THE UNIVERSITY OF CHICAGO | DEPARTMENT OF STATISTICS

MASTER'S THESIS PRESENTATION

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Understanding the Transcriptional Regulation with 3D Genomic Structure

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Zoom Meeting

ABSTRACT

Single-cell RNA sequencing (scRNA-seq) analysis has been used as an important tool to interpret the transcriptional regulations across cells, to understand the mechanisms of transcriptomes, and to detect cell types and tumor heterogeneity. Meanwhile, the High-throughput Chromosome Conformation Capture (Hi-C) data analysis allows us to study the 3D chromatin structure in genomes. In this work, we present a framework to incorporate the results from both analyses to interpret the relationship between distance and correlations of gene pairs, by identifying the highly correlated gene pairs and self-interacting genomic regions.