

The Sixth International Conference on Bioinformatics of Genome Regulation and Structure

Dear colleagues and friends!

As in the previous year, we plan to organize the Sixth International Conference on Bioinformatics of Genome Regulation and Structure (BGRS'2008) from June 22- 28, 2008 at Akademgorodok, Novosibirsk.

The BGRS'2008 is an interdisciplinary conference concerned with furthering a new generation of methods of computer and theoretical analysis and their application to a broad range of problems that includes the structural-functional organization of genomes, transcriptomics, proteomics, metabolomics, evolutionary and systems biology. At the BGRS'2008, it is planned to cover new research directions that are currently emerging with reference to the application of computer methods for processing experimental data in the areas of proteomics, genomics, transcriptomics, also nanobiotechnology. Novel achievements in these research areas will be presented at the BGRS'2008.

The scientific program will consist of plenary and program reports, round tables raising timely issues in bioinformatics and systems biology. The participants will be provided with ample opportunities to demonstrate and freely discuss their work.

The BGRS'2008 will include an innovation business-forum aimed at the discussion of possible ways and means for implementing scientific developments in the bioinformatics area and potential collaboration between scientists, biotechnological companies and venture funds.

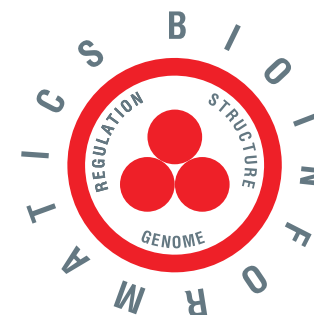
As the BGRS'2008 co-event, an International school-seminar for young scientists will be held under the auspices of the BGRS'2008 from June 29-July 2, 2008.

The conference www page is available at
<http://www.bionet.nsc.ru/meeting/bgrs2008/>

The e-mail address of the BGRS'2008 organizing committee: bgrs2008@bionet.nsc.ru

It is my pleasure to invite you to visit Novosibirsk this time and participate in the BGRS'2008.

Best regards,
Dr.Biol.Sci., Prof. Nikolay Kolchanov,
BGRS'2008 Chairman.



INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE BGRS'2008

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NOVOSIBIRSK, 2008

THE SIBERIAN CENTER FOR GENOMICS, PROTEOMICS AND BIOINFORMATICS TECHNOLOGIES

The increasingly common practice of using expensive high-efficiency biology equipment is the creation of shared multidisciplinary centers.

The Siberian Center for Genomics, Proteomics and Bioinformatics Technologies (SCGPBT) will be created by three institutes of the Siberian Division of the Russian Academy of Sciences to provide researchers access to the most advanced technologies available in molecular biology, cell biology, genetics and bioinformatics.

The Siberian Center for Genomics, Proteomics and Bioinformatics Technologies will include specialized centers for research and technology that promote the following:

1. Genomics research (the sequencing of prokaryotic and eukaryotic genomes and the study thereof);
2. Proteomics research;
3. The development of genetic animal models for use in post-genomic medicine;
4. Post-genomic medical research;
5. Bioinformatics research.

The first priorities for the specialized centers are as follows:

- the shared use of expensive equipment;
- the recruitment of highly skilled personnel to maintain this equipment;
- the provision of support to cutting-edge research technologies, improvement and replacement thereof as new solutions become available;
- The Siberian Center for Genomics, Proteomics and Bioinformatics Technologies will address the following research issues:
 - The sequencing of the entire genomes of bacteria that live in extreme environments
 - The cloning of new enzymes from the metagenomes of hyperthermophilic organisms for use in DNA diagnostics

- The development of microarray-based techniques for the genotyping of viral pathogens, the ascertainment and characterization of genetic polymorphisms
- The study of the molecular mechanisms of leucosis
- The identification of key regulatory genes responsible for atopic diseases, using the most up-to-date approaches in the bioinformatics and experimental analyses of the entire transcriptome
- The development of experimental/computer-based modeling approaches to searching the entire human and mammalian genomes for transcription factor binding sites
- The study of molecular-biological mechanisms that control traits with relevance to domestication
- The study of the role of copy number variation in the human genome in cancer and complex diseases; the study of the role of copy number variation in mammalian genomes for evolution and genome plasticity.
- The study of the genetic/physiological and molecular mechanisms of stress-dependent arterial hypertension
- The study of molecular-genetic mechanisms that underlie the regulation of energy homeostasis; the development of new approaches to the prevention and treatment of metabolic diseases (obesity, type II diabetes)
- The elucidation of the genetic background of premature aging and associated diseases
- The study of proteomic markers of human diseases
- The proteomic study of the proteins that enable the transport and entry of their complexes with extracellular nucleic acids into the cell
- The development of genetically engineered variants of the anti-cancer drug candidate Lactaptin and its structural analogues
- The conformation analysis of immunodeficiency virus proteins

- Control over the differentiation of embryonic stem cells and the reprogramming of the genomes of differentiated cells
- The study of the flexibility of human embryonic stem cells
- The development of post-genomic approaches to the study of regulatory networks that coordinate cell differentiation, proliferation and apoptosis in organs and tissues
- The study of the distribution and signal transduction pathways of auxin in plant tissues
- The complex modification of plant metabolisms using systems biology and genetic engineering approaches
- The computer-assisted development of the pedigree-based maps of human and animal genes for complex characters
- The development of software products for use in structural proteomics, bioinformatics and the design of DNA nanostructures
- The development of an experimental/computer-based modeling approach to studying the functional properties of the regulatory elements of bacterial genomes and creating artificial molecular-genetic systems with properties customized for particular needs.

