

Special Issue on Computational Methods for Identification and Modelling of Complex Biological Systems

CALL FOR PAPERS

The dynamics of biological systems are often nonlinear, complex, and poorly characterized. Dynamic models are fundamental tools for the mechanistic description of biological systems, the quantitative analysis of their behaviour, and the prediction of their temporal evolution. Likewise, certain complex, adaptive biological phenomena may inspire successful engineering solutions. However, the high degree of uncertainty typically present in biological models makes the task of system identification particularly difficult in this context. This difficulty hampers the use of dynamic models for the purpose of understanding and simulating biological processes. Important advances have been made in the last decades, enabling the emergence of new areas of research such as systems biology, synthetic biology, and precision medicine. However, the complexity of many processes of interest (e.g., neurodegenerative diseases, cancer pathways, cell differentiation, and reprogramming) continues to challenge the researchers that try to build or exploit biological models.

The purpose of this special issue is to provide an overview of current open problems in mathematical modelling and identification of complex biological systems and to present a collection of recent results. The type of models to be analysed includes metabolic, signalling, genetic, physiological, and neuronal systems that are often modelled as complex biological networks. Submissions that present new theoretical or methodological contributions motivated by biological problems are especially welcome. We also encourage articles that demonstrate the use of advanced mathematical and computational tools to obtain new biological insight. Review articles that provide a comprehensive description of the state of the art in some of the covered topics will also be considered.

Potential topics include but are not limited to the following:

- ▶ Parameter estimation in large-scale systems biology models
- ▶ Uncertainty quantification in dynamic biological models
- ▶ Identifiability and distinguishability of dynamic biological models
- ▶ Nonlinear observability and controllability
- ▶ Optimal experiment design for biological systems
- ▶ Optimization in complex systems modelling
- ▶ Genetic and evolutionary computation
- ▶ Ensemble modelling
- ▶ Multiscale modelling
- ▶ Cellular automata in biological modelling
- ▶ Analysis of complex biological networks
- ▶ Network inference

Possible application areas include systems biology, synthetic biology, systems biomedicine, biomedical engineering, computational neuroscience, developmental biology, metabolic engineering, and industrial biotechnology.

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/complexity/cbsi/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

Lead Guest Editor

Alejandro F. Villaverde, IIM-CSIC,
Vigo, Spain
afvillaverde@iim.csic.es

Guest Editors

Carlo Cosentino, Università degli Studi
"Magna Græcia", Catanzaro, Italy
carlo.cosentino@unicz.it

Attila Gabor, JRC-COMBINE, Aachen,
Germany
gabor.attila87@gmail.com

Gábor Szederkényi, PPKE, Budapest,
Hungary
szederkenyi@itk.ppke.hu

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