



Fabian Horn

Prediction of gene regulatory networks involved in the differentiation, secondary metabolism and cross talk of *Aspergillus nidulans*

Biological data is collected in many hundreds of different experiments where each consists of thousands of data points. They are published and stored in several databases and scientific journals in different data formats and abstraction layers. The challenge for bioinformatics is to gather, preprocess and model these data consistently. By the integration of the information from several experiments, new scientific findings can be obtained with the help of methods from systems biology and comparative analysis.

Aspergillus nidulans is a filamentous fungus which is able to form sexual spores through meiosis. It is therefore used to research the eukaryotic cell biology. *A.nidulans* has been completely sequenced and there has been great progress in elucidation of the molecular regulation of the biosynthesis of secondary metabolites. In this project there are two main methods which are to be applied to *A.nidulans*:

1. A new microarray probe design has already been developed and is currently applied to investigate the transcriptome under different environmental conditions. To improve the quality of the data, published microarray data for *A.nidulans* can be integrated and methods which mine gene expression across different experiments are to be developed and employed.
2. We are looking for the connection of transcriptome data with metabolome data. Until now such

relationships have only be analyzed for the primary metabolism, e.g. in *Escherichia coli*. The project aims to adapt these existing methods for the specific characteristics of secondary metabolite pathways. The methods should be applicable for organisms like *A.nidulans*, where less prior knowledge is available.

Publications

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