



# THE UNIVERSITY OF CHICAGO

Department of Statistics

STATISTICS COLLOQUIUM

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Topics in the analysis of high-throughput molecular data and  
the bootstrap in high dimensions

MONDAY, November 11, 2019 at 4:30 PM

Eckhart 133, 5734 S. University Avenue

*Refreshments before the seminar at 4:00 PM in Jones 111*

## ABSTRACT

In this talk I will discuss my work in two areas: analysis of single-cell sequencing data and the bootstrap in high dimensions. mRNA sequencing of single cells is a relatively recent biological technology that allows researchers to query what genes are active in a single cell. I discuss our work in analyzing this data, including our method for charting the progression of cells as they differentiate during development (Slingshot). With respect to the bootstrap, we consider the setting of inferential problems in moderate and high-dimensions where we have a diffuse signal. In this setting, results in random matrix theory can prove useful for creating theoretical inferential techniques, but are limited in scope and can be sensitive to the distributional assumptions. The bootstrap is often helpful for such situations where theoretical inferential techniques are difficult. However, we show, through a mix of numerical and theoretical investigations, that in the relatively simple case of linear regression that when there is a diffuse signal and the number of predictors is not small relative to the sample size the performance of the bootstrap is generally poor.

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<https://lists.uchicago.edu/web/subscribe/statseminars>.