

Gene regulatory network inference: data integration in dynamic models-a review.

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Abstract

Systems biology aims to develop mathematical models of biological systems by integrating experimental and theoretical techniques. During the last decade, many systems biological approaches that base on genome-wide data have been developed to unravel the complexity of gene regulation. This review deals with the reconstruction of gene regulatory networks (GRNs) from experimental data through computational methods. Standard GRN inference methods primarily use gene expression data derived from microarrays. However, the incorporation of additional information from heterogeneous data sources, e.g. genome sequence and protein-DNA interaction data, clearly supports the network inference process. This review focuses on promising modelling approaches that use such diverse types of molecular biological information. In particular, approaches are discussed that enable the modelling of the dynamics of gene regulatory systems. The review provides an overview of common modelling schemes and learning algorithms and outlines current challenges in GRN modelling.

Beteiligte Forschungseinheiten

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