

基于微阵列数据的基因网络预测方法研究进展

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DNA微阵列技术可同时定量测定成千上万个基因在生物样本中的表达水平，从这一技术获得的全基因组范围表达数据为揭示基因间复杂调控关系提供了可能。研究人员试图通过数学和计算方法来构建遗传互作的模型，这些基因调控网络模型有聚类法、布尔网络、贝叶斯网络、微分方程等。本文对网络重建计算方法的研究现状进行了较为全面的综述，比较了各种模型的优缺点，并对该领域进一步的研究方向进行了展望。

Progress on methods for inferring the gene networks from microarray data

DNA microarray technology makes it feasible to obtain quantitative measurements of expression of thousands of genes that present in a biological sample simultaneously. Genome-wide expression data generated from technology are promising to uncover the complex relationships between these genes. Mathematical and computational methods are being developed in order to construct formal models of genetic interactions. There have been a number of attempts to model gene regulatory networks, including clustering, Boolean networks, Bayesian networks and differential equations. In this paper, the state of the art in computerized gene network reconstruction techniques is reviewed. The specific advantages and disadvantages of these models are explained. Moreover, some issues valuable for future exploration in this area are indicated and discussed.

关键词