Preface

This ENTCS volume contains the post-proceedings of the *fifth International Workshop on Interactions between Computer Science and Biology* (CS2Bio'14) held in Berlin on the 6th of June 2014. This workshop was organized as an affiliated event of the eighth *International Federated Conferences on Distributed Computing Techniques* (DisCoTec 2014).

For the fifth edition of CS2Bio, the program consisted of three invited lectures by Marco Pettini (Universit DAix Marseille, France), Vincent Danos (University of Edinburgh, UK) and Roberto Barbuti (Dipatimento di Informatica, Università di Pisa, Italy) complemented by six technical contributions (two regular papers, two tool presentations, and two project presentations). The workshop also had a half-day tutorial by Jeffrey Johnson. In line with the theme of the workshop the presentations and the tutorial addressed topics in the area of formal languages and methods for the representation of biological systems and their dynamics, and of analysis and simulation approaches to biological case-studies. Moreover, in this CS2Bio edition, the attempt to launch a new scientific community interested on integrative sciences that focus on novel computational paradigms for understanding biological complex systems, as Quantum information and life sciences; Geometry, algebraic and computational topology and biomathematics; Information processing and biomedicine; Statistical mechanics and biophysics.

In his invited talk Marco Pettini spoke about molecular biology challenging problem that stems from the observation that biochemical reactions which commonly involves a huge number of actors are coordinated simultaneously to be achieved in due time, thus granting the reality of well organized dynamic systems. He discussed the hypothesis that the encounters of distant cognate partners of biomolecular reactions are actively driven by selective (resonant) attractive forces of electrodynamic nature, and how it can be proven by means of an interdisciplinary approach involving theoretical and experimental physics, molecular biology, biochemistry, and computer modelling and simulation. The lecture of Vincent Danos focused on joining graph transformation systems stemming off of concurrency and formal language theories, and mean field approximations, a group of techniques used to great effect in statistical physics to obtain simplified descriptions of complex dynamics. He discussed how to build the associated mean field machinery, when the dynamics

of interest is underpinned by a graph transformation system. The talk of Roberto Barbuti was centered on a specific ecosystem problem regarding the impact of hybridization between different species. He discussed the peculiarities of a reproduction system called hybridogenesis, by which some hybrid species of European water frogs are originated and proposed a P System model as the suitable tool for analyzing stable complexes that, by mutations, give rise to new species or drive to their extinction.

In the two short presentations interesting projects results were presented. Eduardo Hermo Reyes reported on "The Selfish Algorithm", a concrete description on how to test Generalized Natural Selection in the setting of cellular automata. Emanuela Merelli overviewed the on-going research of "TOPDRIM: topology driven methods for complex systems", a European FET projects, among which, the proof that any P-persistent object X in the category of finite topological spaces there is a P- weighted graph, whose weighted clique complex has the same P-persistent homology as X; the explanation of how topology of data reflects on dynamical (temporal) complexity of parameters characterizing the probability distributions of a statistical model by using a Max Entropy principle; the non-trivial topological interpretation of regular expressions modulo bisimulation and the shapes definition of interacting RNA complexes. TOPDRIM sponsored the CS2BIO 2013 and CS2BIO2014".

During the tutorial on Hypernetworks, Jeffrey Johsnson introduced the audience into the world of n-ary relations represented as simplicial complexes of the algebraic topology. He discussed how the new formalism called hypernetworks overcomes the well-known hypergraphs formalism used for many years, along with the beautiful Galois lattice structure they possess, and by several examples of use of the Q-analysis, he intrigued people attending the course.

The workshop in Berlin attracted 22 participants and the interdisciplinary atmosphere was productive and pleasant. The tutorial in hyper networks was followed by 13 participants, mostly young researchers. The organizers express their thanks to all speakers and participants of CS2Bio'14 for their contributions that made this year's edition a success. In particular, we are grateful to Marco Pettini, Vincent Danos, Roberto Barbuti and Jeffrey Johnson for their interesting talks and inspiring contribution to the interdisciplinary discussions. We also acknowledge the efforts of the members of the program committee for the reviewing process.

The Program Committee of CS2Bio'14 was composed by:

- Luca Cardelli (Microsoft Research Cambridge, UK)
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