

学术报告会

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Modelling biochemical and biomedical systems: from theory to applications

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摘要:

One of major objectives in systems biology is to extract information from data to make reliable predictions. In most cases, however, this is very difficult due to the limited amount of data. One major obstacle is the lack of mathematical tools tailored to the specific needs of systems biology. This talk presents both theoretical and practical advancements in building dynamical network models from limited time-series data. The theoretical aspect discusses experimental requirements that guarantee identifiability of dynamical networks. The application part showcases recent tools developed in our group applied to real world data. Since biological systems are highly complex, there are numerous unanswered questions where control systems and related fields can have a significant impact.

简介:

Jorge Goncalves is a Professor at the Luxembourg Centre for Systems Biomedicine, University of Luxembourg and a Principal Research Associate at the Department of Plant Sciences, University of Cambridge. He received his Licenciatura (5-year S.B.) degree from the University of Porto, Portugal, and the M.S. and Ph.D. degrees from the Massachusetts Institute of Technology, Cambridge, MA, all in Electrical Engineering and Computer Science, in 1993, 1995, and 2000, respectively. He then held two postdoctoral positions, first at the Massachusetts Institute of Technology for seven months, and from 2001 to 2004 at the California Institute of Technology with the Control and Dynamical Systems Division. At the Information Engineering Division of the Department of Engineering, University of Cambridge he was a Lecturer from 2004 until 2012, a Reader from 2012 until 2014, and from 2014 until 2019 he was a Principal Research Associate. From 2005 until 2014 he was a Fellow of Pembroke College, University of Cambridge. From June to December 2010 and January to September 2011 he was a visiting Professor at the University of Luxembourg and California Institute