



生物信息学研究中心

Center of Bioinformatics

学术报告

题目： Data-Driven ODE Model Constructors for Dynamic Network Modeling with Biomedical Applications

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地点： 思源楼 712 室

摘要：

Biological systems such as gene regulatory networks and the interactions with gene products are very complex. Identification of the dynamic networks will help us understand the biological process in a systematic way. However, the construction of such a dynamic network is very challenging for a high-dimensional system. We propose to use a set of ordinary differential equations (ODE), coupled with dimensional reduction by clustering and mixed-effects modeling techniques, to model the dynamic gene regulatory network (GRN). The ODE models allow us to quantify both positive and negative gene regulations as well as feedback effects of one set of genes in a functional module on the dynamic expression changes of the genes in another functional module, which results in a directed graph network. A six-step procedure, Significance screening, Clustering, Smoothing, regulation Identification, parameter Estimates refining and Function enrichment analysis (SCSIEF) is developed to identify the ODE-based dynamic GRN. In the proposed SCSIEF procedure, a series of cutting-edge statistical methods and techniques are employed. We apply the proposed method to identify the dynamic GRN for yeast cell cycle progression data and T cell activation in vitro experiments. We are able to annotate the identified modules through function enrichment analyses. The proposed procedure is a promising tool for constructing a general dynamic GRN and more complicated dynamic networks.