



THE UNIVERSITY OF  
CHICAGO

Department of Statistics  
STATISTICS COLLOQUIUM

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Data Denoising for Single-cell RNA Sequencing

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Eckhart 133, 5734 S. University Avenue

ABSTRACT

Single-cell RNA sequencing (scRNA-seq) measures gene expression levels in every single cell, which is a 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. I'll also briefly discuss our ongoing work on post-denoising inference for scRNA-seq.

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For further information and inquiries about building access for persons with disabilities, please contact Jonathan Rodriguez at 773.702.8333 or send him an email at [jgrodriguez@galton.uchicago.edu](mailto:jgrodriguez@galton.uchicago.edu). If you wish to subscribe to our email list, please visit the following website:  
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