Preface

The 3rd International Conference on Bioinformatics of Genome Regulation and Structure (BGRS 2002)

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This ISB special issue is a follow-up of the International Conference on Bioinformatics of Genome Regulation and Structure (BGRS-2002) held in Novosibirsk, Russia, in June 2002. BGRS-2002, the third in the series, was organized by the Laboratory of Theoretical Genetics, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia. It kept and continued the traditions of the previous two conferences, BGRS-98 and BGRS-2000, held in Novosibirsk in August 1998 and 2000, respectively.

Undoubtedly, the greatest scientific event that occurred in the period between the Conferences BGRS-2000 and BGRS-2002, was the completion of sequencing the draft of the human genome. This event marked the beginning of a post-genome era in biology, which was characterized by a sharp increase in research in the fields of transcriptomics, proteomics and systemic biology (gene interaction, gene network functioning, signal transduction pathways, *etc*.), together with an increased interest in studying the basic structure-function genome organization.

The huge volume of experimental data on genome structure and function and gene expression regulation acquired so far continues to grow explosively. The development of new generation informational and computational technologies is a challenging problem for bioinformatics. Bioinformatics has entered that very phase of development when solutions to these challenging problems determines the realization of large-scale experimental research projects directed to studying genome structure, function and evolution.

The most important items of bioinformatics considered at the conference were: (i) regulatory genomic sequences: databases, knowledge bases, computer analysis, modeling and recognition; (ii) large-scale genome analysis and functional annotation; (iii) gene structure detection 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: structure-function organization of genomic DNA, RNA and proteins; (vi) gene networks, signal transduction

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[*]Chairman and [**]Co-Chairman of the Conference.

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.

We believe this issue will be of interest to scientists who are involved in both theoretical and experimental studies of pro- and eukaryotic genomes.