

Use of systems biology to decipher host-pathogen interaction networks and predict biomarkers.

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Abstract

In systems biology, researchers aim to understand complex biological systems as a whole, which is often achieved by mathematical modelling and the analyses of high-throughput data. In this review, we give an overview of medical applications of systems biology approaches with special focus on host-pathogen interactions. After introducing general ideas of systems biology, we focus on (1) the detection of putative biomarkers for improved diagnosis and support of therapeutic decisions, (2) network modelling for the identification of regulatory interactions between cellular molecules to reveal putative drug targets and (3) module discovery for the detection of phenotype-specific modules in molecular interaction networks. Biomarker detection applies supervised machine learning methods utilizing high-throughput data (e.g. single nucleotide polymorphism (SNP) detection, RNA-seq, proteomics) and clinical data. We demonstrate structural analysis of molecular networks, especially by identification of disease modules as a novel strategy, and discuss possible applications to host-pathogen interactions. Pioneering work was done to predict molecular host-pathogen interactions networks based on dual RNA-seq data. However, currently

this network modelling is restricted to a small number of genes. With increasing number and quality of databases and data repositories, the prediction of large-scale networks will also be feasible that can be used for multidimensional diagnosis and decision support for prevention and therapy of diseases. Finally, we outline further perspective issues such as support of personalized medicine with high-throughput data and generation of multiscale host-pathogen interaction models.

Involved units

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