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## Newsletter Archives

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### NEW OFFICERS AT THE HELM At ISMB 2000, the new officers of the society began their terms.

- Russ Altman (Stanford) is the President
- Alfonso Valencia (Centro Nacional de Biotecnologia) is the Vice President
- Teri Klein (Stanford) is the Treasurer
- Phil Bourne (UC San Diego) is the Secretary

Contact information for all are at <http://www.iscb.org>. At the ISCB Board of Directors meeting, it was decided that, effective 2001, officers will be nominated and elected by the general membership. All officers automatically serve three year appointments on the board, so over time, the board will become entirely member-elected. Seven new members were elected to the board of directors to serve a three-year term. They are:

- Dietlind L. Gerloff of the University of Edinburg, Scotland
  - Minoru Kanehisa of the Institute of Chemical Research in Kyoto University, Japan
  - Masaru (Tommy) Tomita, professor and Director for Laboratory for Bioinformatics, Keio University, Japan
  - Gary Stormo, Professor, Dept of Genetics, Washington University Medical School
  - Gunnar Von Heijne Stockholm University, Dept of Biochemistry
  - Cathy Wu, director of Bioinformatics, National Biochemical Research Foundation at Georgetown University Medical Center
  - Hershel Safer of Compugen Ltd in Israel
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**ISMB2000 IN SAN DIEGO A TREMENDOUS SUCCESS** ISMB 2000 in San Diego placed special emphasis on knowledge discovery from the modeling and simulation of complex biological systems. The intense interest in the field was reflected by an attendance of 1211 scientists from 44 countries - almost double the 1999 attendance. Attendees heard 42 papers selected from 141 submitted as well as 7 keynotes, including a wonderful lecture delivered by David Searls as the first Chris Overton Memorial Lecture. Approximately 280 posters were presented over the four days of the conference and 14 tutorials were presented before the main conference. An exhibitor showcase, job fare, and software demos completed the program. In a survey conducted at the end of the conference 19% considered the scientific content outstanding, 64% good, 14% okay, 1% poor and 2% did not respond. Full details of the conference remain on the Web site at <http://ismb00.sdsc.edu> including pointers to what will likely be an equally exciting and rewarding conference in Copenhagen in 2001. Not only has bioinformatics arrived as a serious endeavor, so has ISMB as a major scientific conference. In fact, more scientists attended ISMB than the Protein Society Meeting held in San Diego two weeks prior to ISMB. Phil Bourne & Michael Gribskov ISMB 2000 Co-chairmen

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# **FOURTH ANNUAL CONFAB ON COMPUTATION GENOMICS**

Title: Fourth Annual Conference on Computational Genomics

Time and place: November 16 - 19, 2000, Renaissance Harborplace Hotel, Baltimore, MD

Organized by: The Institute for Genomic Research

URL: <http://www.tigr.org/cet/gss/cg/index.shtml>

Contact information: [cg@tigr.org](mailto:cg@tigr.org) This conference will bring together practitioners of the science of computational genomics and promote the further interaction between the fields of computer science and molecular biology in support of genomics.

# **CALL FOR PAPERS CPM 2001**

The Twelfth Annual Symposium on Combinatorial Pattern Matching will be held in Jerusalem, Israel, on July 1-4, 2001. The conference will be followed by STOC 2001 in Crete, a mere swimming distance away. Papers in all areas related to combinatorial pattern matching and its applications will be considered, including, but not limited to: string algorithms pattern recognition applications in molecular biology text searching information retrieval data mining symbolic computing natural language processing coding and data compression. string processing in databases Both papers reporting on original research unpublished elsewhere and surveys of important results are welcome. In addition, this year the committee welcomes poster submissions as well. Proceedings will be published in the Springer-Verlag series, Lecture Notes in Computer Science. Important dates:

Submission deadline: Jan 29, 2001

Notification of Acceptance/Rejection: Mar 5, 2001

Camera-ready copies: Mar 31, 2001

Conference contact:

The conference web site is: <http://csweb.haifa.ac.il/cpm/>

Ami Amir [amir@cs.biu.ac.il](mailto:amir@cs.biu.ac.il)

Gadi Landau [landau@cs.haifa.ac.il](mailto:landau@cs.haifa.ac.il)

# **CALL TO PARTICIPATE IN FIRST INTL SYSTEMS BIOLOGY CONFAB**

The First International Conference on Systems Biology (ICSB2000) -The 9th JST International Symposium-14-16

November, 2000 Royal Park Hotel@TCAT, Tokyo Japan

Organized by Japan Science and Technology Corporation

ADMISSION FREE / Registration deadline: Oct. 31, 2000

Registration can be made from our website: <http://www.systems-biology.org> The First International Conference on Systems Biology aims at bringing together researchers working in the field of Systems Biology and related field to present the current status of their research and to discuss future directions of the field. The importance of the system-level understanding of biological systems is receiving increasing recognition recently. Nevertheless, the efforts are still sporadic and there is no conference specifically focused on this topic. While there are conferences on bioinformatics, the threads of these conferences are the use of computers in various aspects of biology, and not necessarily viewed from the system-level perspectives. Thus, these conferences cover broadly from sequence database, protein structures to gene networks, and less emphasis on the system-level understanding. Therefore, the goal of the conference is to create a forum of discussion for those who are interested in system-level understanding from various approaches for various biological systems, so that such efforts can form a coherent landscape. Systems Biology that focuses on system level understanding can be a major thrust in biology in the 21st century. A book based on this conference will be published from The MIT Press, Springer. Inquiries on the participation shall be addressed to the ICSB2000 Secretariat

E-mail: [isjst@jsf.or.jp](mailto:isjst@jsf.or.jp)

TEL:03-3212-2454

FAX:03-3212-0014

# **COMPUBIO AND BIOINFORMATICS POSITION AVAILABLE AT UCSD**

Tenure-track Position The Department of Computer Science and Engineering at UCSD has a tenure-track faculty position in computational biology and bioinformatics open for Fall, 2001. The department is looking for applicants with outstanding research credentials. Successful applicants are expected to lead a vigorous research program and to have a strong commitment to teaching. The department is in a period of exciting growth and has attracted extraordinary faculty in the past few years. It has strong research programs in computer science and computer engineering as well as a strong interdisciplinary research program in computational biology and bioinformatics. UCSD's bioinformatics community includes

not only the Computer Science Department but also the Departments of Bioengineering, Physics, Chemistry, Mathematics, and Biology, as well as UCSD Medical School and San Diego Supercomputing Center. For more information, please consult our web page <http://www-cse.ucsd.edu>. We encourage the candidates to send applications as soon as possible. Faculty applications received by January 15, 2001, will be given full consideration. Salary and rank will be commensurate with qualifications in conformance with University of California policies. CSE faculty position announcement may be found at <http://www-cse.ucsd.edu/recruitment>. Please send a letter of interest (cover letter), curriculum vitae including research interests and plans, the names and email addresses of at least four references to the Recruiting Chairman ( [recruit@cs.ucsd.edu](mailto:recruit@cs.ucsd.edu) ), and cite the position reference number 3-757-W. Recruiting Chairman; Dept of Computer Science and Engineering-0114 University of California, San Diego; La Jolla, CA 92093-0114

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### COMPUTATIONAL BIOLOGIST/GENETICIST FACULTY POSITION AT UNM

The University of New Mexico School of Medicine (SOM) invites applications for one or more tenure track positions at the rank of Assistant, Associate or Full Professor. The successful applicant will develop an independent research program focused on the development and application of computational methods that complement and support institutional interests in functional genomics, proteomics, structure-activity relationships and drug design, cell signaling or modeling of complex biological processes, systems and networks. Areas of emphasis include cancer, diabetes, asthma, cardiovascular physiology and neuroscience. Participation in graduate teaching activities also will be expected. Ongoing collaborations with the UNM-Albuquerque High Performance Computing Center, Sandia National Laboratory and Los Alamos National Laboratory provide a multidisciplinary environment with state-of-the-art resources and capabilities. The position also will be supported by a full time systems analyst. Requirements of the position include a Ph.D., M.D., or equivalent degree, and post-doctoral research experience. Demonstrated productivity, as evidenced by peer-reviewed publications, teaching and extra-mural research support are highly desirable. For best consideration applicants must submit the following before November 20, 2000: a curriculum vitae, the names of three references and a concise description of their research program or plan to:

*Dr. Jeffrey Griffith*

*Computational Biologist Search Committee*

*Department of Biochemistry and Molecular Biology*

*University of New Mexico School of Medicine*

*Albuquerque, New Mexico, 87131-5221.*

UNM School of Medicine is an Equal Opportunity/Affirmative Action Employer and Educator

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### MEMBERSHIP NEWS

Did you move, change your email address or simply want to check your record, personal information or address? Go to membership: regular and read and review your record. All you need is your membership id# and the email you used to register. Also, if you did move and have changed your address - snail mail and email, PLEASE notify Oxford University Press (BIOINFORMATICS): [thomsonp@oup.co.uk](mailto:thomsonp@oup.co.uk) and/or Mary Ann Liebert, Inc. (JOURNAL OF COMPUTATIONAL BIOLOGY): [pmasi@liebertpub.com](mailto:pmasi@liebertpub.com) . Renew Now! While reviewing your membership, we urge you to renew your membership as early as November for membership for the year 2001. By getting an early start, you will get all the conference and publication discounts you are entitled to without the hustle of having to do it later! And, don't forget to also urge your friends and colleagues to take advantage of an ISCB membership. We are growing - and growing fast!

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### THIRD INTL BIOINFORMATICS MEETING IN SCANDINAVIA

Bioinformatics 2001 is the third major international bioinformatics meeting in Scandinavia. It is organized jointly by bioinformatics groups from the Nordic countries, and aims to cover current developments in research on all aspects of bioinformatics. For more information, visit the website: <http://www.ida.his.se/ida/bioinformatics2001>

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### ELECTRIC GENETICS STACKPACK AVAILABLE

Free academic availability of Electric Genetics' stackPACK clustering tools for SGI Irix. Electric Genetics is happy to announce the availability of stackPACK v2.0 for SGI Irix 6.5 Academic users are now able to download stackPACK v2.0 for Irix, in addition to Linux, with Sun and Compaq to follow soon, from the following address: [http://www.sanbi.ac.za/CODES/STACKPACK\\_REQUEST/](http://www.sanbi.ac.za/CODES/STACKPACK_REQUEST/) The stackPACK system processes EST and mRNA data through a pipeline consisting of a series of steps including masking, loose clustering, assembly and alignment, alignment analysis for variation in

clusters/transcripts and linking non-overlapping clusters by clone ID. The system is unique not only because of its scientific schema but also because of its efficient management of the clustering data, using a relational database the program can be accessed through an effective web-based interface and viewing tools or through command line. The method employed and assessment of quality of the resource is fully described in: A Comprehensive Approach to Clustering of Expressed Human Gene Sequence: The Sequence Tag Alignment and Consensus Knowledge Base Robert T. Miller, Alan G. Christoffels, Chella Gopalakrishnan, John Burke, Andrey A. Ptitsyn, Tania R. Broveak, and Winston A. Hide. November 1999: Genome Research: 9:1143-1155 and d2\_cluster: A Validated Method for Clustering EST and Full-Length cDNA Sequences. John Burke, Dan Davison, and Winston Hide. November 1999: Genome Research: 9:1135-1142 Please also refer to the Electric Genetics website at <http://www.eugenetics.com/?Section=Stackpack&Parent=products> for further information on stackPACK.

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If you want to contact all of our members or if you have news or information that you want disseminated to all our members, use our society newsletter. Send to the ISCB office ([admin@iscb.org](mailto:admin@iscb.org)) a one or two paragraph blurb. Your society newsletter goes to all members. We also ask that you consider a discount for ISCB members in exchange for this mailing. For example, Stanford's Bioinformatics Certificate program offered a 10% discount in a recent newsletter.

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