



## Preface

The huge amount of data produced by high-throughput tools in biology makes it impossible to handle it manually. Furthermore, the success of the genome project has rapidly moved the focus of life science research towards the functions (behaviour) rather than the structure of the biological systems and their basic components.

To better understand the dynamic of life, biological research is experiencing a paradigmatic shift from the classical reductionist approach (in which complex systems are broken down into their constituents) to an hypothesis driven one (in which abstract models of complex systems are devised and then validated through experiments). This new way of doing research in biology is called systems biology.

The approach of systems biology is very similar to the way in which computer scientists perform research. Actually also computer science is an experimental science, although experiments are not “wet”, but carried out in silico. Computer systems are first modelled (thus generating hypothesis), then they are implemented and tested (experiments) to refine/validate the model (feedback loop). Therefore, if we abstract from the kind of experiments performed, we can state that systems biology is computer science in the applicative domain of life sciences.

Furthermore, the paradigmatic shift joined with the focus on functions rather than on structure views bio-components as computational devices in which millions of computational threads are simultaneously active (e.g., metabolic networks, gene regulatory networks, signalling pathways) and interactions change the future behaviour of the whole systems. The description just reported of biological systems fits very well to the description of mobile and distributed systems, hence the possible application of methods and results from concurrency theory in the realm of life science.

This special issue collects extended versions of papers presented at the international workshop on Computational Methods in Systems Biology held in Rovereto, 24–26 February 2003.

The papers selected for this issue (which have been refereed to journal standards) cover aspects of programming language theory that can help in understanding biological systems. This is the first step to reach a long-term goal of deriving from living systems new abstractions and new computational models to tackle the complexity of emerging applications in computer science.

The first paper of the issue, by Eveillard, Ropers, de Jong, Branlant and Bockmayr, shows how constraint programming can be used to model key processes in post-transcriptional regulation.

The second contribution by Chabrier-Rivier, Chiaverini, Danos, Fages and Schachter introduces a formalism to represent and analyze protein-protein and protein-DNA interaction networks. Furthermore, the Computation Tree Logic CTL is suggested as a query language for querying the possible behaviours of the system.

Antoniotti, Piazza, Policriti, Simeoni and Mishra use hybrid automata equipped with bisimulation and collapsing to model complex biological systems in the third paper of the issue.

The fourth contribution is related to process algebras as modelling mechanism of biological interaction. Here Danos and Laneve propose a formal calculus for protein interaction.

The fifth paper by Curti, Degano, Priami and Baldari shows how causality can help in understanding the relations between the triggering events of signalling pathways.

Finally, the last paper by Regev, Panina, Silvermann, Cardelli and Shapiro introduces a new process calculus that can take care of boundaries and compartments in biological systems.

Corrado Priami

*Dipartimento di Informatica e Telecomunicazioni  
Universita' di Trento, Via Sommarive, 14  
Povo (TN) 38050, Italy  
E-mail address: priami@dit.unitn.it*