

Computational prediction of molecular pathogen-host interactions based on dual transcriptome data

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Abstract

Inference of inter-species gene regulatory networks based on gene expression data is an important computational method to predict pathogen-host interactions (PHIs). Both the experimental setup and the nature of PHIs exhibit certain characteristics. First, besides an environmental change, the battle between pathogen and host leads to a constantly changing environment and thus complex gene expression patterns. Second, there might be a delay until one of the organisms reacts. Third, towards later time points only one organism may survive leading to missing gene expression data of the other organism. Here, we account for PHI characteristics by extending NetGenerator, a network inference tool that predicts gene regulatory networks from gene expression time series data. We tested multiple modeling scenarios regarding the stimuli functions of the interaction network based on a benchmark example. We show that modeling perturbation of a PHI network by multiple stimuli better represents the underlying biological phenomena. Furthermore, we utilized the benchmark example to test the influence of missing data points on the inference performance. Our results suggest that PHI network inference with missing

data is possible, but we recommend to provide complete time series data. Finally, we extended the NetGenerator tool to incorporate gene- and time point specific variances, because complex PHIs may lead to high variance in expression data. Sample variances are directly considered in the objective function of NetGenerator and indirectly by testing the robustness of interactions based on variance dependent disturbance of gene expression values. We evaluated the method of variance incorporation on dual RNA sequencing (RNA-Seq) data of *Mus musculus* dendritic cells incubated with *Candida albicans* and proofed our method by predicting previously verified PHI as robust interactions.

Beteiligte Forschungseinheiten

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Awards

<http://www.rna-seqblog.com/dual-rna-seq-enables-computational-prediction-of-molecular->

pathogen-host-interactions/

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