

## QUANTITATIVE & SYSTEMS BIOLOGY COLLOQUIUM:

Assembling Terabases of Environmental Metagenomes: Applications to Soils and Beyond



Date: 11/20/2025

<u>Time:</u> 10:30 AM – 11:45 AM

Location: SSB 130

## Robert Riley DOF Joint Genome Institute

## **About The Speaker:**

Robert Riley is a bioinformatics data scientist with over two decades of experience analyzing large-scale biological data in genomics centers, university research, and biotechnology. He holds a Ph.D. in Human Genetics from UCLA and a B.S. in Biochemistry and Molecular Biology from UC Santa Cruz. Dr. Riley's work at the DOE-JGI focuses on advanced methods for genome assembly and analysis with applications to environmental microbiology, fungal and algal genomics, metagenomics, bioenergy, and the structure and evolution of genomes. He applies artificial intelligence (AI) and machine learning-informed approaches to the analysis of biological big data, with the aim of developing, optimizing, and scaling complex genome and metagenome assembly workflows for the latest genomic technologies, and demonstrating their scientific impacts.

## Abstract:

Genome assembly is the inference of the complete, contiguous DNA sequence of an organism's genome from numerous shorter segments, or reads. Due to the limitations of current sequencing technologies, these reads are often significantly shorter than full chromosomes or even genomic features such as genes, operons, or biosynthetic gene clusters, thereby necessitating computational methods for genome assembly. The assembly of metagenomes, representing the collective genomes of environmental microbial communities, presents additional complexities. These include substantial variations in species abundance, population heterogeneity, a paucity of reference genomes, and the broad diversity of community members in complex environments such as oceans, lakes, and soils. This presentation will provide an overview of the theoretical foundations and practical application of metagenome assembly, encompassing both short- and long-read data, often operating at extreme scales. The discussion will feature applications to soil metagenomes derived from the U.S. National Science Foundation's National Ecological Observatory Network (NEON).