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Computational methods for characterizing transcriptomic and spatial heterogeneity at the single-cell level

Abstract: The emergence of single-cell sequencing technologies has highlighted the potential to discover novel cellular subpopulations and states within heterogeneous tissues and tumors. Likewise, recent advancements in imaging-based technologies have enabled spatially-resolved targeted transcriptomic profiling at the single-cell level. In both cases, such single-cell measurements are often variable and sparse, owing to both the stochasticity of biological processes and inconsequential technical noise. Therefore, new statistical methods and computational tools are needed to analyze and model the inherently statistical nature of these single-cell measurements and to extract biological insights from within a probabilistic framework. In this talk, Jean will highlight the statistical approaches and computational tools I've developed to connect aspects of genetic, transcriptomic, and spatial heterogeneity and how I've applied these tools to study cancers as well as the mammalian brain.

Bio: Jean is currently an NCI F99/K00 post-doctoral fellow in the lab of Dr. Xiaowei Zhuang at Harvard University. She received her PhD in Bioinformatics and Integrative Genomics at Harvard under the mentorship of Dr. Peter Kharchenko at the Department of Biomedical Informatics and in close collaboration with Dr. Catherine Wu at the Dana-Farber Cancer Institute. Her research interests center around developing computational methods for identifying and characterizing heterogeneity at the single cell level, particularly in the context of cancer, using multi-omic and imaging-based approaches.