

# Fifth International Conference on Bioinformatics of Genome Regulation and Structure-BGRS'2006

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## PREFACE

This issue of the *In Silico Biology* journal covers the materials reported at the *Fifth International Conference on Bioinformatics of Genome Regulation and Structure-BGRS'2006* (Akademgorodok, Novosibirsk, Russia, July 16–22, 2006; <http://www.bionet.nsc.ru/meeting/bgrs2006/index.html>). At the Conference, a wide range of basic issues of bioinformatics resolved by *in silico* methods, in conjunction with the modern experimental ones, were addressed. The issues were related to the structural-functional organization of the essential components of the living systems at the levels of genomes, transcriptomes, proteomes, gene, and metabolic networks.

Bioinformatics emerged over 30 years ago, in an (ongoing) endeavor to develop a quantitative framework for comparing nucleotide and protein sequences. Today, it is a vibrant multidisciplinary research area linked to the modern high-throughput biotechnical methodology. Contemporary bioinformatics embraces mathematical treatment of the data generated by biological experiments, comparative analysis of genetic macromolecules, evolutionary analysis, molecular modeling, etc. Among other things, bioinformatics is concerned with the analysis of complex biological objects such as gene and metabolic networks, computational performance of modeling and simulation tools that describe the behavior of the biological systems, and issues related to warehousing and processing of massive amounts of data generated by modern genomics and genetic epidemiology research. The materials presented by a truly interdisciplinary research community at the Conference demonstrated that the major breakthroughs resulted from synergy of methods employed in the different bioinformatics areas. It should be noted that bioinformatics is rooted in biology; and biology does not make any sense without evolution. Hence, the cornerstones of bioinformatics are comparative analysis of macromolecules and their interactions, and their manifold evolutionary aspects. The materials included in this issue emphasize the interplay of evolutionary and other bioinformatics approaches in attempt to meet and address pressing biological challenges.

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To illustrate, the combination of methods of genomics, and comparative analysis of the DNA sequences as the preprocessing step, makes it feasible to efficiently control the quality of the gene expression data, as Orlov *et al.* reported in this issue [1]. Application of the methods of numerical modeling of biological systems evolution provided Lashin *et al.* with answers to interesting questions related to gene transfer mechanisms in populations of bacteria [2]. Bukin *et al.* revealed interesting features of evolutionary history of the contemporary polychaetes inhabiting the Baikal Lake by combining population genetics and phylogenetic analysis approaches [3].

Rubanov and Lyubetsky showed that complex methods for modeling RNA secondary structure allowed to successfully tackle problems related to the attenuation regulation of gene expression in bacteria [4]. The work of Rodin, A. and Rodin, S. was devoted to the analysis of the tRNA structural, functional and evolutionary features in terms of origin and evolution of the genetic code [5]. Pintus *et al.* reported on their sophisticated analysis of the evolution of the p53, p63 and p73 gene families; in their analysis of mutations in these families they combined methods for detection of positive Darwinian's selection with protein structure modeling by molecular mechanics simulations [6]. Gunbin *et al.* evaluated evolutionary modes of genes involved in the Hh-signalling pathway and compared the results with known information about the structure of this gene network [7]. This comparison proved effective in highlighting the relationship between evolutionary modes of genes and their roles in the Hh-signalling pathway.

Taken together, the studies gathered in this volume demonstrate that the alliance of methodological approaches originating from various subfields of bioinformatics is arguably the most promising, unified, strategy for addressing a number of important issues in modern biology.

Prof. N.A. Kolchanov, BGRS'2006 Chair of the Organizing Committee, In Silico Biology editor, Prof. S.N. Rodin, invited issue editor.

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