

Preface

The 4th International Workshop on Hybrid Systems Biology (HSB 2015) was held during September 4–5, 2015, at the Facultad de Matemáticas, Universidad Complutense de Madrid.

HSB 2015 was co-located with the week-long Madrid Meet 2015, which also hosted CONCUR 2015, QEST 2015, and FORMATS 2015, among other scientific events. Previous editions of the HSB Workshops were held in Newcastle upon Tyne (UK, with CONCUR 2012), Taormina (IT, within ECAL 2013), and Vienna (AT, within VSL 2014).

The scope of the HSB 2015 workshop has broadened since the earlier editions, and now covers the general area of dynamical models in biology. HSB 2015 retained the emphasis on *hybrid* approaches – by no means restricted to a narrow class of mathematical models – and in particular stressed the importance of taking advantage of techniques developed separately in different areas. Topics featured at the workshop included models of metabolic, signaling, and genetic regulatory networks; models of tissues; biological applications of quantitative and formal analysis techniques; parametric and non-parametric system identification techniques; efficient techniques for combined and heterogeneous simulations of biological models; modeling languages for biological systems; models coping with incomplete and uncertain biological information; stochastic and hybrid models in biology; hierarchical approaches for multi-scale, multi-domain analysis; abstraction, approximation, discretization, and model reduction techniques; control architectures in biological systems; and modeling and synthesis for synthetic biology.

HSB 2015 was a packed two-day event, featuring invited talks, single-track regular podium sessions, and an interactive session with posters and software tool demos. We hosted about 40 registered participants, plus two invited speakers, and a constant inflow of attendees from other co-located events at Madrid Meet 2015. The 30-minute contributed talks were of high quality and the participation lively, interactive, and stimulating.

In all, 46 Program Committee (PC) members helped to provide at least four reviews (with in some cases up to six) of the submitted contributions, out of which 13 high-quality articles were accepted to be presented during the single-track sessions, and appear (possibly after further feedback from a shepherding process by the PC members) as full papers in these proceedings. The articles were bundled in four thematic sessions, which is reflected in the organization of these proceedings: statistical analysis; analysis and verification of continuous and hybrid models; quantitative analysis of biological models; and application of advanced models on case studies. In the afternoon of the first day we also hosted a poster/demo session, with 11 presentations, of which five with interactive tool demonstrations.

A highlight of HSB 2015 was the presence of two high-profile invited speakers, whom we selected also in view of the breadth of the event: computer sciences and

control and dynamical systems; theoretical work and laboratory experiments. Luca Cardelli, principal researcher at Microsoft Research Cambridge (UK) and Royal Society research professor at the Department of Computer Science, University of Oxford (UK), gave a seminar titled “Morphisms of Reaction Networks.” Mustafa Khammash, professor of Control Theory and Systems Biology at the Department of Biosystems Science and Engineering at ETH Zürich (CH), gave a talk titled “Cybergenetics: Synthetic Circuits and Systems for the Precise Control of Living Cells.”

Further details on HSB 2015 are featured on the website: <http://hsb2015.fi.muni.cz>

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