# Thesis Defense

Computer Science Master's Program

## "Identifying Interchromosomal Interactions using a Graph-Based Computational Pipeline"

By **Ethan Outangoun**

**Abstract:**

Current computational tools for analyzing chromatin organization are mainly focused on intrachromosomal interactions, despite growing evidence that suggests long-range interactions across chromosomes contribute to transcriptional regulation and disease development. This thesis aims to address this gap in interchromosomal genome analysis, presenting a robust computational pipeline that identifies a clique (i.e., a subgraph) of highly interacting trans-chromosomal regions anchored at a user-specified seed locus. A weighted interaction network is constructed from an input Hi-C contact matrix, a widely used experimental assay for measuring genome-wide chromatin interactions. We model this input contact matrix as a graph and devise three different strategies to computationally find biologically important cliques: a greedy heuristic for efficient local exploration, a simulation-based random walk with restarts, and an analytical formulation of the same random walk process. To validate the performance of this pipeline, we focus on TTN, a key muscle gene whose splicing is essential for human heart development. Hi-C data from wild-type and TTN promoter knockout cardiomyocytes are used to compare structural differences in TTN's long-range interactors. Though sparse contacts in the knockout data limit definitive comparison, cliques built from the wild-type matrix reveal loci with strong gene correlation. We further design several different background models to statistically assess the significance of these interactions. Our results highlight the effectiveness of network-based methods in uncovering functionally relevant interchromosomal interactions and lay the groundwork for future analyses.

**Date: Wednesday, June 11th, 2025**
**Time: 2:00 PM – 4:00 PM**
**Location: 14-232b**
**Committee: Dr. Hristov, Dr. Stanchev, and Dr. Anderson**