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几何模式动态贝叶斯网络推理基因调控网络

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摘要　　针对趋势相关(两基因在其表达水平随时间上升与下降的变化趋势上相关)关系在重建基因调控网络中十分重要却尚未被挖掘利用的问题，提出了几何模式动态贝叶斯网络(Gp-DBN)方法. Gp-DBN将每个基因的表达数据转换为一个几何模式，依据几何模式确定潜在的调控子和调控时滞，并通过推理这些几何模式之间的相关关系来发现基因间的调控关系. 该方法解决了挖掘具有趋势相关的基因调控关系的问题，能够很大程度地提高重建的基因调控网络的性能. 对Yeast和 E. coli基因数据的实验结果表明无论是在无先验知识还是在有先验知识时Gp-DBN重建的基因调控网络的性能都比传统的动态贝叶斯网络方法有大幅度提高.

关键词　　几何模式　动态贝叶斯网络　基因调控网络

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Geometric-pattern dynamic Bayesian networks reasoning gene regulatory networks

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Abstract

<P>Trend correlations (i.e., two genes are correlated in their varying trends that rise and descend with time) between genes are very important but usually neglected in reconstruction of gene regulatory networks (GRN). To mine trend correlations to enhance the reconstruction performance of GRN, we propose geometric-pattern dynamic Bayesian networks (Gp-DBN). In Gp-DBN the time series of each gene is transformed to a geometric pattern, by which potential regulators and time lags are estimated, and regulatory relations between genes are discovered by reasoning correlations between these geometric patterns. Gp-DBN realizes the mining of regulatory relations with trend correlations so that it can improve the performance of GRN reconstruction. Experimental results on Yeast and E. coli data sets show that Gp-DBN improves greatly the performance of GRN reconstruction in the cases with / without prior knowledge, compared with traditional dynamic Bayesian networks.
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Key words　 geometric pattern　 dynamic Bayesian networks　 gene regulatory networks

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