ANNOUNCE A SEMINAR BY

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WHO WILL SPEAK ON

Base Calling, Binning, SNP Calling on Meta-genomic Sequencing Data

Time: 3:00 PM - 4:00 PM
Date: Friday, April 21, 2017
Place: Speakman Hall 318

Abstract

Recently, the emerging new field of metagenomics facilitated by the advent of next-generation sequencing (NGS) technology enables genome sequencing of unculturable and often unknown microbes in natural environments, offering researchers an unprecedented opportunity to delineate bio-diversity of any microbial organism. While the sequencing technologies are evolving at unprecedented speed, researchers engaged in this enterprise are facing major computational, algorithmic and statistical challenges in the analysis of the massive metagenomic data. In this talk, I will introduce a new integrated statistical and computational pipeline empowered by high performance computing that consists of (1) base-calling; (2) binning; and (3) SNP detection on NGS sequencing data.