

Meeting abstract

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Visualizing and sharing results in bioinformatics projects: GBrowse and GenBank exports

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Background

Effective tools for presenting and sharing data are necessary for collaborative projects, typical for bioinformatics. In order to facilitate sharing our data with other genomics, molecular biology, and bioinformatics researchers, we have developed software to export our data to GenBank and combined the export utilities with our customized and augmented version of GBrowse. The GBrowse bioinformatics software provides a way for users to graphically view genomic feature data stored in a back-end database. GenBank is an open-access database, maintained by the National Center for Biotechnology Information (NCBI), containing annotated versions of all publicly available DNA sequences. To support exports relevant to our data, we have developed a tool that processes a list of expressed sequence tags (ESTs), correlates these tags with information from our database, and constructs a set of files for batch submission to the GenBank EST database (dbEST).

We are using this tool in combination with our *Epichloe festucae* genome database (Figure 1), used also as a back-end for GBrowse, to prepare dbEST submissions for the transcriptome of the fungal endophyte *E. festucae*, as well as one of its host plants, *Festuca pratensis* (meadow fescue). ESTs from infected plants are compared against the fungal genome sequence using alignment tools such as

Exonerate. We are using this tool to prepare batch EST submissions of 35,000 fungal and 75,000 plant ESTs, containing a total of 32 million and 60 million base pairs, respectively. The software can be adapted for use with other bioinformatics projects.

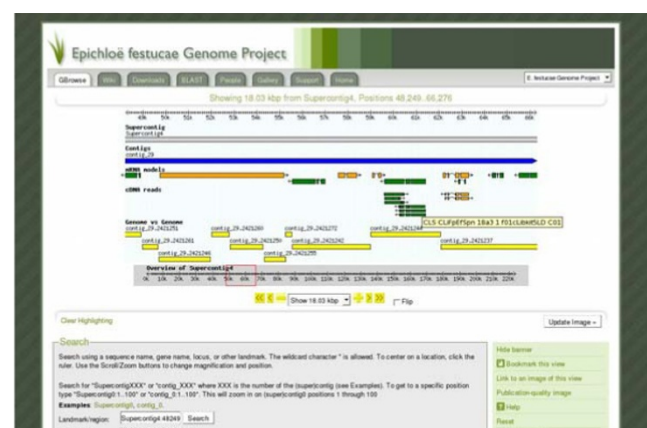


Figure 1
GBrowse for the *Epichloe festucae* genome project.

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