Important Dates:
Abstract deadline 23 September 2018 **(new)**
Full paper deadline 25 September 2018 **(new)**
Author notification 25 October 2018 **(new)**
Final version deadline 30 October 2018

Invited Speakers:
Marta Kwiatkowska (U. Oxford, U.K)
Hidde de Jong (Inria, Grenoble, France)
Alexandre Madeira (U. Minho, Portugal)

PC Chairs:
Manuel A. Martins (U. Aveiro, Portugal)
Madalena Chaves (Inria, France)

OC Chairs:
Claudio Fuentes (U. Diego Portales, Chile)
Daniel Figueiredo (U. Aveiro, Portugal)
Pablo Razeto-Barry (IFICC, Chile)
Tomás Veloz (IFICC, Chile)

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Marta Kwiatkowska (U. Oxford, U.K)
Alexandre Madeira (U. Minho, Portugal)
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Stefan Mitsch (Carnegie Mellon U., USA)
Renato Neves (U. Minho, Portugal)
Loic Pauleve (CNRS/LRI, France)
Ion Petre (Abo Akademi Turku, Finland)
Tatjana Petrov (U. Konstanz, Germany)
Élisabeth Remy (IML Luminy, France)
Eugénio Rocha (U. Aveiro, Portugal)
Marie-France Sagot (ERABLE, Inria, France)
Amilra P. de Silva (Queen's U. Belfast, UK)
Regivan Santiago (UFRN, Brasil)
Ana Sokolova (U. Salzburg, Austria)
Meng Sun (Peking University, China)
Carolyn Talcott (SRI International, USA)
Antonio Tallón (U. Seville, Spain)
P.S. Thiagarajan (Harvard University, USA)
Delfim F. M. Torres (U. Aveiro, Portugal)
Adelinde Uhrmacher (U. Rostock, Germany)
Boyan Yordanov (Microsoft Research, UK)
Paolo Zuliani (Newcastle University, UK)

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Springer Lecture Notes in Computer Science
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International Symposium on Molecular Logic and Computational Synthetic Biology

Santiago de Chile, Chile, 17-18 December, 2018

Synthetic biology aims at the design of biological systems in a systematic way, a process whose hallmark characteristics closely resemble the composition of software: off-the-shelf parts and devices with standard connections, the usual ingredients for assembling components into increasingly complex systems. Of course, a number of key enabling technologies are specifically biological, for example, DNA sequencing and fabrication. But, on the other hand, there is also a need for new models to cope with the complex and heterogeneous nature of biological systems.

In this context, the Symposium starting point is to regard a network of interacting genes and proteins as a dynamic system evolving in time according to fundamental laws of reaction, diffusion and transport. These laws govern how a regulatory network, confronted by any set of stimuli, determines the appropriate response of a cell. The emerging behavioural patterns can be described in precise mathematical terms, combining discrete, continuous and stochastic features, and resorting both to specific or general-purpose analysis and verification techniques.

Molecular logic, focussed on computing logical operations on molecules, a fruitful conceptual crossover between chemistry and computation with unsuspected applications, is a possible path in this research map. Actually, this Symposium emerged from a series of informal workshops on Molecular Logic which, for the last four years, have brought together researchers from different latitudes and backgrounds.

The new International Symposium aims at harnessing logical and algebraic methods for modelling and verifying systems on the interaction of Nature and Computation, around two main themes:

- *development of biological computation models and devices*
- *application of new computing paradigms to the design of biological systems.*

Original submissions are required in any topic from the following, non exclusive list:

- Molecular logic
- Chemistry, biology and computation
- Quantum computing applications to biology
- Computational synthetic biology
- Control theory and/or algorithms for biological systems
- Reconfigurabilility and adaptation
- Probabilistic biological models
- Hybrid systems for biology

Submissions on general computational models that are applicable to a biological context, such as probabilistic, hybrid, weighted, resource-based, and time-based are also welcome.

Submission

Both fully mature contributions and work-in-progress submissions on the topics above are welcome. All contributions should be written in English, prepared in LaTeX, using llncs style, and submitted as PDF files following instructions available from the symposium website. A page limit of 15 pages for full papers is established.

Extended abstracts with preliminarily results and work in progress (2-5 pages) are also welcomed for short presentations. They are subject to a light reviewing and will be available at the conference in an informal booklet.

All contributions must be original, unpublished and not submitted simultaneously for publication elsewhere. Both kinds of submissions should be done via the Online Conference System (OCS) of Springer using the link https://ocs.springer.com/ocs/home/MLCSB2018.

Publication

Proceedings with full papers will be published by Springer Lecture Notes in Computer Science Series. A journal Special Issue, with extended and revised versions of selected papers, is currently under consideration.

The KLEE Project

The workshop is promoted by the KLEE project (FCT 030947, 2018-21) on *Coalgebraic Modeling and Analysis for Computational Synthetic Biology.*