



# CMSB '09

computational methods  
in systems biology

7<sup>th</sup> International Conference on  
Computational Methods in Systems Biology

Bologna, Italy, August 31<sup>st</sup> – September 1<sup>st</sup>, 2009

## FIRST CALL FOR PAPERS

The CMSB (Computational Methods in Systems Biology) conference series was established in 2003 to help catalyze the convergence of modellers, physicists, mathematicians, and theoretical computer scientists (from fields such as language design, concurrency theory, program verification) with molecular biologists, physicians and neuroscientists interested in a systems-level understanding of cellular physiology and pathology.

CMSB 2009 solicits original research articles, surveys of current research and posters. These may cover theoretical or applied contributions that are motivated by a biological question and can demonstrate actual or potential usefulness towards answering that question. Additionally, they may cover models of computation inspired by biological processes; of which the motivation may be either computational or biological. In particular, relevant case studies and open biological questions that demand modelling of systems are of significant interest.

Topics of interest (biological systems and networks: inference, properties, modelling, dynamics, simulation and reverse engineering) include, but are not limited to: Modelling:

- Re-engineering and synthesis of biological systems and networks
- Definition and study of theoretical properties of biologically-inspired formal languages
- Qualitative and quantitative languages and calculi
- Theoretical comparisons between different formal models of cellular processes
- Models including symbolic evolution and learning
- Spatial, multi-level, and multi-formalism modeling

Simulation/Analysis:

- Simulation and analysis methods for computational biology
- Biologically-inspired extensions to concurrency theory, constraint programming, logical methods or language equivalences
- Emergence of properties in complex biological systems
- Parallel, distributed, and multi-resolution simulation methods
- Methods to predict biological network behavior from incomplete information

Tools/Frameworks/Libraries:

- Modelling, analysis and simulation tools
- Differential, discrete and/or stochastic modeling-language frameworks
- Visualization methods for computational biology
- Biological databases and exchange formats for biological data and standards

Applications:

- Detailed biological case-studies on which formal models successfully apply
- Computer models in nano-sciences applied to biological domains
- Model-driven analysis of biological systems

## Submission

The CMSB 2009 conference solicits high quality full papers reporting research results and/or experience reports related to the topics mentioned above. All papers must be original, unpublished, and not submitted for publication elsewhere. Contributions should be submitted electronically as PDF via EasyChair at <http://www.easychair.org/conferences/?conf=cmsb09>, using the Springer LNCS style. Papers should not exceed 15 pages in length. If necessary, the paper may be supplemented with a clearly marked appendix, which will be reviewed at the discretion of the program committee.

The proceedings of the conference will be published with Springer under the series named Lecture Notes in Bioinformatics, sub-series of Lecture Notes in Computer Science. The best papers presented at the Conference will be selected for a special issue of the journal Theoretical Computer Science - C (Theory of Natural Computing).

## Important Dates

|                    |  |
|--------------------|--|
| March, 20:         | Submission of abstract of the full paper to be submitted |
| March, 27:         | Submission of full papers                                |
| May, 18:           | Notification of paper acceptance                         |
| June, 15:          | Revised version of papers                                |
| Aug. 31 – Sept. 1: | Conference   |

## Program Committee (provisional)

**Pierpaolo Degano**, Università di Pisa, Italy (co-chair)  
**Finn Drablos**, Norwegian University of Science and Technology, Norway  
**François Fages**, INRIA Rocquencourt, France  
**Stephen Gilmore**, University of Edinburgh, UK  
**Roberto Gorrieri**, Università di Bologna, Italy (co-chair)  
**Monika Heiner**, TU Cottbus, Germany  
**Adaoha Elizabeth C. Ihekweba**, CoSBI, Italy  
**Marta Kwiatkowska**, University of Oxford, UK  
**Pietro Liò**, Computing Lab Cambridge, UK  
**Satoru Miyano**, University of Tokyo, Japan  
**Grzegorz Rozenberg**, Leiden University, Leiden, NL  
**Mark van Rossum**, University of Edinburgh, UK  
**Carolyn Talcott**, Stanford Research Institute, USA  
**Adelinde M. Uhrmacher**, University of Rostock, Germany