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MSIS-Kadelka: Algebraic Methods for Inferring Discrete Models of Biological Networks

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Biological data science is a field replete with many substantial data sets from laboratory experiments and myriad diverse methods for modeling, simulation, and analysis. As a data set can have a large number of associated models, model selection is often required as a post-processing step. In parallel experimental design can be utilized as a preprocessing step to minimize the number of resulting models, many of which may be biologically irrelevant.

In this talk we provide an overview of algebraic methods for building polynomial models of biological networks from discrete data, and for performing model selection and experimental design simultaneously. This work draws from algebraic geometry and algebraic combinatorics, and has been used to model a variety of biological processes including tissue development and tumor progression.