Learning gene regulatory networks from gene expression measurements using non-parametric molecular kinetics

Revealing the structure and dynamics of gene regulatory networks (GRNs) is of great interest and represents a considerably challenging computational problem. The GRN estimation problem is complicated by the fact that the number of gene expression measurements is typically extremely small when compared to the dimension of the biological system. Many recent GRN inference methods are founded on ordinary differential equations (ODE). However, because gene regulation process is intrinsically complex, commonly used parametric models can provide too simple description of the underlying phenomena and, thus, can be unreliable.

The presented novel framework [1] is based on the use of Bayesian analysis with ODEs and non-parametric Gaussian process modeling for the transcriptional level regulation. It is applicable to structure learning and prediction of the dynamic behavior of a GRN. The uncertainty in measurements is taken into account by using a noise model and Bayesian analysis, and uncertainty in the phenomena is tackled by utilizing non-parametric modeling.

The performance of the proposed structure and dynamics inference method is evaluated using the recently published in vivo reverse-engineering and modeling assessment (IRMA) data set. By comparing the obtained structure inference results with those of existing ODE-based inference methods we demonstrate that the proposed method provides more accurate network structure learning. By splitting the IRMA data set into training and test sets, we also demonstrate that the model is able to capture dynamics of the system.

References

[1] Äijö, T. & Lähdesmäki, H., Learning gene regulatory networks from gene expression measurements using non-parametric molecular kinetics, Submitted.