AUTOMATED ANNOTATION OF NGS TRANSCRIPTOME DATA USING ISGA AND ERGATIS

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Keeping up with next-generation sequencing data requires the use of automated analysis pipelines

Ergatis is a(n awesome) workflow management tool for designing and running such pipelines

http://ergatis.sourceforge.net/

Ergatis: A web interface and scalable software system for bioinformatics workflows

Orvis et al. (2010) Bioinformatics

ISGA is a Biologist's tool for running and customizing Ergatis pipelines previously designed by experts

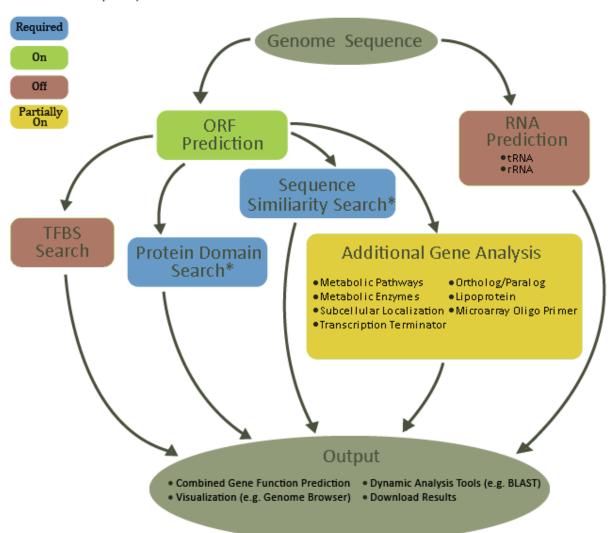
http://isga.cgb.indiana.edu/

An Ergatis-based prokaryotic genome annotation web server Chris Hemmerich, Aaron Buechlein, Ram Podicheti, Kashi Revanna & Qunfeng Dong, (2010) Bioinformatics

chemmeri Pipeline 4

Template Pipeline: Prokaryotic Annotation Pipeline

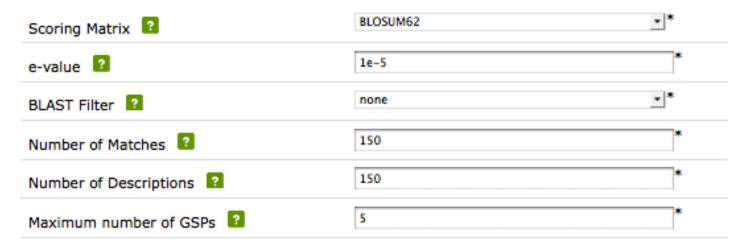
Created At: Apr 02, 2010 11:48



Pipeline Building: Edit Parameters

BLASTP vs COG

Required Parameters

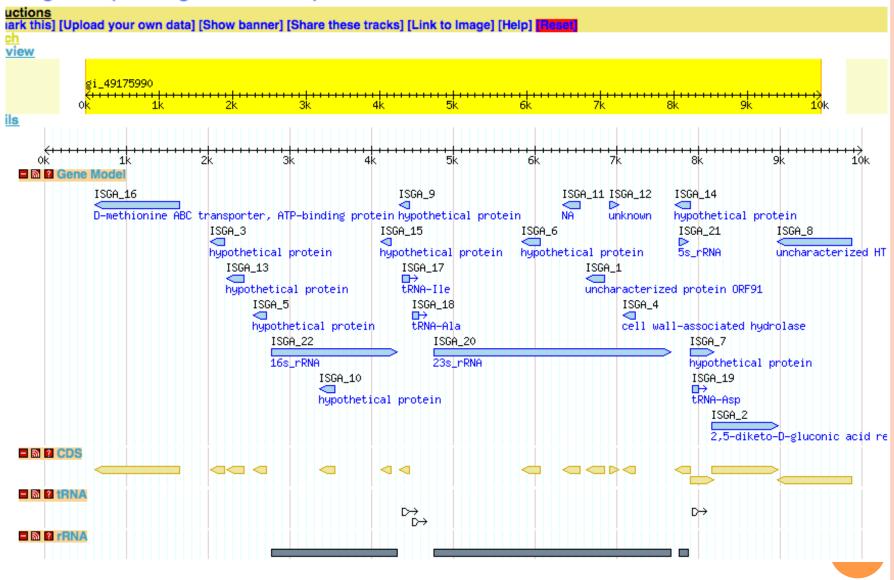


Optional Parameters +

Cancel Reset Form

Save Parameters

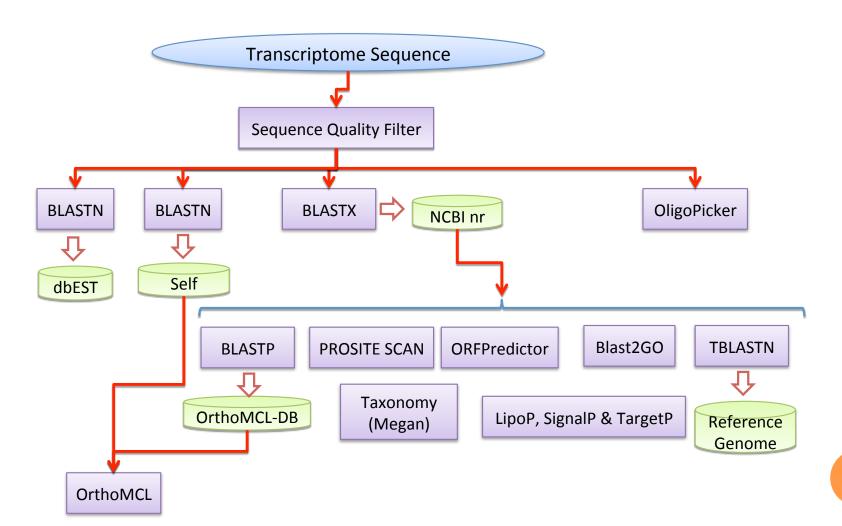
owing 10 kbp from gi_49175990, positions 1 to 10,001



INTEGRATIVE SERVICES FOR GENOMIC ANALYSIS

- Account system protects user data and enables easy retrieval of previous results
- Integrated visualization, query, and analysis tools to explore pipeline results
- File upload and download managed through browser
- ISGA pipelines can be run in Ergatis

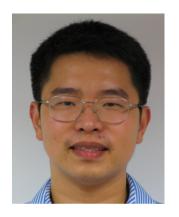
TRANSCRIPTOME PIPELINE



Transcriptome pipeline is running in Ergatis. We are optimizing performance and evaluating additional functionality.

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CREDITS



Qunfeng Dong



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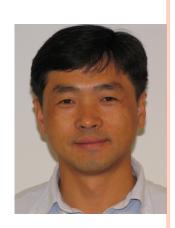
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