عنوان مقاله:

Computational methods for gene regulatoryNetwork construction from expression data

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خلاصه مقاله:

Biological networks provide a natural representation of complex biological systems and thus have been used in a variety of applications, from gene function prediction to identifying disease genes. Many biological research areas such as drug design require gene regulatory networks to provide clear insight and understanding of the cellular process in living cells. This is because interactions among the genes and their products play an important role in many molecular processes. Gene regulatory networks describe control at the gene expression level and could be inferred from expression profiles and interactions between regulatory targets. Due to its importance, several computational approaches have been proposed to infer gene regulatory networks from gene expression data. The approach of inferring gene regulatory networks has been flourishing for many years, and new methods from mathematics, information science, engineering and social sciences have been applied. In this review, different kinds of computational methods biologists use to infer networks of varying levels of accuracy and complexity are discussed: Boolean network, probabilistic Boolean network, ordinary differential equation, neural network, Bayesian network, and dynamic Bayesian network. These approaches are also compared in the discussion section. Furthermore, the strengths and weaknesses of these computational approaches are described.

کلمات کلیدی:

Gene regulatory network; Computational approaches; Gene expression data; Bayesian network; Boolean network

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