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ISCB NEWSLETTER April 30, 1999
Volume 2, Number 3

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1) PACIFIC SYMPOSIUM ON BIOCOMPUTING (PSB 2000) DATA MINING AND DISCOVERY IN MOLECULAR DATABASES

(Call for Papers)
A Full List of Tracks at PSB 2000 can be Found at:
http://www.cgl.ucsf.edu/psb/
This announcement solicits papers for a special track to be held as part of the Pacific Symposium on Biocomputing (PSB-2000). The track will focus on the automated process of discovery of novel and useful patterns or motifs in molecular databases. A primary objective of the session will be on the mining of sequence and structure databases in order to gain an increased understanding of the underlying relationships among sequence, structure and function. Papers should describe the underlining computational techniques that were performed. Preference will be given to papers that apply and evaluate novel data mining techniques to real molecular databases. Of particular interest are applications in areas such as protein structure prediction and drug design. As well, papers that discuss the advantages/limitations of alternative computational methods to the mining of molecular data will be considered.
Co-chairs:

Janice Glasgow, Queen's University (janice@qucis.queensu.ca)
Igor Jurisica, University of Toronto (juris@cs.toronto.edu)
Raymond Ng, University of British Columbia (rng@cs.ubc.ca).

Deadlines:

** July 12 - papers due to PSB-00 as above
** Aug 27 - final paper decisions announced
** Sept 24 - camera ready papers due
** Oct 1 - poster abstracts due (after this date, posters will be accepted on a space available basis; space will be limited especially for interactive/computational posters after this date)

Submission Requirements:

All papers must be submitted to altman@smi.stanford.edu in electronic format. The file formats we accept are: postscript (*.ps), adobe acrobat (*.pdf) and Microsoft Word documents (*.doc). Attached files should be named with the last name of the first author (e.g. altman.ps, altman.pdf, or altman.doc). Hardcopy submissions or unprocessed TEX or LATEX files will be rejected without review.

Each paper must be accompanied by a cover letter. The cover letter must state the following:

* The email address of the corresponding author.

* The specific PSB session that should review the paper or abstract.

* The submitted paper contains original, unpublished results, and is not currently under consideration elsewhere.

* All co-authors concur with the contents of the paper.

Submitted papers are limited to twelve (12) pages in our publication format. Please format your paper according to instructions found at ftp://ftp-smi.stanford.edu/pub/altman/psb/. If figures can not be easily resized and placed precisely in the text, then it should be clear that with appropriate modifications, the total manuscript length would be within the page limit. Color pictures can be printed at the expense of the authors. The fee is $500 per page of color pictures, payable at the time of camera ready submission.

2) ACADEMIC PRESS DISCOUNT

Academic Press is pleased to offer International Society for Computational Biology members 15% off a select group of books, including just released titles such as:

-PCR Applications
-Protocols for Functional Genomics
-Genetics Databases
-Practical Protein
-Crystallography, 2nd ed.
-Statitistics in Medicine

Simply go to *http://www.academicpress.com/lifesci/iscb.htm* for full details on each title and ordering instructions.

Hurry! This exclusive offer expires June 15, 1999.

3) FELLOWSHIPS IN COMPUTATIONAL BIOLOGY

** Fellowships in Computational Biology **
** Section on Molecular Statistics and Bioinformatics **
** National Cancer Institute **

April 19, 1999 --- Please distribute widely

Applications are invited for two anticipated research fellowships in computational approaches to understanding the molecular nature of cancer. One position is specifically dedicated to developing tools and techniques for analyzing gene expression data from the National Cancer Institute's Advanced Technology Center. The other position is more open-ended, intended for researchers interested in any aspect of the development and application of advanced machine learning or statistical techniques in the molecular biology of cancer.

The positions will be in the section on Molecular Statistics and Bioinformatics, a recently formed group under the leadership of Dr. Lawrence Hunter. We are machine learning researchers, statisticians, molecular biologists and physicians working to develop computational methods to take advantage of the rapid growth of molecular biological data about cancer, including sequences of oncogenes, gene expression profiles of neoplastic tissues, high throughput screening of anti-tumor compounds, and allellic variation assays such as SNPs. The lab has abundant computational resources, and ready access to all NIH facilities. Candidates should be highly motivated, with excellent programming and writing skills, and a solid understanding of molecular biology. We expect to fill these positions with post-doctoral researchers, but good candidates at more junior or more senior levels may be accommodated. Salaries will be on

To apply, send a CV, one or two (p)reprints, a brief description of your motivations and goals, and the names, email addresses and phone numbers of at least three references to the address below. Email is preferred, but fax or mail applications are also acceptable.

Larry Hunter
Molecular Statistics and Bioinformatics
National Cancer Institute, MS-9105
7550 Wisconsin Ave., Room 3C06
Bethesda, MD 20892-9015

tel: +1 (301) 402-0389
fax: +1 (301) 480-0223
email: lhunter@nih.gov

4) CALL FOR ISMB'99 POSTERS AND SOFTWARE DEMONSTRATIONS

DEADLINE: May 28, 1999
NOTIFICATION: June 10, 1999

ATTEND ONE OF THE PREMIER INTERNATIONAL MEETINGS IN BIOINFORMATICS AND ENJOY THE RARE SIGHT OF A TOTAL SOLAR ECLIPSE

The Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB '99) announces a call for posters and software demonstrations. The conference will take place in Heidelberg, Germany on August 6 - 10, 1999. For more information on the conference visit the web site.

http://ismb99.gmd.de POSTERS:

Please send a one-page abstract by the above deadline. We only accept electronic submissions (PS or PDF format). Please use font size at least 10pt and format to fit European Standard A4 but make sure that all of the text is also displayed in US letter size. Please include the following information in this order: title, author(s), affiliation, email address in the header, then followed by the abstract text and completed with a list of references.

Please send all of this information to ismb99@gmd.de

The actual poster space will be 190x100 cm (HEIGHT x WIDTH). A booklet with the accepted poster abstracts will be available at the conference.

SOFTWARE DEMONSTRATIONS:
If you represent an academic group you can present your software at our university booth. We intend to set one table including space for a temporary poster (for the time of demonstration) aside for software demonstrations. The table will feature electricity and network connection as well as a large monitor screen. The default will be for you to bring your own laptop for the presentation. A time schedule for software demonstrations will be prepared ahead of the conference. If you want to demonstrate your software, please send a one-page abstract describing your system, adhering to the guidelines for posters. In your email sending the abstract, please qualify your contribution as a software demonstration.

DEADLINE: May 28, 1999
NOTIFICATION: June 10, 1999

5) WASHINGTON UNIVERSITY INTENSIVE SHORT COURSE FOR COMPUTATIONAL MOLECULAR BIOLOGY

Dates: July 26 to 30th, 1999

http://www.ibc.wustl.edu/CMB/shortcourse99.html

The faculty of the computational molecular biology program at Washington University in St. Louis offers an introduction to computational molecular biology as a 5 day intensive short course. The course combines an introduction to the theory and practice of molecular sequence analysis with an intensive session on programming in PERL. The course is offered at a graduate level and is intended to be accessible to professional scientists in molecular biology and biotechnology. Our aim is to provide an understanding of how and why different analytic approaches are used including their limitations as well as capabilities. We emphasize the use of public domain software tools rather than focusing on a specific commercial package. The PERL programming sessions are offered in two sections one targeted to professional software developers and the other to scientists with a limited background in computer programming.

The format is a 5-day course with 6 hours of class time each day (3 hrs. in the morning and 3 hrs in the afternoon) for a total of 30 contact hours. The course (BME-72-537A) is offered through the Washington University Summer School and carries two units of graduate credit at Washington University. It is an intensive and challenging course that covers most of the material offered in our regular graduate course on computational biology in a format that is accessible to working scientists as well as faculty and staff with interests in learning new technology.

A CD-ROM containing course lecture notes, problem sets, programming exercises, public domain software and reference material will be distributed. All students are asked to bring a laptop computer (Windows/Intel) for use in the programming sessions.

Faculty Department

David States Institute for Biomedical Computing
Michael Zuker Institute for Biomedical Computing
Volker Nowotny Institute for Biomedical Computing
Warren Gish Department of Genetics

Location: Newman Educational Center, Washington University in St. Louis

To register for this course you must bring in or fax your registration form to the continuing Education Department at Washington University. Forms can be obtained from:

Washington University
Continuing Education Department
Lopata Hall #303
Campus Box 1220
St. Louis, MO 63130
Phone: 314-935-5484
Fax: 314-935-5449
http://www.seas.wustl.edu/classes/SumSchl98.html