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#### ISMB2000 LECTURE TO HONOR CHRIS OVERTON

David Searls, Vice President, Bioinformatics, of GlaxoSmithKline, will deliver a lecture to commemorate the work of his longtime colleague, G. Christian Overton, founding director of the Center for Bioinformatics at the University of Pennsylvania, at the International Conference on Intelligent Systems for Molecular Biology (ISMB 2000) in San Diego, California. Dr. Overton, who died May 31, was well known as a pioneer of the emerging field of bioinformatics. He recognized early the potential impact of applying computational technology to the study of biological problems. In 1997, he established Penn's Center for Bioinformatics (<http://www.pcbi.upenn.edu>), which houses the Computational Biology and Informatics Laboratory (CBIL). At the time of his death, Dr. Overton was a member of the board of directors of the International Society for Computational Biology. Prior to joining SmithKline, Dr. Searls was a Research Associate Professor of Genetics, with a secondary appointment in Computer and Information Science, at the University of Pennsylvania. ISMB 2000 is the Eighth Annual International Conference for the latest developments in bioinformatics. It will be held August 19 - 23 on the University of California campus in San Diego. Searls's talk is among the seven keynote addresses to be given by noted biologists, including Nobel prizewinner Gerald Edelman and Leroy Hood, another bioinformatics pioneer. ISMB2000 Keynote Talks:

- Gerald Edelman, The Neurosciences Institute, La Jolla, CA How Matter Becomes Imagination: From Brain Dynamics to Consciousness
- Leroy Hood, Institute for Systems Biology, Seattle, WA Globally Deciphering and Integrating Information Expressed by Living Organisms
- Minoru Kanehisa, Institute for Chemical Research, Kyoto University, Japan Graph Comparison and Path Computation Methods for Predicting Molecular Networks from Genome Information
- J. Andrew McCammon, Chemistry and Biochemistry, UC San Diego, CA, Dynamics of Molecular Recognition
- Gene Myers, Celera Genomics Corporation, Rockville, MD A Whole Genome Assembly of Drosophila and a Progress Report on the Human Genome
- Harold A. Scheraga, Chemistry and Chemical Biology, Cornell University, NY Ab Initio Folding of Proteins
- David B. Searls, GlaxoSmithKline Reading the Book of Life

ISMB2000 will also feature the presentations of more than 40 research papers and more than 300 posters, as well as software demonstrations, exhibits by vendors and researchers, and pre- and post-conference forums. Phil Bourne of the San Diego Supercomputer Center (SDSC) (<http://www.sdsc.edu>), co-chair with Michael Gribskov of ISMB 2000, says the conference "is shaping up to be a very important meeting, coming as it does immediately upon the milestone announcement by the Human Genome Project and Celera." For registration information and a detailed agenda of the event, please refer to the website, (<http://ismb2000.sdsc.edu>), or contact Nancy Jensen, SDSC, [jensenn@sdsc.edu](mailto:jensenn@sdsc.edu), 858-534-5039.

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#### SEARCH FOR NEW NIH BIOINFORMATICS DIRECTOR

A search is underway for the directorship of a new NIH office. The Office of Bioengineering, Bioimaging and Bioinformatics is newly formed within the office of the NIH Director. Information about the position is available at <http://www1.od.nih.gov>

</ohrm/hrinfo/ses/vacancy/announcement/OD-Dir-OBBB.htm> If you are interested or if you know of anyone who would be uniquely qualified (and might be convinced to apply) for this position, contact Jeffery A. Schloss, Ph.D., e-mail: [jeff\\_schloss@nih.gov](mailto:jeff_schloss@nih.gov), who will forward the application to the search committee. Should you have any question about the job, you may also contact Dr. Schloss. -Jeffery A. Schloss, Ph.D.  
Program Director  
Technology Development Coordination  
National Human Genome Research Institute  
National Institutes of Health  
e-mail: [jeff\\_schloss@nih.gov](mailto:jeff_schloss@nih.gov)

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#### **FIRST SCANDINAVIAN EMBOSS WORKSHOP EMBnet**

Norway and Bioinformatics Forum in Bergen will conduct the first Scandinavian EMBOSS workshop on September 4-5, 2000 in Bergen, Norway. The EMBOSS suite is a freely available open source package of libraries and applications for bioinformatics. Developed over the last few years by EMBnet with many of the developers responsible for EGCG, EMBOSS is a public licensed standalone package that can be readily integrated into existing workflows and user interfaces without the need for inflexible proprietary packages. The workshop is aimed at three target participants:

- Those who wish to set up and configure EMBOSS on their own site
- Those who wish to develop new bioinformatics applications using the EMBOSS libraries
- Those who wish to use EMBOSS for bioinformatic analysis

All inquiries should be directed to workshop organizer Dr. David Martin ( [admin@embnet.uio.no](mailto:admin@embnet.uio.no) ) of the Norwegian EMBnet node at the Biotechnology Centre of Oslo, or visit the website: <http://www.no.embnet.org/Courses/emboss.php3>

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#### **PROTOMAP NEEDS YOUR FEEDBACK**

ProtoMap (<http://protomap.stanford.edu>) is an automatic hierarchical classification of all protein sequences in the SWISSPROT and TrEMBL databases.

- Classification of SWISSPROT 38 and TrEMBL 12
- Online classification of new protein sequences.
- Over 10,000 multiple alignments
- Links to more than 100,000 3D models (from the BioSpace website)

The third release offers the classification of SWISSPROT and TrEMBL databases up to December 1999 with a total of 365174 proteins. Sequences can also be submitted via the website for online classification. A new mirror site (that will be the main site starting January 2001) at <http://protomap.cornell.edu> will be released in the next few weeks. You are invited to check out the site and offer feedback about the classification and the tools developed to present the results.

- Golan Yona

Department of Structural Biology

Stanford University

<http://csb.stanford.edu/golan/>

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#### **GENOME INITIATIVE SEEKS COMMENTS**

A review paper (<http://biodatabases.com/whitepaper.html>) on Database Mining in the Human Genome Initiative has recently been written in the spirit of Open Source software. Comments and updates are requested by the authors in order to define and shape the future of the Initiative. The Human Genome Initiative is an international research program for the creation of detailed genetic and physical maps of the human genome. Genome research projects generate enormous quantities of data. Database mining is the process of finding and extracting useful information from raw datasets. Computational genomics has identified a classification of three successive levels for the management and analysis of genetic data in scientific databases: genomics, gene expression and proteomics. For further correspondence, please contact:

Sylvain Henry

[henry@biodatabases.com](mailto:henry@biodatabases.com)

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**CALL FOR PAPERS ON DISCRETE APPLIED MATH**

This is a new call for papers in Computational Molecular Biology Series of "Discrete Applied Mathematics" Submission deadline for the next volume is November 1, 2000 Manuscripts are solicited for a volume of "Discrete Applied Mathematics" on topics concerning the development of new combinatorial and algorithmic techniques in computational molecular biology. This volume will be the fourth in the Computational Molecular Biology Series of Discrete Applied Mathematics, which publishes papers on the mathematical and algorithmic foundations of the inherently discrete aspects of computational biology. The traditional partnership of mathematics and physics has advanced and enriched both disciplines. In a similar partnership, mathematics and algorithms have become crucial tools in the rapid advancement of molecular biology. At the same time, the computational challenges of these biological disciplines raise exciting new problems in discrete mathematics and theoretical computer science. Further information on the series is available from:

<http://www.elsevier.nl/mcs/dam/Menu.html> (The Netherlands)

<http://www.cs.sandia.gov/~scistra/DAM> (USA)

<http://www.math.tau.ac.il/~shamir/dcb.html> (Israel)

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**STRUCTURAL GENOMICS CONFAB SEPT 20-22, 2000**

"Structural Genomics: From Gene to Structure to Function" conference will be held at Robinson College, Cambridge, UK on September 20-22, 2000. Structural Genomics promises to be one of the most important subjects in the post-genome sequencing era. This conference is one of the first of its kind to be held in Europe. The conference aims to discuss the major issues and developments related to Structural Genomics, including target selection, protein expression, functional genomics, structure determination and bioinformatics. Information regarding speakers, registration and other details of the conference can be found on the web site: <http://www.mgms.org/cambs2000> Bursaries For Young European Scientists Attention is drawn to the availability of funding from the European Union Framework V programme for young researchers (aged 35 and under) who wish to attend the conference. The bursaries will cover conference registration, accommodation and meals, and will additionally include a contribution towards travel costs (up to a maximum of 300 pounds). Further details, and an application form, can be found on the web site: <http://www.mgms.org/cambs2000/grants.html>

- Robert B. Russell, Bioinformatics

SmithKline Beecham Pharmaceuticals

e-mail: [russelr1@mh.uk.sbphrd.com](mailto:russelr1@mh.uk.sbphrd.com)

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**CALL FOR PAPERS RECOMB 2001**

FIRST CALL FOR PAPERS FIFTH ANNUAL INTERNATIONAL CONFERENCE ON COMPUTATIONAL MOLECULAR BIOLOGY (RECOMB 2001) April 21-24, 2001

Montréal, Canada Organized by

Centre de recherches mathématiques

Université de Montréal Sponsored by

ACM (Association for Computing Machinery) - SIGACT with support from

Celera Genomics

Compugen

IBM Corporation

International Society for Computational Biology

SLOAN Foundation

SmithKline Beecham

US National Science Foundation

US Department of Energy <http://recomb2001.gmd.de> The Fifth Annual Conference on Research in Computational Molecular Biology (RECOMB 2000), sponsored by the Association for Computing Machinery Special Interest Group on Algorithms and Computation Theory (ACM-SIGACT) with support from the SLOAN Foundation, US Department of Energy, US National Science Foundation, SmithKline Beecham, IBM Corporation, Compugen and ISCB will be organized by Centre de recherches mathématiques, Université de Montréal, in Montreal, Canada on April 20-24, 2001. The conference will be held at the Wyndham Montréal Hotel. Papers reporting on original research (both theoretical and experimental) in all areas of computational molecular biology are sought, including surveys of important recent results/directions. Typical but not exclusive topics of interest include:

- Genomics,
- Molecular sequence analysis,
- Recognition of genes and regulatory elements,
- Molecular evolution,

- Protein structure,
- Gene Expression,
- Gene Networks,
- Computational proteomics,
- Functional genomics.

**ABSTRACT SUBMISSION:** Authors are encouraged to submit their abstracts ELECTRONICALLY. Electronic submission instructions can be found at <http://sigact.csci.unt.edu/~recomb01/RECOMB2001.html>. Authors who are unable to do so are requested to send 10 copies (preferably two sided copies) to:

*Prof. Dr. Thomas Lengauer*

*Program Chair RECOMB 2001*

*Institute for Algorithms and Scientific Computing*

*GMD - German National Research Center for Information Technology*

*Schloss Birlinghoven*

*53754 Sankt Augustin*

*Germany*

*Tel: +49 2241 14 2777*

*Fax: +49 2241 14 2656*

[lengauer@gmd.de](mailto:lengauer@gmd.de)

Abstracts must be received by September 30 2000, 23:59 local time. This is a firm deadline. Simultaneous submission to another conference or journal is allowed. Authors are asked to inform the program chair at the time of submission of the simultaneous submission. **CONFERENCE PROCEEDINGS:** The extended abstracts for the Conference will be published by ACM Press and will be available at the Conference. If the paper has been accepted to another conference or a journal before RECOMB 2001, the authors will be allowed only a short abstract (1 page) in the proceedings of RECOMB 2001 and not an extended abstract. A selection of the accepted extended abstracts in their final journal versions will be invited to appear in a special issue of the Journal of Computational Biology devoted to RECOMB 2001. **NOTIFICATION:** The conference submissions will be refereed by the program committee. Authors will be notified of acceptance or rejection by a letter mailed on or before December 8, 2000. A final copy of each accepted paper is required by January 5, 2001. An author of each accepted paper is expected to attend the Symposium and present the paper; otherwise alternative arrangements should be made to have the paper presented. **ABSTRACT PREPARATION:** An abstract should start with a succinct statement of the problem, the results achieved, their significance and a comparison with previous work. This material should be understandable to non-specialists. A technical exposition directed to the specialist should follow. The length, excluding cover page and bibliography, should not exceed 10 pages. The manuscript should be easy to read, using at least 11 point font size on U.S. standard 8 1/2 by 11 inch paper with no less than one inch margin all around. If authors believe that more details are absolutely necessary to substantiate the claims of the paper, they may include a clearly marked appendix. An E-mail address for the contact author should be included. Abstracts that deviate significantly from these guidelines risk rejection without consideration of their merits. **POSTERS:** RECOMB 2001 will include a poster session. Accepted posters will appear in a special poster book published by the Centre de recherches mathématiques. Poster submission instructions will be announced later. **CONFERENCE EVENTS:** RECOMB 2001 will feature 9 Plenary Lectures (to be announced later) including the following conference events: The Stanislaw Ulam Memorial Computational Biology Address: awarded by RECOMB to a scientist who has made major contributions in the computational aspects of the field. The Distinguished Biology Lecture: awarded by RECOMB to a scientist who has made major contributions in the biological aspects of the field. The Distinguished New Technologies Lecture: describing emerging, new technologies. Best Paper by a Young Scientist Award: This award will be given to the best paper written solely by one or more recent graduates or students. An abstract is eligible if all authors are recent graduates (within 3 years from Ph.D.) or full-time students at the time of submission. This should be indicated in a letter to the program chair that accompanies the submission. The program committee may decline to make the award or may split it among several papers. The Conference occasionally awards the "Fred Howes Distinguished Service Award Lecture" in recognition of exceptional service on behalf of the Computational Biology community. **CALENDAR:**

Deadline for submission of papers: Sep 30, 2000

Notification of acceptance/rejection: Dec 5, 2000

Deadline for reception of final papers: Jan 5, 2001

#### STEERING COMMITTEE:

Sorin Istrail, RECOMB General Vice-Chair

Richard Karp

Thomas Lengauer

Pavel Pevzner, RECOMB General Chair

Celera Genomics, Rockville, MD, USA

University of California, Berkeley, CA, USA

GMD-SCAI, Sankt Augustin, Germany

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Ron Shamir	Tel-Aviv University, Tel Aviv, Israel
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Ron Shamir	Tel Aviv University, Tel Aviv, Israel
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Terry Speed	University of California, Berkeley, CA, USA
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Ralf Zimmer	GMD, Sankt Augustin, Germany

## ORGANIZING COMMITTEE:

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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 monthly. 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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