第 10 回 2013 年 1 月 11 日（金）14:50 ~ 15:40

State transition of living cells and time series analyses

細胞の状態変化と時系列データ解析

Daisuke Tominaga / 富永　大介

Computational Biology Research Center (CBRC)

National Institute of Advanced Industrial Science and Technology (AIST)

産業技術総合研究所　生命情報工学研究センター

Several mathematical models based on systems of ordinary differential equations (ODEs) have been proposed for the representation of RNA interference (RNAi) dynamics. These consist of equations for molecular elements involved in RNAi, and so there are many real-value parameters that must be optimized in order to identify the models. They also have many `hidden variables', which cannot be observed directly by experiment. Calculation of the values or profiles of the hidden variables is generally difficult, if not impossible, and identification of the ODE models is also quite difficult in this situation.

We show that the simplified logistic Lotka-Volterra model, which is one of the most well-established ODE models for biological and biochemical phenomena, can represent RNAi dynamics as a predator-prey system that models the apoptosis of HeLa cells by small interfering RNA (siRNA). Although there is a hidden variable, the values can be determined, or made visible as dynamic profiles of RNA decomposing effects of siRNAs. Model parameters correlate highly with the total effect of the siRNA.

Keywords: time series analysis, state transition, gene expression analysis, statistical models, optimization