

SECOND EDITION

COMPUTATIONAL SYSTEMS BIOLOGY

FROM MOLECULAR MECHANISMS TO DISEASE

Edited by
Roland Eils
and **Andres Kriete**



Computational Systems Biology Second Edition From Molecular Mechanisms To Disease

Léo Pomar



Computational Systems Biology Second Edition From Molecular Mechanisms To Disease:

Computational Systems Biology Andres Kriete,Roland Eils,2005-11-10 Systems Biology is concerned with the quantitative study of complex biosystems at the molecular cellular tissue and systems scales Its focus is on the function of the system as a whole rather than on individual parts This exciting new arena applies mathematical modeling and engineering methods to the study of biological systems This book is the first of its kind to focus on the newly emerging field of systems biology with an emphasis on computational approaches The work covers new concepts methods for information storage mining and knowledge extraction reverse engineering of gene and metabolic networks as well as modelling and simulation of multi cellular systems Central themes include strategies for predicting biological properties and methods for elucidating structure function relationships Computational Systems Biology Helder I Nakaya,2013-11-26 Computational Systems Biology Hans V. Westerhoff,Fei He,Ettore Murabito,Frédéric Crémazy,Matteo Barberis,2013-11-26 Systems Biology brings the potential to discover fundamental principles of Life that cannot be discovered by considering individual molecules This chapter discusses a number of early more recent and upcoming discoveries of such network principles These range from the balancing of fluxes through metabolic networks the potential of those networks for truly individualized medicine the time dependent control of fluxes and concentrations in metabolism and signal transduction the ways in which organisms appear to regulate metabolic processes vis vis limitations therein tradeoffs in robustness and fragility and a relation between robustness and time dependences in the cell cycle The robustness considerations will lead to the issue whether and how evolution has been able to put in place design principles of control engineering such as infinite robustness and perfect adaptation in the hierarchical biochemical networks of cell biology **Computational Systems Biology** Robert B. Russell,,Gordana Apic,Olga Kalinina,Leonardo Trabuco,Matthew J. Betts,Qianhao Lu,2013-11-26 The best understanding of complex biological systems ultimately comes from details of the underlying atomic structures within it In the absence of known structures of all protein complexes and interactions in a system structural bioinformatics or modeling fill an important niche in providing predicted mechanistic information which can guide experiments aid the interpretation of high throughput datasets and help provide key details to model biological systems This introductory review discusses the current state of this field and suggests how current datasets in systems studies can profit from a better integration of predicted or known structural information *Computational Systems Biology* Andres Kriete,Roland Eils,2013-11-26 This comprehensively revised second edition of Computational Systems Biology discusses the experimental and theoretical foundations of the function of biological systems at the molecular cellular or organismal level over temporal and spatial scales as systems biology advances to provide clinical solutions to complex medical problems In particular the work focuses on the engineering of biological systems and network modeling Logical information flow aids understanding of basic building blocks of life through disease phenotypes Evolved principles gives insight into underlying organizational principles of biological

organizations and systems processes governing functions such as adaptation or response patterns Coverage of technical tools and systems helps researchers to understand and resolve specific systems biology problems using advanced computation Multi scale modeling on disparate scales aids researchers understanding of dependencies and constraints of spatio temporal relationships fundamental to biological organization and function **Computational Systems Biology** Joseph Xu

Zhou,Xiaojie Qiu,Aymeric Fouquier d'Herouel,Sui Huang,2013-11-26 In this chapter we introduced the basic concepts of cell attractors and showed that Waddington's metaphoric epigenetic landscape has a formal basis in the attractor landscape This conceptual framework helps to understand core properties of cell differentiation and ultimately multicellularity Specifically we developed the concept of relative stability of network states on the epigenetic landscape thus providing the elevation in the landscape picture a formal quantifiable basis We proposed methods to quantify the relative stability of attractor states in discrete gene networks models We show in two examples that even with incomplete information about network structures the use of Boolean networks can capture the essential outlines of cell fate dynamics and more importantly permit the estimation of relative stability and the attractor transition barriers These measures hold great promise for the rational design of the perturbation protocols for cell reprogramming in regenerative medicine As the knowledge of the structure of GRNs for the development of various tissues will undoubtedly increase in the next decade the utilization of such network information for therapeutic reprogramming may benefit from the concepts developed here **Computational Systems Biology** Julien

Delile,René Doursat,Nadine Peyri  ras,2013-11-26 We propose a theoretical yet realistic agent based model and simulation platform of animal embryogenesis called MecaGen centered on the physico chemical coupling of cell mechanics with gene expression and molecular signaling This project aims to investigate the multiscale dynamics of the early stages of biological morphogenesis Here embryonic development is viewed as an emergent self organized phenomenon based on a myriad of cells and their genetically regulated and regulating biomechanical behavior Cells mechanical properties such as division rate adhesion strength or intrinsic motility are closely correlated with their spatial location and temporal state of genetic and molecular dynamics such as internal protein and external ligand concentrations and affect each other concurrently In a second part we illustrate our model on artificial data gene regulation motifs and cell sorting then demonstrate a customization and application to a real biological case study in the zebrafish early development We use as an example the episode of intercalation patterns appearing during the first phase of epiboly and the movements of the deep cells between the yolk and the enveloping layer A domain of the model's multidimensional parameter space is explored systematically while experimental data obtained from microscopy imaging of live embryos is used to measure the fitness of the virtual embryo and validate our hypotheses **Computational Systems Biology** Hong-Wu Ma,An-Ping Zeng,2013-11-26 Understanding the

complex interactions among cellular components genes proteins and metabolites at a network level is a key issue in systems biology In this chapter we give an overview of metabolic network reconstruction from genome information and its structural

analysis First two approaches for genome scale metabolic network reconstruction high throughput reconstruction and high quality reconstruction are discussed Then the various means for mathematical representation of metabolic networks are explained with particular emphasis on the problem arising from currency metabolites Several topological features of metabolic network such as the power law connection degree distribution and the bow tie global connectivity structure are explained in detail In the last section we discuss the different types of methods for network decomposition which can be used to identify somehow structurally and functionally independent modules in a complex network This allows us to understand the functional organization of metabolic network from a modular perspective

Computational Systems Biology Stefan M. Kallenberger, Stefan Legewie, Roland Eils, 2013-11-26 Apoptosis is a form of cellular suicide central to various aspects in biology including tissue homeostasis and embryonic development It is typically dysregulated in cancer Understanding the apoptotic signal transduction network is thus a central goal of cancer research Quantitative modeling approaches provided valuable insights into determinants of cell fate decisions and promise to become a valuable tool to optimize therapeutic strategies In this chapter we summarize modeling approaches used in systems biology of apoptosis In addition we give an overview of apoptosis related research questions that can be addressed by modeling Moreover we review top down and bottom up modeling approaches applied to apoptosis and particularly focus on ordinary differential equation ODE modeling We describe bistability temporal switching crosstalk between death and survival and discuss approaches to model cell to cell variability

Computational Systems Biology Juergen Eilsa, Elena Herzoga, Baerbel Felder, Christian LawerENZA, Roland Eils, 2013-11-26 Systems biology combines experimental and computational research to facilitate understanding of complex biological processes In this chapter we describe data repositories data standards modeling and visualization tools as prerequisites for systems biology research in order to help us to better study and understand biological processes In addition we propose improvements of these tools providing an example application JUMMP developed in our laboratory We suggest that flexibility interoperability and modularity of novel applications contribute to better acceptance and further development of these tools We also emphasize that having flexible and extendable standards describing complex and incomplete biological data allow new discoveries to be incorporated in a seamless way into systems biology tools Overall we discuss here advances challenges and perspectives of data and other platforms in systems biology which we believe will continue to make an impact on biomedical research

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