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PSB 2001 CALL FOR PARTICIPATION

<http://www.cgl.ucsf.edu/psb>

The 6th Pacific Symposium on Biocomputing (PSB), will be held January 3-7, 2001 in Honolulu, Hawaii. PSB provides a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology. PSB intends to attract a balanced combination of computer scientists and biologists, presenting significant original research, demonstrating computer systems, and facilitating formal and informal discussions on topics of importance to computational biology. PSB 2001 Sessions To provide focus for the very broad area of biological computing, PSB is organized into a series of specific sessions. Each session involves both formal research presentations and open discussion groups. The 2001 PSB sessions are:

- Human Genome Variation and Clinical Genotypics
- Genome, Pathway and Interaction Bioinformatics
- NLP and IE for Biology
- High Performance Computing for Computational Biology
- Phylogenetics in the Post-Genomic Era
- Integrated Study of Protein Evolution
- Disorder in Protein Function
- DNA Structure, Interactions, and Expression
- Bioethics and Fiction Science

Papers, Abstracts and Demonstrations The core of the conference consists of rigorously peer-reviewed full-length papers reporting on original work. Accepted papers will be published in a hard-bound archival proceedings, and the best of these will be presented orally to the entire conference. Workstations and internet connections will be available for demonstrations. Open submissions of posters and abstracts are also encouraged. See the web site <http://www.cgl.ucsf.edu/psb> for information about submission requirements. Important Dates

Paper submissions due: July 17, 2000

Abstract deadline: November 6, 2000

Meeting: January 3-7, 2001

For More Information See our web site <http://www.cgl.ucsf.edu/psb> or send email to the conference coordinator: psb@cgl.ucsf.edu

SIGs ISCB has begun to offer special interest groups (SIGs) to its members. SIGs are intended to create communities of interest in particular topics in computational biology. All ISCB SIGs will have space on the ISCB web site, and ISCB will consider funding particular projects proposed by its SIGs. The first ISCB SIG was just approved on the topic of Biological Simulations. Please contact the SIG chair, Masaru Tomita (mt@sfc.keio.ac.jp) for more information. If you are interested in starting an ISCB SIG in any subarea of computational biology, please send an informal proposal to exec@iscb.org. Your proposal should specify the rationale for creating the SIG, your plans for initial activities, and evidence that there is a critical mass of participants interested in contributing to SIG activities. Larry Hunter

ISCB President

SECOND INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE We are announcing the Second International Conference on Bioinformatics of Genome Regulation and Structure, that is to be held in Novosibirsk on August 7-11, 2000. This conference will be the second in the series. The First International Conference on Bioinformatics of Genome Regulation and Structure held in Novosibirsk in August 1998 revealed that accumulation, analysis and recognition of genomic regulatory sequences have become now the actual problems in Bioinformatics. BGRS'2000 will bring together experts in Bioinformatics to discuss the progress in this field achieved at the end of 20th century. The researchers working in the fields of experimental biology and interested in application of Bioinformatics methods in their work are also welcome. This conference is also expected to be a stimulating event to establish new links between Bioinformatics and experimental research. It will focus mainly on the following topics:

- Databases on regulatory genomic sequences and regulatory proteins;
- Representation and integration of data on regulation of gene expression, genetics;
- Databases, computer analysis, and modeling of metabolic pathways;
- Computer methods of analysis and recognition of regulatory genomic sequences;
- Methods of analysis and prediction of functional site activity;
- Computer technologies for automatic knowledge discovery on gene regulation;
- Gene structure prediction;
- Models of transcription, splicing and translational control;
- Large-scale genome analysis and functional annotation of nucleotide sequences;
- The search for objective methods in annotating and finding signals in genomic sequences;
- Evolution of regulatory genomic sequences;
- Aspects of protein structure and structural genomics related to regulation;
- Interactive links between Bioinformatics and experimental research on functional genomics (Micro array/biochips and other genome technologies)

Scientific program of the conference will include plenary lectures, symposia, posters and Internet computer demonstrations, round table sessions. The deadline for submission of extended abstracts (up to 4 pages) is March 15, 2000. The notification of acceptance will follow by April 15, 2000. The exhaustive information on our conference can be found at the URL <http://www.bionet.nsc.ru/bgrs2000/>. If you are going to participate in our conference, please help us by filling the registration form [http://www.bionet.nsc.ru/bgrs2000/registration_form.html] as soon as possible. Sincerely yours,

Prof. Nikolay Kolchanov
Institute of Cytology and Genetics,
Novosibirsk, 630090 Russia:
TEL, +7(3832) 333468
FAX: +7(3832) 331278
e-mail: kol@bionet.nsc.ru

SPECIAL INTEREST GROUP OF BIOLOGICAL SIMULATION (SIGSIM) INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY Scope: A vast amount of biological knowledge in molecular level will be rapidly accumulated in the near future, and it is clear that computer simulation is indispensable to understand dynamic behavior of cellular metabolisms by integrating these pieces of knowledge. Constructing cell models in computers and conducting "in silico experiments" will possibly become one of the most important paradigms of biology in the 21st century. Special Interest Group of Biological Simulation (SIGSIM) focuses on, but not limited to, the following three areas:

- Basic and applied technologies in simulation software and biological knowledge representation.
- Cell metabolism models of various kinds constructed with the above technologies.
- Standardization of biological knowledge representation and simulation software to make cell models sharable and exchangeable.

Activities:

- Annual SIGSIM meetings will be organized, possibly as satellite workshops of ISMB from 2001.
- A mailing list and a web page will be created shortly.
- More to be announced.

Steering Committee members: Hamid Bolouri (U of Hertfordshire), Dennis Bray (Cambridge), Doug Brutlag (Stanford), Andrea Califano (IBM), George Church (Harvard), Igor Goryanin (GlaxoWellcome), Larry Hunter (NCBI), Peter Karp (SRI), Hiroaki Kitano (Sony CSL), Nikolay Kolchanov (Russian Academy of Sciences), Leslie Loew (U of Connecticut), Pedro Mendes (NCGR), Chris Ouzounis (EMBL), Masaru Tomita (Keio U).

[more to be added]. Contact:

Masaru Tomita

Laboratory for Bioinformatics, Keio University

5322 Endo, Fujisawa, 252 JAPAN

mt@sfc.keio.ac.jp

NIH POSITION IN BIOMEDICAL COMPUTATION The NIH National Center for Research Resources is seeking an individual with a background in biomedical computation with strength in one or more of the following areas: molecular simulation on terascale computers, storage and analysis issues in large biological databases, display and analysis of large-scale data sets, or biological image processing and fusion. The individual who fills this position will develop and manage an extramural research program in bioinformatics that impacts the entire spectrum of biomedical research supported by the NIH. Application information can be found at http://careerhere.nih.gov/CHPublic/HRShowVac.taf?&VACANCY_uid1=3497 Questions should be directed to Dr. Michael Marron, 301-435-0753.

IEEE SYMPOSIUM "IEEE International Symposium on Bioinformatics and Biomedical Engineering" The web site for the announcement is: <http://pinon.cs.unr.edu/~bebis/BIBE/> The deadline for the submission is May 15, 2000.

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