

1116-AA-2890 **Brandilyn Stigler*** (bstigler@smu.edu), 3200 Dyer Street, Dallas, TX 75275. *Reducing Ambiguity in Biological Network Inference via Grobner Bases.*

Predicting mathematical models of biological phenomena from experimental data is sensitive to the amount of data used as input. When there are too few data, the number of possible models that explain the data are too numerous, thereby reducing the probability of selecting biologically relevant models. In the context of systems biology where substantial costs are incurred in laboratory experiments, having an estimate of the amount of data required to infer the network becomes important and aids in minimizing wasted resources.

In this talk, we describe a class of discrete models, called polynomial dynamical systems (PDSs), for gene regulatory networks as well as a method for constructing PDSs from data. We also establish a connection between model ambiguity and existence of multiple Groebner bases, which capture the distinct vector space basis representations associated to the input data. Furthermore we provide criteria for determining whether a set of data uniquely identifies a PDS and a strategy for selecting candidate data points for unique model identification. (Received September 22, 2015)