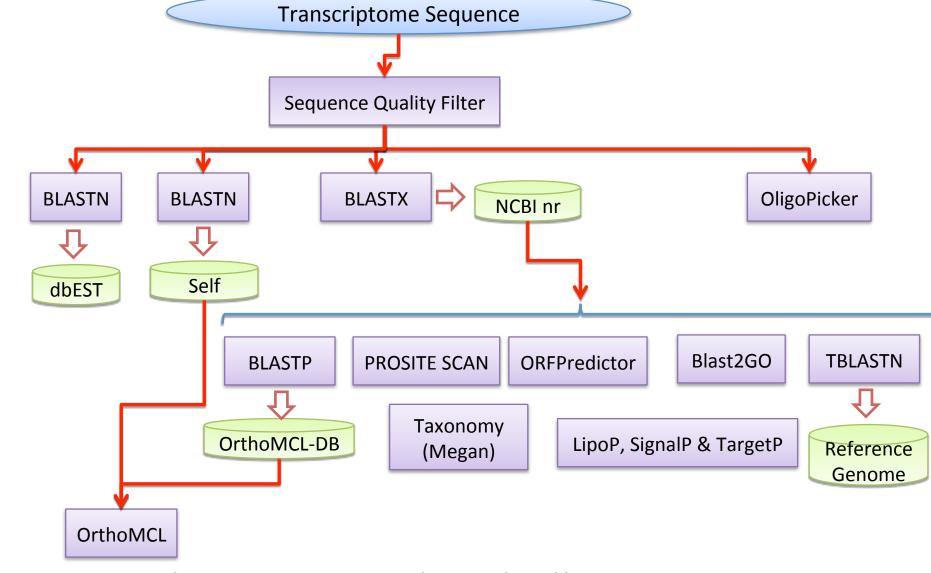
http://isga.cgb.indiana.edu/

Key Features:

- Easy-to-use web interface for bioinformatics pipelines
- Free demonstration site and download for local install
- Run pipelines immediately or customize to meet your needs
- Form validation catches pipeline errors immediately
- Account system allows data privacy and future retrieval
- Integrated analysis of pipeline results
- Pipelines are built and run with Ergatis Workflow System
- Integrated tools for analyzing pipeline results

Available Pipelines:

- Prokaryotic Genome Annotation (see left)
- Prokaryotic Assembly

Pipelines In Development:

- Transcriptome Annotation (see below)
- Gene Clustering against a Phylogenetic Tree
- Functional Genomics Analysis of NGS Data

ISGA Toolbox:

- View pipeline results in GBrowse
- Standalone BLAST Search
- Database query of annotation results
- Convert assembly results to Hawkeye

Prokaryotic Genome Annotation Pipeline

Transcriptome Annotation Pipeline

Step 1: Select and Customize Pipeline

Toggle components and open parameter editor

Customize the component and parameters of a pipeline or run with defaults
Edit program parameters (w/ help and validation)

Step 2: Run Pipeline

Upload new input file or selecting existing file in ISGA
Provide any run-specific parameters (e.g. Organism species)
Monitor run progress and download results

Step 3: Analyze Results

Load results of annotation into integrated GBrowse genome browser
View feature details and BLAST sequences

Manuscript:

An Ergatis-based prokaryotic genome annotation web server

Chris Hemmerich, Aaron Buechlein, Ram Podicheti, Kashi Revanna & Qunfeng Dong, (2010) Bioinformatics