

Workshop: *Deconstructing Biochemical Networks*
22–23 September 2007

*Dynamic Modeling of Signaling Pathways and
Their Interaction with Cell Cycle Progression in
Budding Yeast*

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Abstract

Investigation of cellular systems is more and more supported by mathematical modelling, such as the description of reaction system dynamics by sets of ordinary differential equations. The structure of the equations is based on the network structure, i.e pathways or protein-protein interactions, while the parameters are determined from quantitative experimental measurements. We investigate the stress response processes in a model organism, the yeast *Saccharomyces cerevisiae*. The adaptation of cells to environmental changes like nutrient supply or pheromone stimulation is mediated by signalling pathways that eventually adjust the expression of many genes, which in turn regulate metabolism or cell cycle progression in order to compensate for or adapt to the external stimuli. We specifically investigate the response of yeast cells to osmotic stress [1] and its implications on cell cycle [2] as well as on energy metabolism. To test model predictions, we consider different stress conditions and experimental scenarios. The analysis shows that mathematical model can be helpful to formulate experimental knowledge in a testable form, to explain hitherto unsolved phenomena and to predict the outcome of new experiments.

References

- [1] E. Klipp et al., *Minimum information requested in the annotation of biochemical models* (MIRIAM), Nat. Biotechnol. **23** (2005), 1509–1515.
- [2] M. Barberis et al., PLoS Comp. Biol., 2007.