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### ISCB NEWSLETTER July 6, 1999 - Vol. 2 #5

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#### ISCB ANNOUNCES CORPORATE MEMBERSHIP SCHEME

ISCB's efforts to establish computational biology as a vibrant scientific discipline continue apace, with the announcement of a new institutional membership scheme. ISCB believes that forging links between industry and the Society will result in great benefit to the computational biology community as a whole, and invites companies to participate in this important enterprise. Two levels of institutional membership are offered:- Full membership: is aimed at companies with significant investment in bioinformatics, wishing to contribute to the development of this critical interdisciplinary field through the ISCB, and thereby support the establishment of bioinformatics as a scientific profession and the development of new career opportunities for bioinformatics scientists. Associate membership: is for companies who wish to contribute in a more limited way, but who also wish to benefit from some of the ISCB initiatives as a broker for recruitment and consultancy. Benefits for all institutional subscribers include a subscription to Bioinformatics, discounted registrations at ISCB-affiliated conferences, and a preferred position at the ISMB Job Fair. Further information on the benefits of institutional membership can be found on the ISCB web site: <http://www.iscb.org> Alternatively, mail your enquiry to: [iscb-corporate@iscb.org](mailto:iscb-corporate@iscb.org)

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#### GENOME INFORMATICS WORKSHOP (GIW) 1999

December 14-15, 1999

Yebisu Garden Place, Tokyo, Japan

(see <http://www.hgc.ims.u-tokyo.ac.jp/giw> for CFP) The Tenth Workshop on Genome Informatics (GIW '99) focuses on Genome Informatics, including but not limited to research and development on theory, software tools, and application for the analysis, prediction and understanding of sequential, structural and functional information which is included in Genome and their network of relations. Kiyoshi Asai Board of Directors member of ISCB Electrotechnical Laboratories

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#### THE FIRST INTERNATIONAL BIOINFORMATICS SUMMER SCHOOL

Devoted To Information Systems and Network Analysis of Gene Regulation and Metabolism Magdeburg, Germany September 5 -10, 1999 You can see detailed information in the electronic poster at [http://www.witi.cs.uni-magdeburg.de/iti\\_bm/ibss/](http://www.witi.cs.uni-magdeburg.de/iti_bm/ibss/) [please distribute to colleagues and graduate students] Post-genomic methods in molecular biology generate large amounts of expression data, which require computational methods for their storage, management, and analysis. Knowledge databases with information on genes not only as genome constituents but also as the elements of regulatory, signaling, and metabolic pathways are essential resource for "reverse engineering" regulatory and metabolic networks in the cell. An updated illustrative list of different methodologies available in the internet can be obtained at ([http://www.witi.cs.uni-magdeburg.de/iti\\_bm/dagstuhl/demos.html](http://www.witi.cs.uni-magdeburg.de/iti_bm/dagstuhl/demos.html) ). The conclusion when looking at such a variety of approaches is that in order to support the analysis of gene regulation and metabolic network control we need distributed data access integrated with visualization, simulation, and analysis tools. Based on the experience of two International Dagstuhl Seminars on this topic (1995 and 1998 Schloß Dagstuhl with URL: <http://www.dag.uni-sb.de> ) we invited scientists to prepare specific courses in the following areas:

- Basic Molecular Database Systems (R. Apweiler, EMBL Cambridge)
- Global Gene Expression Studies (A. Manson McGuire, Harvard Medical School)
- Gene Regulation (J. Collado-Vides, UNAM; E. Wingender, GBF)

- Metabolic Pathways (M. Kanehisa, University Kyoto)
- Cell Signaling (N. Kolchanov, Russia Academy of Science)
- Gene Expression and Cell Differentiation (J. Reinitz, Mt. Sinai Med. School)
- Modeling and Simulation of Metabolic Networks (M. Tomita, University Keio)
- Database Integration (T. Møck, University Vienna)
- Molecular Information Systems (R. Hofest"dt, University Magdeburg)
- Metabolic Engineering (M. Reuss, University Stuttgart)

The summer school will be supported by the Volkswagen-Stiftung. Therefore we can offer grants to approximately 25 graduate students of Biology, Medicine, Computer Science, Biophysics, Biomathematics, and Biochemical Engineering who are already working in the interdisciplinary field of this Summer School and who have experience using molecular database systems. Graduated students and junior scientists are asked to send their CV and a short paragraph about their main motivation to apply for this course to the organizers. They should not be older than 35 years. Sincerely Yours, Organizing Committee:

- J. Collado-Vides (UNAM, Mexico)
- R. Hofest"dt (University Magdeburg, Germany)
- J. Reinitz (Mt. Sinai Med. School, NYC, USA)
- M. Reuss (University Stuttgart, Germany)

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[http://www.cifn.unam.mx/Computational\\_Biology/](http://www.cifn.unam.mx/Computational_Biology/) Currently on sabbatical leave at:

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### **NIGMS "Individual Postdoctoral Fellowships in Genomics and Related ELSI Topics"**

NIGMS is a co-sponsor of a new program announcement entitled "Individual Postdoctoral Fellowships in Genomics and Related ELSI Topics." The purpose of these fellowships is to train scientists in the multidisciplinary skills that will enable them to engage in research to accomplish the short- and long-term objectives of the Human Genome Project and similar genomic projects, as well as to take full advantage of the resulting genomic data and resources to solve biomedical and bioethical problems. Broad areas of research that are relevant include genomic analysis (including technology development) and the ethical, legal, and social implications of human genetics research. NIGMS will support fellowships that provide training in functional genomic analysis in non-human model systems. The full announcement is available at <http://www.nih.gov/grants/guide/pa-files/PA-99-122.html>

### **NIGMS: Annual MARC/MBRS Biomedical Research Symposium Support for the Annual MARC/MBRS**

Biomedical Research Symposium NIGMS items in this week's NIH Guide for Grants and Contracts: Support for the Annual MARC/MBRS Biomedical Research Symposium <http://www.nih.gov/grants/guide/rfa-files/RFA-GM-99-008.html> This RFA solicits applications for a cooperative agreement (U13) to conduct a national biomedical research symposium starting in the fall of 2001 and continuing every year for the next four years. The symposium would be targeted to students supported by the NIGMS Division of Minority Opportunities in Research and could focus on such areas as:

- undergraduate research
- exposure of students to outstanding science and scientists
- workshops that offer skills development for students
- workshops for Minority Access to Research Careers (MARC) and Minority Biomedical Research Support (MBRS)

program directors in such areas as advising, tutoring, educational technology, grant writing, grants management, and professional development

- booths for graduate program recruiters

Protein Structure Initiative (Structural Genomics) <http://www.nih.gov/grants/guide/pa-files/PA-99-116.html>  
<http://www.nih.gov/grants/guide/pa-files/PA-99-117.html> (for SBIR/STTR grants) These program announcements encourage research on the methodology and technology underpinning the emerging field of structural genomics, whose goal is the understanding of protein structural families, structural folds, and the relationship of protein structure to function. Projects related to high-throughput structure determination by X-ray crystallography and NMR, as well as those addressing other constituent tasks of structural genomics, are relevant to these announcements.

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