Joint Genome Institute/UC Merced
Genomics Distinguished Graduate Internship Program
2017 Summer Research Science Program
June-August 2017

The JGI/UCM Genomics Distinguished Graduate Internship Program is jointly sponsored by the Department of Energy (DOE) Joint Genome Institute (JGI) and School of Natural Sciences, UC Merced (UCM). The objectives of this program are to:

1. Introduce students to emerging genomics technologies and informatics,
2. Provide hands-on experience in cutting edge genomics research,
3. Apply experimental and computational tools to research level problems, and
4. Analyze results using data and translate into scientific context.

This is an 8 week summer program located at the JGI campus in Walnut Creek, CA with a projected start date of June 5, 2017. Two students will be selected to participate in research projects (specific projects are attached). Students will be expected to participate in weekly group meetings to get input for their projects, make midterm and final presentations to summarize their research findings.

Note: You must be a current graduate student with the UC Merced to be eligible for this opportunity.

HOW TO APPLY:

Interested students must apply by **April 15th, 2017**. To formally apply, please directly contact the mentor of your favorite project (see attached project description) and copy your communications to program directors. As part of the application process, please submit the following attachments as part of your application.

1. A copy of your resume
2. A letter of recommendation from a UC Merced Faculty
3. A copy of transcript from UC Merced (non-official transcripts will be acceptable).

Students will be hired through the Lawrence Berkeley National Laboratory to work at the Joint Genome Institute in Walnut Creek, CA. Berkeley Lab/JGI is dedicated to the goal of building a culturally diverse and pluralistic workforce committed to teaching and working in a multicultural environment and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

CONTACT Information

If you have questions about this program, please contact one of the following professors:

Program Director: Prof. Zhong Wang (zhongwang@lbl.gov)
Program Co-Director: Prof. Axel Visel (avisel@lbl.gov)
Program Co-Director: Prof. Suzanne Sindi (ssindi@ucmerced.edu)
Program Support: Ms. Stephanie Canon (stephaniecanon@lbl.gov)

Project 1: FUNgal genome Analysis

Mentor: Igor Grigoriev ivgrigoriev@lbl.gov

Genomes of fungal species relevant to energy and environment are in the focus of the Fungal Genomic Program at the US Department of Energy Joint Genome Institute (JGI). In collaboration with research groups around the world we sequenced, assembled, and annotated over 700+ fungal genomes, which are integrated with omics data and analytical tools in the JGI fungal genome portal MycoCosm (jgi.doe.gov/fungi). Analysis of this Big Data requires analysis of gene families, development of new approaches and further automation.

Requirements: Graduate students with some experience in programming or bioinformatics.

Project 2: Hunting for new structural proteins in uncultivated viral genomes

Mentor: Emiley Eloe-Fadrosh eaeloefadrosh@lbl.gov

Viruses are the most abundant entities in the biosphere, displaying a high morphological and genomic diversity. In nature, viruses strongly influence microbial population dynamics, long-term evolution, and ecosystem functions. A fundamental feature of all viruses is their ability to create a protein-based capsid to protect their genome when outside of the host cell. Identifying the capsid machinery of a new virus is thus fundament to understanding its biology, evolution, and potential host interactions.

Recently, the number of sequenced viral genomes has increased 200fold, opening an unprecedented window into viral diversity. However, these new viral genomes have not been isolated in the lab, hence no information is available on their morphology, and most lack any identifiable capsid-associated genes. This project will aim to detect capsid proteins from uncultivated viral genomes captured from metagenomic data. The student will work closely with scientists in the Metagenome Program to (i) identify candidate genes putatively encoding capsid proteins from thousands of metagenomes collected globally, (ii) generate 3D structural predictions for these candidates and compare to known capsid protein folds, and (iii) propagate these newly validated capsid annotations across genome clusters and families. This work will help identify the capsid machinery of abundant uncultivated viruses, and potentially detect new types of capsids in understudied environments.