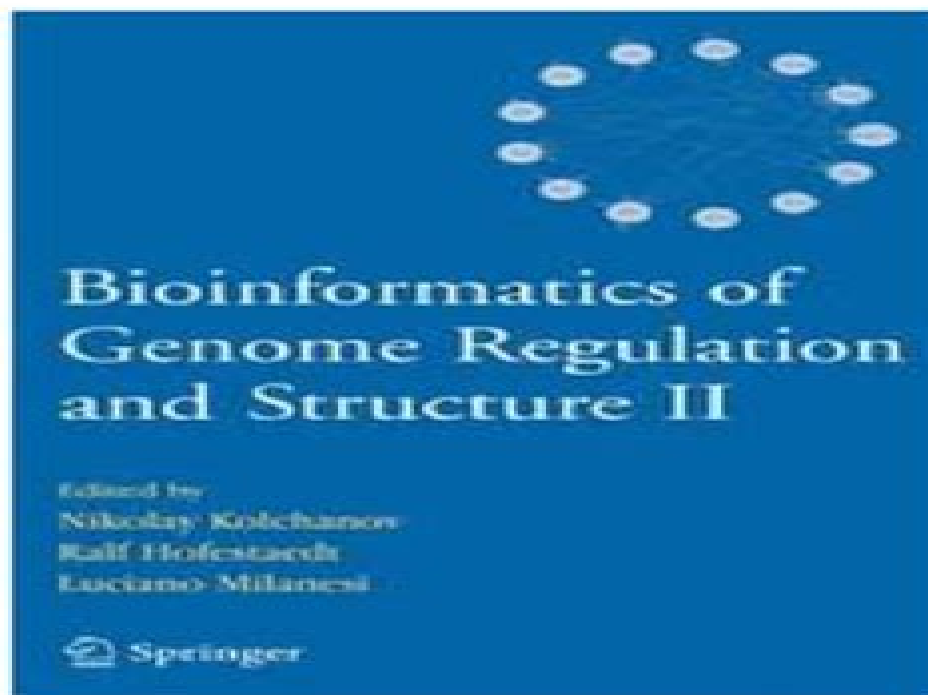


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The last 15 years in development of biology were marked with accumulation of unprecedentedly huge arrays of experimental data. The information was amassed with exclusively high rates due to the advent of highly efficient experimental technologies that provided for high throughput genomic sequencing of functional genomics technologies allowing investigation of expression dynamics of large groups of genes using expression DNA chips of proteomics methods giving the possibility to analyze protein compositions of cells, tissues and organs, assess the dynamics of the cell proteome and reconstruct the networks of protein-protein interactions and of metabolomics. In particular, high resolution mass spectrometry study of cell metabolites and distribution of metabolic fluxes in the cells with a concurrent investigation of the dynamics of thousands of metabolites in an individual cell. Analysis, comprehension and use of the tremendous volumes of experimental data reflecting the intricate processes underlying the functioning of molecular genetic systems are unfeasible in principle without the systems approach and involvement of the state-of-the-art information and computer technologies and efficient mathematical methods for data analysis and simulation of biological systems and processes. The need in solving these problems initiated the birth of a new science: postgenomic bioinformatics or systems biology in silico.

Bioinformatics of Genome Regulation, Volume II Yuriy L. Orlov, Ancha Baranova, Tatiana V. Tatarinova, Anastasia A. Anashkina, 2022-01-27 Proceedings of the Second International Conference on Bioinformatics of Genome Regulation and Structure International Conference on Bioinformatics of Genome Regulation and Structure 2, 2000, Novosibirsk, 2000

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Progress in Analysis and Its Applications Michael Ruzhansky, Jens Wirth, 2010. The International Society for Analysis, its Applications and Computation (ISAAC) has held its international congresses biennially since 1997. This proceedings volume reports on the progress in analysis, applications and computation in recent years as covered and discussed at the 7th ISAAC Congress. This volume includes papers on partial differential equations

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Gene Regulation and Metabolism Julio Collado-Vides,Ralf Hofestädt,2002 An overview of current computational approaches to metabolism and gene regulation

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