



生物信息学研究中心

Center of Bioinformatics

学术报告

题目 : Inferring Genetic Networks by Datasets of Different Experiments

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摘要 : Reconstruction of genetic regulatory network is the field of research that tries to find the underlying network of gene-gene interactions from the measured set of gene expressions. Since typical gene expression data-sets consist of relatively few time-points (e.g. less than 20) with respect to the number of genes (e.g. more than 1000), existing approaches are currently hampered by one major difficulty, i.e. scarcity of time series data or the so-called dimensionality problem. In other words, the number of genes typically far exceeds the number of time points for which data are available, making the problem of determining genetic network structure an ill-posed one although there are many experimental results by different groups. On the other hand, the derived gene networks from the conventional approaches are generally densely connected among nodes, which are not biological plausible. The biologically the resulting gene network is expected to be sparse, which should be reflected in the reconstruction of networks.

We aim theoretically to propose a new algorithm for inferring the dynamical genetic networks by using datasets with different experiments. The method is based on linear programming (LP) and decomposition technique, which not only are efficient from the computational viewpoint, exploring the datasets of different experiments, but also can derive biologically plausible networks with sparseness.