



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Studying eQTL Detection with Methylation Data

TUESDAY, May 9, 2017, at 10:00 AM
Jones 304, 5747 S. Ellis Avenue

ABSTRACT

DNA methylation plays an important role in regulating gene expression. In the past decade, it has become common to conduct genome-wide searches for genetic variants, or eQTLs, associated with gene expression. Recently, increasingly available data on individual epigenomes have made it possible to study the interactions between epigenome, genome, and gene. We examine the feasibility of leveraging DNA methylation data for use in eQTL discovery, investigating multiple methods for modeling the relationships between genes, variants, and methylation sites. We also study patterns in comethylation and correlation between levels of methylation and gene expression.

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