



Department of Mathematics and Statistics

Colloquium

Tuesday February 25

4:00 - 5:00 pm Adel 164

## How cells make decisions - identifying master regulators by Boolean network

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### Abstract

How do cells differentiate into functionally distinct cell types, such as a nerve cell, a skin cell, etc., although they all share the very same genome? This mainly depends on the expression profile of a set of genes. For example, in the gene *GATA1*, a transcription factor stimulates differentiation of blood stem cells into the red blood cell lineage. The differentiation process is thought to be initiated by the activation of master regulators, a set of transcription factors that are specialized to promote the respective cell type. Shinya, a Nobel Prize-winning Japanese researcher, discovered that skin cells can be converted to stem cells by increasing the expression level of 4 master regulators.

So the next question is how do we identify the master regulators that control the cell differentiation lineage. One approach is to use Boolean network, as the status of the transcription factors can be simply modeled as on or off, namely 1 or 0. We can construct the Boolean network with the vertices being the transcription factors that have the weight 0 or 1, and with the weighted directed edges being defined based on the biological observations. The use of Boolean networks can capture the essential outlines of cell fate dynamics and more importantly, permit the estimation of relative stability and the attractor transition barriers. I will talk about some successful applications in finding master regulators using Boolean net, then discuss how to extend this method in the new area – single cell RNA-seq data analysis.

The only prerequisite for this talk is MAT 316 Linear Algebra.

Refreshments at 3:45