

MSc Seminar

Tuesday May 17, 2022 at 1pm via Zoom Rekkab Gill

Predicting Chromosomal Compartments using Machine Learning

Advisor: Dr. Stefan Kremer **Advisory:** Dr. Daniel Gillis

Abstract:

The 3D structure of a genome is critical to gene regulation and the mechanisms that govern gene expression. Genomes can be organized into two distinct compartments, A and B. Compartment A is associated with chromatin that is gene rich, transcriptionally active, and loosely packed. Compartment B is gene poor, expression-inactive, and tightly packed. The research presented here expands on previous work using machine learning to predict compartments directly from DNA sequence basepairs. In total, 10 additional datasets were examined of which five were used to train ABCNet models to predict compartments. The other five were analyzed and compared using customized python scripts to examine compartments for similarities and differences. Preliminary research and methodology to develop a predictive model that can determine whether regions of chromosomes change compartments or remain consistent is discussed as a roadmap for future work.