Introduction

Three volumes of *Proceedings of the Fifth International Conference on Bioinformatics of Genome Regulation and Structure—BGRS’2006* (Akademgorodok, Novosibirsk, Russia, July 16–22, 2006) comprise about 200 peer-reviewed publications on the topical problems in bioinformatics of genome regulation and structure. Biology now is among the most dynamically developing scientific disciplines. The main factor of this progress is an unprecedented, both in the rate and volume, accumulation of new facts due to advent of novel state-of-the-art experimental technologies. The post-genome era in biology brought about a sharp up-scaling of the research in the fields of genomics, transcriptomics, and proteomics. We are the witnesses how new directions of experimental and computer molecular biology emerge and successfully advance, including sequencing and analysis of megagenomes of bacterial communities, regulation of gene expression by short RNAs, microarray analysis technique, construction of proteomic portraits of cells and tissues, metabolomics, high-throughput genotyping of human populations for biomedical purposes, and many others. However, the synthesis of these directions is developing to a lesser degree, while it is a primary need for creation of an orderly theory of development, function, and evolution of the living systems—systems biology (gene interaction, gene network functioning, signal transduction pathways, networks of protein–protein interactions, modeling of ontogenesis, molecular phylogeny, the theory of evolution, etc.). The reasons underlying this gap lie not only in the objective complexity of the living systems, but also in the specialization in various fields of biology, which is ever increasing with accumulation of new data and development of new methods. The holistic vision of the research object is disappearing. The goal of this Conference, similar to the preceding Conferences—BGRS’1998, BGRS’2000, BGRS’2002, and BGRS’2004, which were held in Novosibirsk in 1998, 2000, 2002, and 2004—is, first and foremost, to provide the possibility for a wide exchange of opinions for various experts in *in silico* biology and researchers involved in experimental studies who use computer methods in their work or have interest in applied or theoretical aspects of bioinformatics. BGRS’2006 provides a general forum for disseminating and facilitating the latest developments in bioinformatics in molecular biology. BGRS’2006 is a multidisciplinary conference. The scope covered by the Conference comprises (i) the issues of development of advanced methods for computational and theoretical analysis of structure–function genome organization, proteomics, transcriptomics microarray analysis, etc.; (ii) application of these methods in theoretical (various aspects of evolutionary biology) and applied (search for promising application points in biotechnology and medicine) fields; and (iii) the issues related to general informational support of biological research and education (creation and computer support of databases, retrieval systems, ontologies, etc.). Thus, the final goal of this Conference may be defined as a half the battle for the new synthesis in Biology, which is a long-standing need, via the dialogue...
between the experts in particular fields of biology. This is the reason why BGRS’2006, along with the traditional sections (computational structural and functional genomics and transcriptomics, computational structural and functional proteomics, comparative and evolutionary genomics and proteomics, and bioinformatics and education), includes an essentially expanded section on computational systems biology, which contains the presentations on modeling of molecular genetic systems and processes in bacterial and multicellular organisms and modeling of morphogenesis. Moreover, as compared to the previous conferences, the presentations related to evolution and phylogeny are plentiful. Numerous interdisciplinary studies into various taxa performed by the methods of molecular phylogeny, computer genomics, proteomics, cytogenetics, etc., as well as comparison of these results with the data obtained by classical methods of evolutionary morphology, paleontology, and various directions of ecology revealed the basic differences between the rates and modes of evolution at different hierarchical levels of biological organization (genes, genomes, karyotypes, organisms, populations, and biocenoses). Thus, the actual evolutionary process cannot be reduced to the evolution on one of the listed levels and is, speaking in images, an interference pattern, which is the more complex, the more interacting blocks and hierarchical levels constitute a biological system and the more intricate are their interrelations. Deciphering of this interference pattern is one of the challenges for the biology of the XXI century, which is answerable only by the joint efforts of bioinformatics and experimental sciences. If BGRS’2006 succeeds in contributing to this to any degree, the organizers will reckon their goal fulfilled.

Among the main goals of BGRS is improvement in the quality of education in all its aspects. That is why the success and international acknowledgement of the preceding conferences and the 2005 BGRS Summer School "Evolution, Systems Biology and High Performance Computing Bioinformatics" has encouraged launching the 2006 BGRS Summer School "Evolution, Systems Biology and High Performance Computing Bioinformatics". This School being the co-event of the conference will precede BGRS’2006. This event will attract next generation of scientists to bioinformatics. The scientific scope of the school will include issues of the development and application of advanced methods of computational and theoretical analysis for structure-function genome organization, proteomics, evolutionary and systems biology. We hope that the School of Young Scientists will become a good BGRS tradition.

BGRS’2006 is organized by the Laboratory of Theoretical Genetics with the Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, (Novosibirsk, Russia). The organizational sponsors of the Conference are the Institute of Cytology and Genetics and the Siberian Branch of the Russian Academy of Sciences. The financial sponsor is the Russian Foundation for Basic Research. The School of Young Scientists "Evolution, Systems Biology and High Performance Computing Bioinformatics" is sponsored by the Russian Foundation for Basic Research and INTAS. The organizational support for the School is provided by the Chair of the Informational Biology, Faculty of the Natural Sciences of the Novosibirsk State University and the Council of Young Scientists of the Institute of Cytology and Genetics, SB RAS.

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