



University of Stuttgart

Stuttgart Research Center Systems Biology (SRC SB)

Systems Biology Seminar Talk

„Computational modeling of
the metabolism of lactic acid
bacteria “

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**Wednesday
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10 a.m. – 11 a.m.

Log in:

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Abstract:

Computational modeling is a frequently used approach in microbiology. Both detailed kinetic as well as genome-scale models are used. Whereas kinetic models encompass detailed knowledge of the regulation and speed of individual reactions, whole genome-scaled models offer an integrative view on the metabolic network of an organism without the need to know kinetic information in detail. However, the enormous size of the solution space when using the latter poses problems for the interpretation of the results of e.g. analysis techniques like flux balance analysis (FBA).

In this talk, both approaches are compared and the insights gained by their applications discussed in the context of the study of the metabolism of lactic acid bacteria.

CV:

2018 - Director at BioQuant

2007 - Full Professor for Modeling of Biological Processes, Faculty of Biosciences, Heidelberg Univ.

2000 - 2007 Independent group leader, EML Research gGmbH, Heidelberg

1996 PhD (Dr. rer.nat.) in Biochemistry, University of Tübingen

1994 Vordiploma in Physics, University of Tübingen, Germany

1993 Diploma in Biochemistry, University of Tübingen, Germany

1990 Master of Science in Chemistry, University of Oregon, Eugene, Or, USA