Preface

Molecular biology has until now mainly focussed on individual molecules, on their properties as isolated entities or as complexes in very simple model systems. However, biological molecules in living systems participate in very complex networks, including regulatory networks for gene expression, intracellular metabolic networks and both intra- and intercellular communication networks. Such networks are involved in the maintenance (homeostasis) as well as the differentiation of cellular systems of which we have a very incomplete understanding.

Nevertheless, the progress in molecular biology has made possible the detailed description of the components that constitute living systems, notably genes and proteins. Large-scale genome sequencing means that we can (at least in principle) delineate all macromolecular components of a given cellular system, and microarray experiments as well as large-scale proteomics will soon give us large amounts of experimental data on gene regulation, molecular interactions and cellular networks. The challenge of the 21st century will be to understand how these individual components integrate into complex systems and the function and evolution of these systems, thus scaling up from molecular biology to systems biology. By combining experimental data with advanced formal theories from computer science, "the formal language for biological systems" to specify dynamic models of interacting molecular entities would be essential for: (i) understanding the normal behaviour of cellular processes, and how changes may affect the processes and cause disease – it may be possible to correlate genetic properties and symptoms in new and more efficient ways, based on an actual understanding of how various processes interact; (ii) providing predictability and flexibility to academic, pharmaceutical, biotechnology and medical researchers studying gene or protein functions. In particular, it may save time by reducing the number of experiments needed, if inadequate hypotheses can be excluded by computer simulation.

In response to the call for papers 39 were submitted to CMSB 2003. All the submitted papers were reviewed and the programme committee (listed below) selected 11 high-quality papers for publication in this volume. The care of the reviewers and of the programme committee members in reviewing the papers was surely valuable. A further 11 papers were selected only for presentation at the workshop in order to stimulate discussions (an abstract is included).

At the workshop Ehud Shapiro and Michael Stern gave two invited talks whose topics are described in papers included in this volume. The programme committee decided to accept for publication in this volume also some position papers that highlight the research trends in this new field of computational methods in systems biology. The reason is that because this is the first edition of a workshop in this fast-growing field a large view of potential topics of research was considered extremely important.

Rovereto, December 2002   Corrado Priami

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Corrado Priami, Linda Brodo, Michela de Concini, Debora Schuch da Rosa Machado, and the University of Trento Events and Meetings Office.

List of Referees

F. Abascal, N. Chabrier, A. Cimatti, M. Curti, M.D. Devignes, S. Gnesi,
J. Guijarro, K. Hafez, E. Klipp, C. Laneve, P. Lopez Romero, F. Luccio,
R. Marangoni, M. Padron, M.C. Pinotti, R. Rizzi, S. Tini.

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