

LECTURE SERIES & WORKSHOPS

TRANSLATIONAL BIOINFORMATICS AND SYSTEMS BIOMEDICINE

05

LECTURE

 **Maison du Savoir**
Room N° 4.340

MEET THE SPEAKER*

Light snacks provided
Maison du Savoir
Room N°4.390

DECEMBER 2017

Tuesday

4.00 - 5.00 pm

5.00 - 6.30 pm



*Please register by sending a mail to
florence.henry@lih.lu



SPEAKER

Prof Edda Klipp

Professor for Theoretical Biophysics,
Department of Biology
Humboldt-Universität zu Berlin, Germany

HOST:

Department of Oncology

RESPONSIBLE LIH SCIENTIST:

Dr Gunnar Dittmar
(gunnar.dittmar@lih.lu)

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.

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