Statistical Methods for Single-cell RNA-seq Experiments

Christina Kendziorski, Ph.D., Professor
Department of Biostatistics and Medical Informatics
University of Wisconsin, Madison

ABSTRACT

Single-cell RNA-sequencing (scRNA-seq) has emerged as a revolutionary tool that allows us to address scientific questions that were elusive just a few years ago. With the advantages of scRNA-seq come computational challenges that are just beginning to be addressed. In this talk, I will review statistical methods our group has developed for scRNA-seq experiments with a focus on normalization, denoising, and identifying genes showing differential dynamics across biological conditions.

The Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics, Monday, November 14, 2016, 12:15-1:15, Room W2008 (Refreshments 12:00pm)

Note: Taking photos during the seminar is prohibited.

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Department of Biostatistics
615 N. Wolfe Street, Suite E3527 Baltimore, MD 21205