Bioinformatics and Systems Biology

In the future biology will increasingly focus not only on single molecules but on biological systems. This ‘systems’ approach, which is based on the hypothesis that biology is basically an informational science, requires the generation and formalization of knowledge on different levels including the establishment of links between genes and cell status, and the characterization of co-regulated genes or associating gene changes to pathways or networks. The methods used for these investigations largely stem from the field of machine learning. We were recently able to find generalization error bounds that can be used for model selection and the classification of conjunctions of Boolean variables. We are currently investigating this topic further with the aid of boosting algorithms (PhD project Ludwig Lausser). Another project is how to arrive at these Boolean variables i.e. how to binarize data from gene expression values in a well-defined way (PhD project Martin Hopfensitz). This is also directly linked to modelling signal transduction and gene regulation with Boolean functions from data via reverse engineering (PhD work Alexander Groß). Other approaches being investigated are models based on differential equations, which consist of many parameters that cannot all be calculated based on data alone but also require the inclusion of more global knowledge (PhD project Christian Wawra). In this regard, we were able to extend a model of the Wnt/β-catenin pathway via time-delay differential equations and substantiate the model’s principal behaviour by conducting an extended robustness analysis.

Rule-based random graph model for modelling qualitative interactions. Edge probabilities p are introduced that represent interaction probabilities (in its broadest sense) and then apply rules Φ that modify pt based on the current edge state of the graph (interaction present or not) and the current probability distribution.

Selected Publications: