Sophie Lèbre (LSIIT - UMR7005 - Université de Strasbourg)

Non-homogeneous dynamic Bayesian networks with Bayesian regularization for inferring gene regulatory networks with gradually time-varying structure.

résumé :
The proper functioning of any living cell relies on complex networks of gene regulation.
These regulatory interactions are not static but respond to changes in the environment and evolve during the life cycle of an organism. A challenging objective in computational systems biology is to infer these time-varying gene regulatory networks from typically short time series of transcriptional profiles. While homogeneous models, like conventional dynamic Bayesian networks, lack the flexibility to succeed in this task, fully flexible models suffer from inflated inference uncertainty due to the limited amount of available data.
In the present paper we explore a semi-flexible model based on a piecewise homogeneous dynamic Bayesian network regularized by gene-specific inter-segment information sharing. We explore different choices of prior distribution and information coupling and evaluate their performance on synthetic data.
We apply our method to gene expression time series obtained during the life cycle of Drosophila melanogaster, and compare the predicted segmentation with other state-of-the-art techniques.
We conclude our evaluation with an application to synthetic biology, where the objective is to predict an in vivo regulatory network of five genes in Saccharomyces cerevisiae subjected to a changing environment.