

How to Predict Molecular Interactions between Species?

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Abstract

Organisms constantly interact with other species through physical contact which leads to changes on the molecular level, for example the transcriptome. These changes can be monitored for all genes, with the help of high-throughput experiments such as RNA-seq or microarrays. The adaptation of the gene expression to environmental changes within cells is mediated through complex gene regulatory networks. Often, our knowledge of these networks is incomplete. Network inference predicts gene regulatory interactions based on transcriptome data. An emerging application of high-throughput transcriptome studies are dual transcriptomics experiments. Here, the transcriptome of two or more interacting species is measured simultaneously. Based on a dual RNA-seq data set of murine dendritic cells infected with the fungal pathogen *Candida albicans*, the software tool NetGenerator was applied to predict an inter-species gene regulatory network. To promote further investigations of molecular inter-species interactions, we recently discussed dual RNA-seq experiments for host-pathogen interactions and extended the applied tool NetGenerator (Schulze et al., 2015). The updated version of NetGenerator makes use of measurement variances in the algorithmic procedure and accepts gene expression time series data with missing values. Additionally, we tested multiple modeling scenarios regarding the stimuli functions of the gene regulatory network. Here, we summarize the

work by Schulze et al. (2015) and put it into a broader context. We review various studies making use of the dual transcriptomics approach to investigate the molecular basis of interacting species. Besides the application to host-pathogen interactions, dual transcriptomics data are also utilized to study mutualistic and commensalistic interactions. Furthermore, we give a short introduction into additional approaches for the prediction of gene regulatory networks and discuss their application to dual transcriptomics data. We conclude that the application of network inference on dual-transcriptomics data is a promising approach to predict molecular inter-species interactions.

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[Netzwerke der Wirt-Pilz-Pathogen Interaktion](#)

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