

5th Annual Joint Bioinformatics Workshop

July 19, 2005
2229 Seamans Center
University of Iowa

by

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The Development of a Workflow to Populate a Synteny Browser Database

ABSTRACT

SynBrowse is a web-based synteny browser that provides visualization of genome alignments within and between species. The browser allows scientists to visualize and analyze synteny, homologous genes, and other conserved elements between sequences. It consists of two components: a web-based front end and a set of relational database back ends. Each database stores pre-computed alignments from a focus sequence to reference sequences in addition to the genome annotations of the focus sequence. This project is to create a workflow to populate the SynBrowse databases. The focus of my work is on writing a parser to transfer the outputs of BLASTX into the appropriate format required by SynBrowse. The testing datasets used for this project were genomic BACs of *Zea mays* and *Sorghum bicolor* from GenBank and the whole genome and its annotations of *Oryza sativa* from the TIGR rice annotation database. I wrote a parsing script and used it to parse the BLASTX alignments for the SynBrowse databases. After populating the databases, I have successfully displayed the genome alignments using SynBrowse. My work has led to a workflow to parse BLASTX alignments and populate SynBrowse databases, which will be useful for many SynBrowse users.