2025-2026 Cross-Campus Biomedical Research Collaboration Seminar Series





CHARACTER, TERRAIN, AND DESTINY: SINGLE-CELL AND SPATIAL ANALYSES OF THE MAMMALIAN REPRODUCTIVE SYSTEM



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Gallogly Hall, Room 126



ABSTRACT

Single-cell RNA sequencing (scRNAseq) methods have transformed our ability to measure cellular heterogeneity in complex tissues. The next frontier lies in spatial analysis, adopting imaging approaches that are high-resolution (e.g., visualizing single RNA molecules) and highly multiplexed (for hundreds of genes at a time) to survey the spatial organization of molecules and cells in large tissue sections. Our group has applied the MERFISH technology and scRNAseq to study mammalian spermatogenesis, and contributed to the Human Cell Atlas by creating female reproductive tissue atlases for the fallopian tube, ovary, and uterus. This enhanced understanding of cellular functions in healthy tissues has accelerated translational research, addressing long-standing questions in reproductive aging, infertility, and related cancers. Meanwhile the field faces increasingly pressing challenges in integration across diverse technologies, computational tools, and ontologies More broadly, I will discuss the major trends in genome research that led to the establishment of the Department of Molecular Genetics and Genome Sciences at the OUHSC, and the exciting prospect of joint growth with SBME.

BIO

Dr. Jun Li is Professor and Founding Chair of the newly established Department of Molecular Genetics and Genome Sciences in the College of Medicine (COM) at the University of Oklahoma Health Sciences. Before joining OU in April 2025, he was a Professor of Human Genetics and Professor and Associate Chair of Computational Medicine & Bioinformatics at the University of Michigan Medical School, where he worked for nearly 18 years. His background includes physics (BSc, Peking University), and biophysics/electrophysiology (PhD, Caltech), and genetics/genomics (postdoc, Stanford). As a computational biologist Dr. Li has led many studies to extract knowledge from genetic, genomic, and phenotype data generated from disease cohorts, patient families, or relevant model systems. His group has built expertise in statistical inference (pattern recognition, classification) and bioinformatics. In recent years his team has developed strong collaborations to study rat models of metabolic health, genetics and epigenetic of drug abuse, multi-omic analyses of human response to exercise, and cell and developmental biology of the reproductive system. He was experienced at leading research initiatives in Michigan Medicine, and has been elected as an AAAS Fellow and AIMBE Fellow.