

Lecture Notes in Bioinformatics

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Preface

This is the first issue of a new journal of the LNCS journal subline. The aim of the journal is to encourage inter- and multidisciplinary research in the fields of computer science and life sciences. The recent paradigmatic shift in biology towards a system view of biological phenomena requires a corresponding paradigmatic shift in the techniques from computer science that can face the new challenges. Classical tools usually used in bioinformatics are no longer up to date and new ideas are needed.

The convergence of sciences and technologies we are experiencing these days is changing the classical terms of reference for research activities. In fact clear distinctions between disciplines no longer exist because advances in one field permit advances in others and vice versa, thus establishing a positive feedback loop between sciences. The potential impact of the convergence of sciences and technologies is so huge that we must consider how to control and correctly drive our future activities.

International and national funding agencies are looking at interdisciplinary research as a key issue for the coming years, especially in the intersection of life sciences and information technology. To speed up this process, we surely need to establish relationships between researchers of different communities and to define a common language that will allow them to exchange ideas and results. Furthermore, expectations of different communities can be merged only by running activities like common projects and experiences.

The Transactions on Computational Systems Biology could be a good forum to help life scientists and computer scientists to discuss together their common goals.

This first issue is made up of contributions by members of the Editorial Board to provide a smooth start-up of the journal. The first paper, by Gómez et al., surveys the new methods needed for acquiring data suitable to enable simulation of simple cellular systems. Then Shenhav et al. discuss how system biology can be of help also in studying very early organisms in the time evolution scale. The third contribution is by Roux-Rouquié and Soto and shows how useful is the notion of model and metamodel in the systemic approach to the study of biological systems. Feytmans et al. investigate the relationships between the complexity of a genome and the functional complexity arising from it. The next paper moves inside computer science. Priami and Quaglia show how calculi for describing concurrent systems can be used to model biological systems as well. The last invited contribution is by Uhrmacher et al. and copes with the problem of multilevel and multiscale simulation. Finally, Zobeley et al., in the regular paper of this issue, present a new complexity reduction method which is time-dependent and suited not only for steady states, but for all possible dynamics of a biochemical system.

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