High-dimensional ODEs for Gene Regulatory Network Identification

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Abstract

The gene regulation network (GRN) is a high-dimensional complex system, which can be represented by various mathematical or statistical models. The ordinary differential equation (ODE) model is one of the popular dynamic GRN models. In this talk, I present a sparse additive ODE (SA-ODE) model, coupled with ODE estimation methods and adaptive group LASSO techniques, to model dynamic GRNs. The asymptotic properties of the proposed method are established and simulation studies are performed to validate the proposed approach. An application example for identifying the nonlinear dynamic GRN of T-cell activation is used to illustrate the usefulness of the proposed method.