

Preface

Completion of the human genome sequencing could be undoubtedly viewed as the greatest scientific event of the last three years. This event marked the beginning of the post-genome era in biology. This era is characterized by a drastic elevation in the research scale in the fields of transcriptomics, proteomics, and systemic biology (gene interactions, gene network operation, and signal transduction pathways) without losing the basic interest to studying structure–function genome organization.

The structure and regulation of genome are the counterparts of life at molecular level; that is why the understanding of basic principles underlying operation of the regulatory genomic machinery is impossible unless their detailed structural organization is known, and vice versa.

The huge volume of experimental data that has been acquired on the genome structure, functions, and gene expression regulation is growing by leaps and bounds. Development of informational and computational technologies of the new generation is a challenging problem of bioinformatics. Bioinformatics has entered that very phase of development when solutions for the challenging problems determine realization of large-scale experimental research projects directed to studying genome structure, function, and evolution.

One of the international scientific forums presenting and discussing topical problems of bioinformatics related to genome regulation and structure is the international conference Bioinformatics of Genome Regulation and Structure–BGRS, organized biennially by the Laboratory of Theoretical Genetics with the Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia. BGRS'2002 was the third event in the series.

Participants of BGRS'2002 concentrated their attention on the following hottest items in bioinformatics: (i) regulatory genomic sequences: databases, knowledge bases, computer analysis, modeling, and recognition; (ii) large-scale genome analysis and functional annotation; (iii) gene structure determination and prediction; (iv) comparative and evolutionary genomics; (v) computer analysis of genome polymorphism and evolution; computer analysis and modeling of transcription, splicing, and translation; structural computational biology: genomic DNA, RNA, and protein structure-function organization; (vi) gene networks, signal transduction pathways, and genetically controlled metabolic pathways: databases, knowledge bases, computer analysis, and modeling; principles of organization, operation, and evolution; (vii) data warehousing, knowledge discovery, and data mining; and (viii) analysis of basic patterns of genome operation, organization, and evolution.

This book comprises selected reviewed papers prepared on the basis of results presented at BGRS'2002.

This book may be interesting to the specialists working on development of databases on genome regulation and structure, algorithms and software for analysis and simulation of molecular genetic systems of various organisms at various levels of their function and organization as well as to a wide range of biologists using bioinformatics methods and approaches in their work.

All the papers of this volume passed double reviewing: first, when submitted as presentation to BGRS'2002; second, when preparing the book.

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