Preface

This volume contains the proceedings of the Ninth International Workshop on Parallel and Distributed Methods in Verification (PDMC 2010) joint with the proceedings of the Second International Workshop on High-Performance Computational Systems Biology (HiBi 2010).

For the first time the PDMC and HiBi workshops were joined in a two-day event, held at the University of Twente in the Netherlands, from 30 September to 1 October 2010. The event was co-located with the Fifth International Conference on Graph Transformation (ICGT 2010) and the 17th Annual SPIN Workshop on Model Checking Software (SPIN 2010).

The idea of bringing together the PDMC and HiBi workshops originated in the autumn of 2009, with preliminary discussion started during HiBi 2009 and continued at PDMC 2009. Both PDMC and HiBi are concerned with aspects related to the complex computer (PDMC) and exploration and analysis of large and biological (HiBi) systems in combination with the usage of methods and techniques that exploit state-of-the-art computing hardware. As observed not only by our two communities, computer technology has recently undergone a paradigm shift. Chip producers have shifted their focus from single-core to multi-core chips. Parallel processing has become ubiquitous. Computing platforms such as clusters of multi-core workstations, CUDA technology equipped workstations, and workstations equipped with solid state disks have become easily accessible. As a result, many software tools relying on old-fashioned serial hardware alone have ceased taking advantage of recent technological developments.

To catch up with the continuous increase in the complexity of systems being analyzed it is essential that the tools and procedures employed in both PDMC and HiBi areas of application follow suit. Although the application areas differ for PDMC and HiBi, it appeared to us that bringing together these two communities would foster an inspirational exchange of knowledge that, so we hope, would be beneficial to both. This year's submitted papers consolidate this impression, preliminary signs of which were witnessed already at the 2009 PDMC and HiBi events. The two communities are learning from each other and their knowledge exchange is growing. The PDMC workshop series was established in 2002, motivated by the growing interest in the possibility of fighting the complexity of the automated formal verification process by means of parallel and distributed-memory processing. It is the aim of the PDMC workshop series to cover all aspects related to the verification and analysis of complex, industrial-size computer systems in combination with the usage of methods and techniques that exploit state-of-the-art hardware architectures. The first edition of PDMC was held in Brno (Czech Republic) 2002, with follow-ups in Colorado (USA) 2003, London (United Kingdom) 2004, Lisbon (Portugal) 2005, Bonn (Germany) 2006, Berlin (Germany) 2007, Budapest (Hungary) 2008 and Eindhoven (The Netherlands) 2009.
HiBi, on the other hand, is a much younger workshop. Established in 2009, its first edition was held at The Microsoft Research/Universita di Trento Centre for Computational and Systems Biology (CoSBi), Trento (Italy). The motivation from which the HiBi workshop originated is one of establishing a forum for researchers interested in the application of parallel computing techniques to the vast area of Systems Biology. This requires the adaptation of popular computational methods of Systems Biology. In many cases this entails a thorough re-design of well established sequential algorithms, such as is the case with, for example, the stochastic simulation method.

This year, the PDMC-HiBi workshop attracted a total of 23 submissions (PDMC: 10, HiBi: 13) by researchers from 18 countries. The program committees decided to accept six (PDMC) and nine (HiBi) submissions, respectively, for a total of 15 papers for presentation and for publication in this volume. Each paper was rigorously reviewed by at least three reviewers. In addition, the workshop featured two invited speakers, whose extended abstracts can be found in this volume as well: Youssef Hamadi (Microsoft Research Cambridge, United Kingdom) on Parallel SAT Solving and Peter Schuster (Austrian Academy of Sciences) on Inverse Methods in Systems Biology. We would like to thank the authors of all submitted papers, the invited speakers, the program committee members and the external reviewers for their help in composing this year’s program. Tommaso Mazza is thanked for the cover design. Finally, we thank EasyChair for supporting the electronic submission and reviewing process.

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