

The Integrated Microbial Genomes (IMG) System

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The Joint Genome Institute (JGI) is producing about 25% of the reported number of bacterial genome projects worldwide. The main goal of the Integrated Microbial Genomes (IMG) system is to provide an efficient platform for the review, curation, analysis, and subsequent release of microbial genomes sequenced at JGI. IMG provides support for comparative analysis of microbial genomes in an integrated genome data context. A high level of genome diversity is ensured by collecting data from public sources, such as EBI Genome Reviews, NCBI's RefSeq, and EMBL Nucleotide Sequence Database. IMG incorporates in a coherent biological context primary genomic sequence information, computationally predicted and curated gene models, pre-computed sequence similarity relationships, and functional annotations and pathway information.

Since the release of its first version on March 1st, 2005, IMG has been extended in terms of data content and analytical tools through quarterly updates, whereby it aims at continuously increasing the number of genomes integrated in the system from public resources and JGI as well as improving the efficiency of the analysis process. The latest version of IMG will be demonstrated from both data management and analytical perspectives. IMG is available at: <http://img.jgi.doe.gov/>. The system, including its architecture, requirements, data sources, and key components are described in the "About IMG" section available at http://img.jgi.doe.gov/pub/doc/about_index.html. A user guide for the system is provided at http://img.jgi.doe.gov/pub/doc/using_index.html.

This work was performed under the auspices of the U.S. Department of Energy, Office of Biological and Environmental Research; the University of California; and Lawrence Berkeley, Lawrence Livermore, and Los Alamos National Laboratories.

IMG is using tools and data from a number of publicly available resources. Their availability and value is gratefully acknowledged. IMG software and data are free and available without restrictions on use or access.