UNIVERSITY OF CALIFORNIA
UC RIVERSIDE

STATISTICS DEPARTMENT SEMINAR

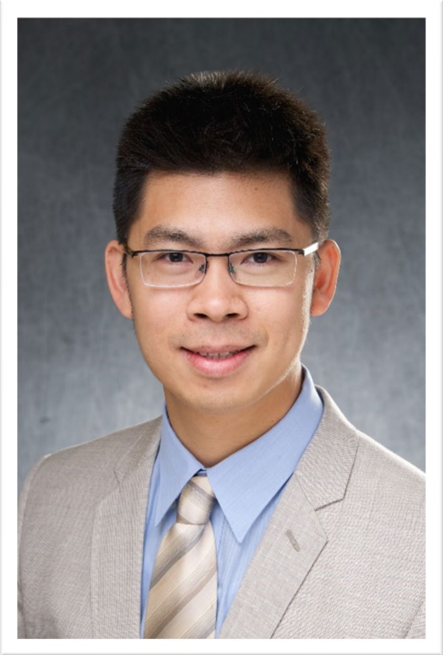
Dr. Kin Fai Au

Department of Computational

Tuesday, October 10th, 2023

Reception: 3:00-3:35pm
Olmsted Hall 1331
-
Talk: 3:45-4:45pm
Olmsted 420
Remote option
Meeting ID: TBA
Passcode: TBA

Medicine & Bioinformatics
University of Michigan



"NEW SEQUENCING TECHNOLOGY, NEW DATA ANALYSIS METHODS AND NEW INSIGHTS IN TRANSCRIPTOMICS AND EPIGENETICS"

Abstract

Third Generation Sequencing/TGS(i.e., Oxford Nanopore Technologies/ONT and Pacific Biosciences/PacBio), a.k.a. long-read sequencing, can generate single-molecule long reads, ranging from a few kb to million bp. These data have been demonstrated very powerful to address many complex biomedical problems that remained unsolved by short reads. For example, the extensive applications of TGS data for genome research have been published in various biomedical contexts. Here, I will present the methodological research of how long reads can advance transcriptome and epigenetics research. The particular focus is the mathematical foundation to model the unique information of long reads in the quantitative analyses of transcriptome, and the discovery of a unique activation pattern of transposable elements over zebrafish early embryonic development.

Biography

Dr. Au is the professor of Computational Medicine and Bioinformatics at University of Michigan, Ann Arbor. He received a B.S. at Tsinghua University and Ph.D. of structural biology at University of Oxford. He also obtained a master's degree of statistics and the postdoctoral training in Dr. Wing H. Wong's group at Stanford University. In the early stage of his career, he published the first long-read RNA-seq methods plus bioinformatics software (PacBio platform: PNAS 2013; Nanopore platform: F1000research 2017). Dr. Au established his independent research team at University of Iowa in 2013 and extended his research to long read-based epigenetics research. Dr. Au relocated to The Ohio State University in 2018, where he founded the PhD program of biomedical informatics as the program director and served as the Vice Chair of Research Development in the department. Dr. Au's research focuses on bioinformatics method development for sequencing data, especially for long reads. His team is also interested in applying these innovative techniques to interrogate the problems of transcript complexity and transposable elements in early embryonic development and stem cell biology.

UC RIVERSIDE
UNIVERSITY OF CALIFORNIA