FICUS JGI-NERSC-KBase FY19

2019 FICUS JGI-NERSC-KBase Biological Data Science Call for Proposals (CLOSED)

The Biological Data Science call will enable users to perform state-of-the-art computational research to explore the wealth of genomic and metagenomic data generated worldwide and translate sequence information into biological discovery. Users will have access to resources and capabilities through two DOE Office of Science User Facilities, the Joint Genome Institute (JGI) and the National Energy Research Scientific Computing Center (NERSC), as well as the DOE Systems Biology Knowledgebase (KBase). The call aims to help users perform large-scale computational analyses of genomics and related omics data to solve problems relevant to the DOE missions in bioenergy and the environment.

Projects are encouraged that relate to:

Large-scale data mining for genes, genomes, metabolic and biosynthetic pathways, and regulatory motifs of interest

Large scale computations for large datasets exploring the power of High Performance Computing

Developing explainable scalable machine learning and artificial intelligence based methods for sequence classification, gene calling or gene functional annotation leveraging high performance computational tools such as HipMCL, MetaHipMer, etc.

Developing new analysis and/or visualization tools for Terabyte (TB)-sized multi-omics data that can be deployed in KBase, IMG, or MycoCosm

Distributing resulting data products through IMG/JGI portals or KBase

DOE JGI, NERSC and KBase core capabilities available through this call include:

Up to 2 million CPU hours on the Cori supercomputer (128GB memory per node, 32 cores)

Access of up to 100TB of high-performance storage on the NERSC parallel file system and burst buffer to overcome I/O bottlenecks

The expertise of DOE JGI, NERSC and KBase staff

The Integrated Microbial Genomes & Microbiomes (IMG/M) database, the largest publicly available integrated resource of assembled metagenomic sequences and isolate microbial genomes

The MycoCosm portal, the largest collection of fungal genomes

An integrated software and data platform, KBase, for metabolic modeling of microbes or microbial communities, custom processing of microbial and fungal genomes and metagenomes and state-of-the-art computational workflows, narratives, and pipelines

Comparative analyses (e.g. large or complex queries) of the IMG system that are not available through the web interface.

Gene/protein family-centric analysis of IMG or KBase data

Proposals will be reviewed for feasibility, scientific excellence and DOE mission relevance by scientific experts in microbial genomics and HPC. All relevant data must be available at the time of submission; proposals requesting sequencing will be rejected without peer review. Applications should be submitted at https://proposals.jgi.doe.gov.

General inquiries about the program should be directed to Susannah Tringe.

Technical inquiries related to JGI resources should be addressed to Nikos Kyrpides.

Technical inquiries related to NERSC resources should be directed to Deborah Bard.

Technical inquiries related to KBase should be directed to Shane Canon.

Proposal Schedule

2019 proposals will only be accepted electronically and should be submitted at https://proposals.jgi.doe.gov/ between August 20 and September 13, 2018.

The full schedule is below:

Calls for proposals issued	August 17, 2018
Proposals received	Sept 24, 2018
Technical and scientific review	mid-Nov 2018
Approval and rejection notices sent	December 3, 2018