

Preface

This volume contains the papers presented at HSB 2016: the 5th International Workshop on Hybrid Systems Biology held during October 19–20, 2016, in Grenoble (France).

In biology, a “hybrid” is the offspring of two different species. Likewise, in the eco-system of scientific workshops and conferences, the International Workshop on Hybrid Systems Biology (HSB) is the offspring of scientists from two different fields of study, hybrid systems and systems biology. The word “systems” makes the connection between the two, and encompasses the theme common to all works presented at the workshop and published in this volume: The modelling and analysis of complex dynamical behaviors emerging from interacting components of a whole.

Biological systems are complex and, to be useful, models¹ need to capture properties of diverse nature: discrete and continuous, stochastic and deterministic, temporal and spatial, etc. A couple of decades ago, the notion of hybrid system was introduced by computer scientists and mathematicians as a unifying mathematical framework mixing two modelling approaches widely studied at the time: finite-state machines, or automata, and ordinary differential equations. Nowadays, the theory and practice have matured and a hybrid system is widely understood as being a dynamical system mixing continuous and discrete components. The hybrid systems community has grown to become a vibrant interdisciplinary community including logicians, software engineers, applied mathematicians, control theorists, physicist, etc., and, thanks to the many relevant applications, biologists. Different actors bring about different contributions from the respective domains of origin, while at the same time acknowledging the need for complementary expertise and profiting from the pluridisciplinary interaction to enrich their appreciation and solution of scientific and practical challenges.

The Workshop on Hybrid Systems Biology partly emerged as a specialization of hybrid systems to biological case studies, i.e., as a *hybrid systems* biology workshop, but the ambition is for it to become a full-fledged biology workshop, i.e., a *hybrid systems biology* workshop. Here, the adjective “hybrid” means in a broader sense that special attention was paid to true interdisciplinary collaborations and contributions, aimed at reaching beyond some arguably advanced Python scripting performance or abstract methodological proposal of questionable applicability. Hardly any other venue to date can attract and critically evaluate, thanks to the wide and excellent expertise of its Program Committee members, such diverse and multifaceted contributions as on spatial and temporal logics of biological systems, on identifiability and estimation of cellular dynamics, or on the simulation, analysis, and controllability of biochemical pathways, all standing at the frontier of and advancing the fields of computer science, control theory, and of course systems biology.

¹ Recall that, quoting George Box, all models are wrong, some are useful.

The first edition of HSB was held in 2012 as a co-located event with CONCUR in Newcastle upon Tyne in the UK. Subsequent editions were HSB 2013, co-located with ECAL 2013 in Taormina (Italy), HSB 2014, co-located with VSL 2014 in Vienna (Austria), and HSB 2015, co-located with CONCUR, QEST, and FORMATS 2015 within the week-long Madrid Meet 2015 in Spain. This year marked a major turning point, because for the first time, the workshop was held as a standalone event. Nevertheless, the workshop attracted as many as 26 submissions. Each submission was reviewed by at least three Program Committee members, with most of them getting four or more reviews. The committee decided to accept 11 high-quality papers, which were organized and presented in four thematic sessions also reflected in this book: Model simulation, model analysis, discrete and network modelling, and stochastic modelling for biological systems. In addition to the oral presentations comprising the main program, the workshop featured an interactive poster and tool demo session, and several high-profile invited talks. The details and full program are available online at <http://hsb2016.imag.fr>.

The organization of the workshop into such a high-quality scientific and social event would not have been possible without the invaluable help of its general chair, Oded Maler, whose ability to think and reach out to people and topics away from his own scientific center of gravity never ceases to amaze. The editors are also grateful to the help, support, and guidance provided by a highly motivated Steering Committee, in particular, the chairs of the previous editions of HSB, notably David Šafránek, Alessandro Abate, Ezio Bartocci, and Luca Bortolussi. Special thanks go to Sergiy Bogomolov and all Program Committee members who helped us spread the word about HSB 2016, and to all reviewers for providing high-quality evaluations within an extremely tight schedule. Warm thanks to Sophie Azzaro and Catherine Bessière for their invaluable assistance in the practical conference preparation and arrangements. We gratefully acknowledge our sponsoring institutions (Inria, Verimag, UGA, INPG, CNRS, see also the conference website) for their financial and organizational support. Finally, we thank Springer for hosting the HSB proceedings in its *Lecture Notes in Bioinformatics series*, a sub-series of *Lecture Notes in Computer Science*, and Easy-chair, which lives up to its name by making chairing a workshop such a smooth experience.

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