

Simon Joyce (Binghamton)

Interaction Graphs Derived From Activation Functions and Their Application to Gene Regulation

Abstract for the Combinatorics Seminar 2017 November 27

Signed interaction graphs are graphic representations of complex networks of mutually interacting components. Their main application is in the field of gene regulatory networks, where they are used to visualize how the expression levels of genes activate or inhibit the expression levels of other genes.

First I develop a natural transformation of activation functions called conjugation that is related to a natural transformation of signed digraphs called switching isomorphism. This is a useful tool for the analysis of interaction graphs.

I then discuss the question of what restrictions, if any, apply to interaction graphs derived from activation functions. Within these restrictions, I then construct polynomial activation functions that have any desired interaction graph. The specific case of threshold activation functions, a commonly used kind of activation function, is also considered.

I then conclude with some discussion and new proofs, using the theory of conjugate activation functions, of the conjectures of René Thomas. These conjectures relate feedback in the interaction graph to the dynamic properties of multi-stationarity and periodic stability. In particular, I have a new counterexample to the local version of Thomas' second conjecture that requires only eight components. This is the smallest counterexample I am currently aware of.

This is Simon Joyce's dissertation defense. The dissertation committee consists of Laura Anderson, Fernando Guzmán, Leslie Lander (outside examiner), and Thomas Zaslavsky (chairone).

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