Speaker: Rong Fan, Yale University
Talk Title: Spatial Multi-Omics Sequencing for Mapping Tissue Function, Aging, and Diseases

Abstract: Despite latest breakthroughs in single cell sequencing that revealed cellular heterogeneity, differentiation, and interactions at an unprecedented level, the study of multicellular systems needs to be conducted in the native tissue context defined by spatially resolved molecular profiles to better understand the role of spatial heterogeneity in biological, physiological and pathological processes. In this talk, I will begin with discussing the emergence of a whole new field – “spatial omics”, two major directions of spatial technologies that were developed over the past decade via either high-plex imaging or spatially encoded omics sequencing, and then focus on the technology platform called Deterministic Barcoding in Tissue (DBiT) for spatial omics sequencing developed in our own laboratory. We conceived the concept of “spatial multi-omics” and demonstrated it for the first time by co-mapping whole transcriptome and proteome (~300 proteins) pixel-by-pixel directly on a fixed tissue slide in a way compatible with clinical tissue specimens including FFPE. It has been applied to the study of developing mouse brain, human brain, and human lymphoid tissues associated with normal physiology, disease, or aging. Recently, our research enabled another new field – “spatial epigenomics” – by developing multiple DBiT-based spatial sequencing technologies for mapping chromatin accessibility (spatial-ATAC-seq), histone modification (spatial-CUT&Tag), or further combined with transcriptome or proteins for spatial co-profiling. These new technologies allow us to visualize gene expression regulation mechanisms pixel by pixel directly in mammalian tissues with a near single cell resolution. The rise of NGS-based spatial omics is poised to fuel the next wave of research revolution in all the areas of biological and biomedical sciences.