Indiana University-Purdue University Indianapolis
Department of Mathematical Sciences

STATISTICS SEMINAR

12:15pm—1:15pm, Tuesday, October 03, 2023
Zoom Meeting: Meeting ID: 845 0989 4694

Speaker: **Victor Jin**
Division of Biostatistics, MCW Cancer Center & Mellowes Center, Medical College of Wisconsin

Title: **Modeling 3D-regulated cell or disease heterogeneity**

Abstract:

Single-cell Hi-C (scHi-C) has been used to delineate the three-dimensional (3D)-regulated heterogeneity of population cells. Although new sets of computational methods have been developed for processing scHi-C data, none of these methods were designed to algorithmically integrate scHi-C and single-cell (sc)RNA-seq data. Recent studies have revealed highly tumor-specific 3D chromatin architecture among different tumor samples, highlighting the important role of 3D chromatin in regulating inter/intra-tumor heterogeneity. However, all of these analyses are not based on any finely designed computational methods. Thus, it is important to develop a novel algorithm to identify individual tumor-specific TADs and looping genes. In this talk, I will present two computational methods newly developed in my lab, to define distinct 3D-regulated and biological-context dependent cell subpopulations, and to identify tumor-specific TADs and looping genes. I will then demonstrate their application in endocrine-resistant breast cancer cells and tumor samples. Our studies provided new insights into the role of 3D chromatin architecture in regulating cell or disease heterogeneity, and better understand how 3D-regulated heterogeneity governs endocrine-resistant breast cancer progression.

Bio:
Victor Jin, Ph.D, a Professor in Division of Biostatistics, Institute for Health Equity (IHE), Medical College of Wisconsin (MCW), a member of MCW Cancer Center and of Mellowes Center for Genome Sciences and Precision Medicine. He holds Linda T. and John A. Mellowes Endowed Chair of Bioinformatics and Data Analytics. He was trained in computational and functional genomics and has established a highly

reputable track record of developing novel computational methods and adapting cutting-edge genomic technologies in cancer systems. In particular, his lab and his collaborators have innovatively modified some cutting-edge omics-seq techniques such as MBDCap-seq, 3C-seq and ChIP-exo, and developed novel computational algorithms to process these omics-seq data. Currently he runs a multi-disciplinary systems biology lab where the research program is focused on the interface between chromatin regulation, cancer progression and drug resistance by utilizing novel computational, genomics and molecular techniques. They have been developing computational and genomic approaches for the identification of three-dimensional (3D) chromatin regulatory networks and epigenetic-regulated splicing variants from NGS data, as well as performing functional and mechanistic characterization of their roles in cancer progression and therapeutic resistance. They have also been adapting genome-wide omics-seq techniques in patient samples to identify epigenetically driven therapeutic targets and molecular biomarkers. His research program is continuously funded by NIH, DOD, CPRIT and other private funding agencies. He has delivered many scientific presentations at different levels of conferences, meetings and seminars and is involved in organizing numerous conferences and meetings. He has been participating in various NIH review panels, particularly in cancer systems biology and computational biology. He is currently an Associate Editor for Genes and an Editorial Board member of BMC Genomics.