8. ANALYSIS AND CONTROL OF DYNAMICAL SYSTEMS

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SCIENTIFIC BACKGROUND: THE SYSTEM THEORETIC POINT OF VIEW

Although models are "really nothing more than an imitation of reality", their widespread utilization not only in research and development but also in the everyday life of developed societies is clearly indispensable. Due to the complexity of system components and their possible interactions, without building, analyzing and simulating appropriate models, we could not predict the outcome of common events, not to mention the operation of involved technological or living systems. When we are interested in the evolution of certain quantities usually in time and/or space, we use dynamic models. The deep understanding and the targeted manipulation of such models' behaviour are in the focus of *systems and control theory* that provides a common framework for handling dynamical models from different application fields and thus supports to form an interdisciplinary viewpoint on electrical, mechanical, thermodynamical or biological systems.

RESEARCH TOPICS

Computational analysis and synthesis of quantitative biological models

The key importance of dynamics in the explanation of complex phenomena occurring in living systems is now a commonly accepted view. Besides the sufficient maturity of systems and control theory, the accumulation of biological knowledge mainly in the form of reliable models and the recent fast development in computer and computing sciences converged to the birth of a new discipline called systems biology, which can hopefully address important challenges in the field of life sciences in the near future. For modeling biological processes, we primarily use two related canonical nonnegative system classes that have clear biological relevance, good dynamical descriptive power, and a computationally advantageous algebraic structure: the quasi-polynomial system class and the kinetic system class coming originally from biochemistry.

The structural non-uniqueness of biochemical reaction network models is an intensively studied area with applications in the structural and parametric identification (inference) of biological networks. We have been developing optimization-based computational procedures for the determination of network structures that are dynamically equivalent or similar to a given initial kinetic system [1]. The existence or non-existence of reversible, weakly reversible, complex, detailed balanced or deficiency zero structures has important consequences regarding the qualitative dynamical properties of the modeled network [2, 3, 4]. Moreover, the developed optimization framework is suitable for the algorithmic building of chemical network structures corresponding to a given dynamics.This framework has been extended for the treatment of rational kinetic systems in [11].

Our other important research topic is the modeling and parameter estimation of biological systems based on real measurement data. We have given an effective method for the parameter estimation of a human blood-glucose dynamics model [7]. The mathematical model of a cell-free transcription/translation process suitable for identification was developed and analyzed in [5].

Nonlinear control

The main question in our work related to the design of controllers for nonlinear systems is how the physical/chemical properties of these models can be used for effective control. In [6] we propose a hierarchically structured model for process systems that gives rise to a distributed controller structure that is in agreement with the traditional hierarchical process control system structure where local controllers are used for mass inventory control and coordinating controllers are used for optimizing the system dynamics. In [8] we give a computational solution for obtaining a closed loop nonlinear polynomial system that corresponds to a weakly reversible deficiency zero network and thus satisfies robust stability properties.

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