

# Fall 2015 Seminar Series

Presented by the CS Division

**THOROUGH MINING OF METAGENOMIC AND METATRANSCRIPTOMIC DATA  
WITH GUIDED REFERENCE-BASED ASSEMBLY OF SHORT PEPTIDES**

THURSDAY AUGUST 20, 2015

11:00 AM – HEC 450

Metagenomic and Metatranscriptomic (MG/MT) data analysis is challenged by the lack of complete reference genomes in the database and low coverage of less-abundant microbes. Currently available computational approaches often leave more than half of the MG/MT data unannotated, which makes it difficult to understand the behavior of the entire microbial community. In this talk, I will present a novel algorithm called the Simultaneous Alignment and Assembly (SAA), which combines both model-based alignment and de novo assembly. To emphasize the utility of the implemented program, I will describe its applications on detecting differential expression in MT data and discovering novel sequences with MG/MT data.

**DR. CUNCONG ZHONG**  
J. Craig Venter Institute

Dr. Cuncong Zhong currently is a postdoctoral fellow at the J. Craig Venter Institute. His research focuses on developing bioinformatics and computational biology algorithms. At JCVI, he is developing a suite of program for metagenomics and metatranscriptomics analysis, and applying these approaches for better understanding of human oral biofilm microbiome. He has published more than 15 peer-reviewed journal and conference papers. Dr. Zhong obtained his Ph.D. in Computer Science from the University of Central Florida in 2013.

*Hosted by: Dr. Shaojie Zhang*

