STATISTICS SEMINAR

UW-Department of Statistics www.stat.wisc.edu

TITLE: Data Denoising for Single-Cell RNA Sequencing

Abstract: Single-cell RNA sequencing (scRNA-seq) measures gene expression levels in every single cell, which is a recent ground-breaking technology over microarrays and bulk RNA sequencing and reshapes the field of biology. Though the technology is exciting, scRNA-seq data is very noisy and often too noisy for signal detection and robust analysis. In the talk, I will discuss how we perform data denoising by learning across similar genes and borrowing information from external public datasets to improve the quality of downstream analysis.
Specifically, I will discuss how we set up the model by decomposing the randomness of scRNA-seq data into three components, the structured shared variations across genes, biological "noise" and technical noise, based on current understandings of the stochasticity in DNA transcription. I will emphasize one key challenge in each component and our contributions. I will show how we make proper assumptions on the technical noise and introduce a key feature, transfer learning, in our denoising method SAVER-X. SAVER-X uses a deep autoencoder neural network to extract transferable gene expression features across datasets under different settings and borrow information from external data. I will show that SAVER-X can successfully transfer information from mouse to human cells and can guard against bias with a careful model setup and design of the algorithm.

Speaker:

Jingshu Wang

Stanford University

Time & Place:

Monday, February 11, 2019 **4pm**, Room 133 SMI
Cookies & Coffee @ **3:30**, Rm 1210 MSC

THE UNIVERSITY of WISCONSIN MADISON