



Emerging Topics in Biological Networks and Systems Biology

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Systematic Integration of Models and Data for Yeast Growth and Division

Abstract:

With the progress of genome-wide experimental approaches we witness the establishment of more and more libraries of genome-wide data for proteins or RNA or metabolites. However, the separated consideration of metabolic networks or gene regulation networks does not tell us how these networks are integrated to allow a cell to grow, divide and respond to changing environments.

We use the yeast *Saccharomyces cerevisiae* as the model organism for eukaryotic cells allowing to comprehensively analyzing regulatory networks and their integration with cellular physiology. We use a modular and iterative approach that allows for a systematic integration of cellular functions into a comprehensive model allowing to link processes that are strongly interlinked in cellular life, but measured separately. Edda Klipp & TBP.

About:

Edda Klipp is full professor for Theoretical Biophysics at Humboldt-Universität zu Berlin. She has a doctoral degree in theoretical biophysics. In 2009 she was awarded an honorary doctor of Göteborg University. 2015 she was awarded the Caroline-von-Humboldt professorship at Humboldt-Universität zu Berlin. Klipp carries out multi-disciplinary research projects to understand cellular organization, dynamics of cellular processes and stress response. Her group has long-standing experience in computational systems biology with focus on dynamic modeling of regulatory processes including signaling, cell cycle, metabolism, transcriptional regulation and growth control.