



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Beta-Poisson Modeling of Single-Cell RNA-Sequencing Data

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Jones 304, 5747 S. Ellis Avenue

ABSTRACT

Genetically identical cells grown in the same condition have been found to have different gene expression levels. While the modern RNA-sequencing tools allow us to count mRNA molecules on the single-cell level, the statistical models to identify the sources of gene expression variability are still being developed.

We present and fit a Beta-Poisson model to the human induced pluripotent stem cells in order to infer the parameters driving the gene transcription process. We also describe the statistical properties of the estimates for genes with different kinetics and separate the genes with identifiable and non-identifiable parameters.

Additionally, we use the genotype information to investigate its influence on the parameter's value. Our model has identified a few significant results at 5% FDR, but we specifically focus on gene ENSG00000197728 as it appears to have significant effects of genotype on all model parameters.