Identification and Characterization of Genomic Variants with High Throughput Data

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https://uclahs.zoom.us/j/780633065

Abstract: Massive datasets generated by modern technologies have enabled great effort toward precision medicine. Researchers have identified various genetics/genomics features as potential biomarkers for disease prevention and diagnosis. The first part of my talk will be on copy number variants (CNVs) analysis. Most of existing methods used algorithms assuming that the observed data of different genetic loci are independent. Our study found that the correlation structure of CNV data is associated with linkage disequilibrium. Therefore, we developed a novel algorithm that will systematically integrate the genomic correlation structure into the modeling. I will show simulations and the application to a whole genome melanoma study. Application to a large cohort lung cancer study to reveal high confidence CNVs predisposing to lung cancer risk will also be illustrated. In the second part of my talk, I will talk about the identification of a gene expression based immune signature for lung adenocarcinoma prognosis using machine learning methods.

Bio: Feifei Xiao, Ph.D, is an Assistant Professor in the Department of Epidemiology and Biostatistics at the University of South Carolina. Dr. Xiao received her Ph.D. in Biostatistics from The University of Texas MD Anderson Cancer Center in 2013. She then got her postdoc training in Biostatistics from School of Public Health at Yale University (2013-2015). Dr. Xiao’s research focuses on high throughput genetic/genomics data, specifically on copy number variations, gene-gene/environment interactions, epigenetics and next generation sequencing data analysis. She has published 27 articles in peer reviewed journals of statistics, genetics and bioinformatics including Nucleic Acid Research, Human Genetics, and Bioinformatics.

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