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Title
Annotation of Eukaryotic Genomes

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Annotation of Eukaryotic Genomes
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Abstract
We annotated over 60 eukaryotic genomes increasing annotation throughput ~10 fold in the last 5 years with improved annotation process, automated annotation pipeline, and further developed genome analysis tools integrated in the Eukaryotic Genome Portal. We developed a Community Annotation model, unique across sequencing centers, to achieve higher quality of annotations, teach and train new users, and build stronger genome user communities. These tools will serve as a platform for programmatic approach to scaling up sequencing and analysis of microbial eukaryotic, for example, JGI Fungal Program, along the directions of (i) sequencing phylogenetic breadth, (ii) deeper sampling DOE mission relevant organisms, and (iii) exploring ecotrophic diversity. A diverse portfolio of microbial eukaryotes (68 fungal and 21 algal projects at different stages in JGI pipeline) and DOE mission positions the JGI to sequence a broad range of microbial eukaryotes.

Fungi and Algae for DOE Mission: Today and Tomorrow

Programmatic Tools

User Inputs:
- Proposals
- DNA/RNA
- Mapstoools
- Manual Curations
- Community Annotation

JGI Tools:
- Projects
- Sequencing
- Assembly
- Annotation
- Genome Portal
- Training, User support, Jamborees

Validation of Annotations and Genome Analysis

Support for H.annosum gene models predicted by different annotation pipelines

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