Editorial

Jérôme Feret and Heinz Koeppl

THIS special section includes a selection of five papers presented at the 15th International Conference on Computational Methods in Systems Biology (CMSB 2017) held at the Technische Universität Darmstadt, Germany, on September 27-29, 2017.

The CMSB annual conference series, created in 2003, provides a unique forum of discussion for computer scientists, biologists, mathematicians, engineers, and physicists interested in a system-level understanding of biological processes. Topics of interest include formalisms for modeling biological processes; approaches for model verification, validation, analysis, and simulation; high-performance methods; model inference from experimental data; model integration from biological databases; multi-scale modeling and analysis methods; and computational approaches for synthetic biology. Case studies were especially encouraged.

The CMSB series of conferences has contributed to making the biological domain an important test-bed of ideas for interdisciplinary computer science applications and, at the same time, showing to biologists common patterns of circuit similarity across different areas (such as biomedical processes, animal, plant, and bacterial physiology) and across scales.

The conference program featured several tracks: regular papers, tool papers, presentation only (for works already published), posters, and tutorials. There were 30 regular submissions and five tools paper submissions among which we decided to accept 17 regular papers and four tools papers. This special section contains a selection of five papers which have been significantly extended with respect to the proceedings version and underwent a new peer-review process. We are extremely grateful to the members of the program committee and the external reviewers for their excellent and meticulous work.

"Bio-Curation for Cellular Signalling: The KAMI Project" was an invited contribution. It describes the current state of KAMI, a bio-curation tool for rule-based modeling, based on rewriting in hierarchies of graphs.

The identification of the disease-induced molecular perturbations and the subsequent development of efficient therapies are challenged by the complexity of the genotype-phenotype relationship. "Causal Reasoning on Boolean Control Networks Based on Abduction: Theory and Application to Cancer Drug Discovery" describes a new method using abductive reasoning principles to address this issue.

"Quantitative Regular Expressions for Arrhythmia Detection" presents a formalization of some arrhythmia-detection algorithms in the language of Quantitative Regular Expressions. These expressions describe precisely complex numerical queries over data streams, with provable runtime and memory consumption guarantees.

"Hidden Markov Modelling Reveals Neighborhood Dependence of Dnmt3a and 3b Activity" extends existing Hidden Markov Models for DNA methylation by describing the occurrence of spatial methylation patterns over time and propose several models with different neighborhood dependences. Correlations between the neighborhood dependence and other genomic information are also investigated.

"Algorithms for the Sequential Reprogramming of Boolean Networks" addresses the issue of cellular reprogramming. It proposes an algorithm to identify sequential perturbations on qualitative models of regulatory networks, that consist in mutations to be applied not only to the initial state, but also during the transient evolution of the model. The approach is applied on models of the literature.

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Guest Editors

Jérôme Feret entered École Normale Supérieure, in 1997, where he received his training in theoretical computer sciences, with a focus on semantics of programming languages and abstract interpretation. In 2005, he defended the PhD degree about abstract interpretation of mobile systems, under the supervision of Prof. Patrick Cousot. He has been trained in applications of computer sciences in systems biology by Vincent Danos since 2006, and by Walter Fontana in 2007. He joined INRIA as a junior researcher in 2008. His research interest is to extend the scope of abstract interpretations by developing new applications. He is one of the co-author of the ASTRÉE static analyser, that is used to prove the absence of run time errors in critical embedded C code. He is also developing static analysis, causality analysis, and model reduction tools within the Kappa modelling platform.

Heinz Koeppl received the MSc degree in physics from the School for Electrical Engineering (HTL), Graz Karl-Franzens University, in 2001 and the PhD degree in electrical engineering from the Graz University of Technology, in 2004. He is a full professor with the Department of Electrical Engineering and Information Technology, TU Darmstadt, with a co-affiliation with the Department of Biology since January 2014. Prior to that, he was a SNSF assistant professor with the Automatic Control Lab of ETH Zurich and a group leader at IBM Research – Zurich. His PhD thesis was done in collaboration with Infineon Technologies within the Christian Doppler Laboratory. After doing his civil service for the Austrian federal government for a year, he went on as a Schroedinger fellow to UC Berkeley to work with Leon Chua in the EECS Department. From Fall 2006 to Fall 2010, he has been a postdoc with the Laboratory of Nonlinear Systems in the School of Communication and Computer Sciences at EPFL (Ecole Polytechnique Federal de Lausanne) Lausanne, Switzerland. In Spring 2008, he did a three month visit with the Department of Systems Biology, Harvard Medical School, Boston. He received an IBM Faculty Award (2014) and has run an ERC Consolidator grant since 2018.

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Digital Object Identifier no. 10.1109/TCBB.2019.2934374

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