ISCB NEWSLETTER

ISMB 2002 FOCUS ISSUE

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INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

A NOTE FROM ISCB PRESIDENT *Phil Bourne*

This newsletter is packed with information on the ISMB2002 conference. With over 200 paper submissions and over 500 poster submissions, the conference promises to be a scientific feast. On behalf of the ISCB's Directors, staff, and membership, I would like to thank the organizing committee, local organizing committee, and program committee for their hard work preparing for the conference. Having co-chaired ISMB 2000, I know how much effort must be directed away from research and teaching to make ISMB happen. Thank you.

In the previous newsletter, the Society's history was discussed *(www.iscb.org/newsletter5-1/history.html)*. The article describes how the Society began as a means to manage the ISMB meeting. ISCB now plays many more roles to support our science worldwide. Since I suspect many members are unaware of how these roles are carried out, let me elaborate a little here. This is particularly timely information, as ISCB is actively seeking nominations from interested scientists to volunteer their time, help run the Society, and make a difference to our science.

As the column to the left shows, the Society consists of an Executive Committee, Board of Directors, and Society staff. Not shown, are the individual committees which can be found at *www.iscb.org/committees.shtml*. The Executive Committee holds a monthly teleconference to discuss issues important to the development and dissemination of bioinformatics. Issues arise from recommendations made by the Society's committees, Board of Directors, and membership at large. Important issues are defined as motions and are discussed by the Board of Directors on a bi-monthly teleconference. Motions that pass are enacted by the Executive Committee which also serves as an oversight body for the Society office and staff. I meet with the Society staff once a week and am continuously in contact via email to track progress and to help as needed.

Much of the work for the Society is done in committees; members are encouraged to contact committee chairs or to join committees to actively share their ideas with the entire Society. Members who wish become more officially involved may seek nomination to the Board or Executive Committee by writing to *nominations@iscb.org*. Board members are elected by the existing Board for a three year term, whereas Executive Committee members are elected for two years by the membership.

With elections occurring in the fall; now is the time to step forward and become involved. ISCB is particularly interested in involving young scientists and those from regions of the globe where bioinformatics is emerging. I am be happy to address questions members have about becoming involved either now by email *(admin@sdsc.edu)* or in person at ISMB 2002.

ISCB Staff *(clockwise from the far left)*: Josh Polterock, Cassie Ferguson, BJ Morrison McKay, Stephanie Hagstrom, Jennifer Matthews, Tracy Zhao, Chris Smith, Phil Bourne, (*not pictured:* Kim Baldridge)

EXECUTIVE COMMITTEE

Philip E. Bourne, Ph.D., *President*
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Cassie Ferguson, *Writer*
Stephanie Hagstrom, *Conference Coordinator*
Jennifer Matthews, *Design*
BJ Morrison McKay, *Administrative Officer*
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Chris Smith, Ph.D. *Finance*
Tracy Zhao, *Programming*

REGISTER NOW FOR ISMB 2002

ISMB 2002 Registration Now Open

www.ismb02.org/regis.htm

Save US$100 by registering by June 28, 2002. Note: previous ISMB conferences have sold out one week after the early registration date.

Registration Fees

The conference fees include all scientific sessions, poster session, exhibit hall entrance, breakfasts, lunches, receptions, and one copy of the ISMB 2002 proceedings.

On or Before June 28, 2002

Academia: US$415 (ISCB members)
US$480 (Non-ISCB members)

Student: US$300 (ISCB members)
US$350 (Non-ISCB members)

Corporate: US$650 (ISCB members)
US$715 (Non-ISCB members)

After June 28, 2002

Academia: US$515 (ISCB members)
US$580 (Non-ISCB members)

Student: US$400 (ISCB members)
US$450 (Non-ISCB members)

Corporate: US$750 (ISCB members)
US$815 (Non-ISCB members)

ISMB Registration

Phone: +1-847-518-1708
Fax: +1-847-518-0735

Tutorial Sessions *(August 3, 2002)*

Individuals may register for one or two optional tutorials. There will be maximum seven (7) concurrent sessions in the morning and eight (8) maximum concurrent sessions in the afternoon. Please note: Tutorials may only accommodate a limited number of participants, consequently, some tutorials may sell out. It is recommended that participants sign up as soon as possible.

Price for one tutorial: US$85
Price for two tutorials: US$130

For more information about the ISMB 2002 tutorials, visit *www.ismb02.org/tutorial.htm*.

Morning Tutorials *(8:30-12:30)*

- *Introduction to Perl Programming for Bioinformatics.* Instructor: James Tisdall
- *Introduction to Computational Sequence Analysis.* Instructor: Frédérique Galisson
- *Molecular Modeling: Building a 3-D Protein Structure from Its Sequence.* Instructor: Shoba Ranganathan
- *DNA Microarrays and Gene Regulation.* Instructor: Pierre Baldi
- *Relational Databases for Biologists.* Instructors: Aaron Mackey and William R. Pearson
- *A Primer on Metabolic Pathway Analysis.* Instructor: Eberhard O. Voit
- *Information Extraction from Biomedical Literature.* Instructor: Dietrich Schuhmann, et. al.

Afternoon Tutorials *(13:30-17:30)*

- *Perl and Bioperl: Tools for Automated Analysis of Biological Sequence Data.* Instructor: Peter Schattner
- *Pattern Discovery in Biosequences.* Instructor: Stefano Lonardi
- *Protein Classification and Meta-organization. Methods for Global Organization of the Protein Universe.* Instructor: Golan Yona
- *In silico Analysis of Gene Regulatory Sequences. Towards Target Gene Identification.* Instructors: Alexander Kel and Edgar Wingender
- *Functional Genomics in 4 Hours: A Practical Guide to Creating Your Own High-Throughput Pipeline.* Instructors: Atul Butte and Isaac Kohane
- *Heterogeneous Data and Algorithm Integration in Bioinformatics.* Instructors: Barbara Eckman, Julia Rice, and William Swope
- *Modelling Biological Data in Hierarchies.* Instructors: Graham Kemp and Peter Gray
- *Comparative Genomics.* Instructor: David Sankoff

REQUEST FOR PROPOSALS TO HOST THE ISMB 2004 AND 2005 CONFERENCES

ISCB is now accepting proposals from potential organizing committees to host future ISMB conferences. Submissions must be received by July 19, 2002. For more information, please access the ISCB website conference page *(www.iscb.org/conferences.html)* or contact Stephanie Hagstrom: *shagstrom@iscb.org*.

CONTACT INFORMATION

ISCB questions, comments, and suggestions may be posted to:

ISCB c/o San Diego
Supercomputer Center
UC San Diego
9500 Gilman Drive
La Jolla, CA 92093-0505 USA

phone: +1-858-822-0852
email: *admin@iscb.org*
internet: *www.iscb.org*

For specific queries, please refer to the following:

Membership:
membership@iscb.org
Corporate:
corporate@iscb.org
Sponsorship:
sponsorship@iscb.org

2002 OVERTON PRIZE

David Baker

The ISCB thanks the following individuals for all their support, dedication, and commitment to producing to the ISMB 2002 conference.

ISMB 2002 ORGANIZING COMMITTEE

David Wishart (Chair), *University of Alberta, Canada*

Søren Brunak, *Technical University of Denmark, Denmark*

Julio Collado-Vides*, *National Autonomous University of Mexico, Mexico*

Frédérique Galisson*, *University of Lausanne, Switzerland*

Warren Gallin, *University of Alberta, Canada*

Janice Glasgow*, *Queen's University, Canada*

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François Major, *University of Montreal, Canada*

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ISMB 2002 LOCAL ORGANIZING COMMITTEE

David Wishart (Chair), *University of Alberta, Canada*

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Bob Parker, *University of Alberta, Canada*

Mark Ragan, *University of Queensland, Australia*

Karim Sayani, *BioAlberta, Canada*

Haiyan Zhang, *University of Alberta, Canada*

** also a member of the ISMB 2002 Scientific Committee*

The Overton Prize was established by the ISCB in memory of G. Christian Overton, a major contributor to the field of bioinformatics and member of the ISCB Board of Directors who died unexpectedly in 2000. The prize is awarded for outstanding accomplishment to a scientist in the early- to mid- stage of his or her career who has already made a significant contribution to the field of computational biology through research, education, service, or a combination of the three. The first Overton Prize was awarded last year to Christopher Burge of the Massachusetts Institute of Technology for his work identifying and modeling genes in higher eukaryotic organisms.

The 2002 Awards Committee was chaired by David States, and included Donna Slonim, Søren Brunak, Mike Waterman, Anders Krogh, and Larry Hunter. In March 2002, members of the Society were invited to submit nominations to the Awards committee for the 2002 Overton Prize. Nominees from around the globe were considered. Several outstanding nominations were received, highlighting the growing talent in bioinformatics.

The Awards Committee unanimously selected David Baker, Howard Hughes Medical Institute (HHMI) Investigator and associate professor at the University of Washington, in recognition of his outstanding contributions in genomics. His computational technique known as the "Rosetta algorithm," predicts protein folds. He continues to extend and apply his work to drug design, genetics, and health care.

2002 Overton Prize Recipient, David Baker
(Photo credit: University of Washington/Mary Levin)

Baker has previously won the HHMI's Assistant Investigator Award, as well as Young Investigator Awards from the Protein Society, the Beckman Foundation, and the National Science Foundation. Since 1988, Baker has established a record of publications in protein folding and outstanding structure prediction using both computational and experimental approaches.

Baker will present a keynote address at this year's Intelligent Systems for Molecular Biology (ISMB) conference in Edmonton, Alberta, Canada, on Wednesday, August 7th, the final day of the conference.

OVERTON PRIZE ENDOWMENT OPPORTUNITIES

ISCB continues to solicit contributions toward the endowment of the annual Overton Prize. Contributions at the level of $5,000 will be acknowledged as Principal Sponsors and all contributions at the level of $1,000 or more will be acknowledged as Sponsors in a brochure distributed at each years award of the prize. The ISCB is a tax-exempt organization and contributions are tax deductible.

ISMB 2002 SPONSORSHIP & EXHIBITOR OPPORTUNITIES

ISMB 2002 is the premiere event in computational biology and is known as an outstanding opportunity for vendors and exhibitors to highlight their products. To maximize exhibitor exposure, the ISMB 2002 Conference Exhibition will be held together with the conference's poster sessions. The combination of poster sessions, food courts and high quality exhibition space will ensure maximal exposure for your company at this year's conference.

To obtain additional information on how to participate in the ISMB conference as a sponsor, please visit: *www.ismb02.org/corporate.html*, or contact Stephanie Hagstrom, ISCB +1-858-623-0050 or *sponsorships@iscb.org*.

ISMB 2002 Sponsors and Exhibitors to date:

Platinum Sponsors

- Hewlett-Packard
- IBM Life Sciences

Gold Sponsors

- Alberta Government: Ministry of Innovation and Science
- GeneData
- Gene Logic
- Genome Prairie
- ICORE
- LionBioscience
- SGI
- Sun Microsystems
- University of Alberta

Silver Sponsors

- Accelrys, Inc.
- University of Calgary

Conference Supporters/Travel Fellowship

- Alberta Government: Alberta Science and Research Authority
- Alberta Heritage Foundation for Medical Research
- Hewlett-Packard
- IBM Life Sciences
- International Society for Computational Biology
- National Institute of Health
- National Science Foundation
- PENCE The Canadian Protein Engineering Network
- Structural Genomix, Inc.
- University of Alberta
- US Department of Energy

Exhibiting Companies

- American Medical Informatics Association
- Biomax Informatics AG
- Cambridge University Press
- Institute of Biomolecular Design, Project Cybercell
- ExerGen
- InforSense
- John Wiley & Sons
- O'Reilly & Associates
- Platform Computing, Inc.
- Protein Data Bank
- Science Factory GMBH
- Silicon Genetics
- Spotfire, Inc.
- The MIT Press

ISMB BEST PAPER AWARD BY SGI

The ISMB Best Paper Award by SGI will be presented to an outstanding paper submitted to ISMB 2002. The finalists are:

- Pier Luigi Martelli, Piero Fariselli, Anders Krogh, Rita Casadio: *A sequence profile based HMM for predicting and discriminating beta barrel membrane proteins*
- Daniel Fasulo, Aaron Halpern, Ian Dew, Clark Mobarry: *Efficiently Detecting Polymorphisms During The Fragment Assembly Process*
- Gianluca Pollastri, Pierre Baldi: *Prediction of Contact Maps by Recurrent Neural Network Architectures and Hidden Context Propagation From All Four Cardinal Corners*

Initial nominations were provided by the program committee and senior reviewers for the conference. The three finalists were chosen by the committee's co-chairs after reviewing all nominations. The winner will be selected by a subset of the senior review committee based on the written paper as well as oral presentation at the conference. The award will be presented after the final session of ISMB.

ISMB 2002 SPECIAL INTEREST GROUP MEETINGS

Over the past 10 years, a number of smaller, more specialized meetings in computational biology have become regularly associated with the ISMB annual meetings. ISMB is pleased to have several special interest group meetings associated with the 2002 conference.

Bioinformatics Open Source Conference (BOSC): August 1-2 (9:00-17:00) *Westin Hotel*
BOSC is a two-day conference focusing on the development of open source software for the life sciences. Keynotes will be delivered by Michael Eisen, Winston Hide, and Ewan Birney. Leaders from many of the major open source toolkit projects will present progress reports and current applications of their toolkits. Additionally, the conference will include technical talks, a poster session, mini-tutorials, and software demonstrations, and Birds of a Feather gatherings to discuss specialized interests. More information (including a full speaker list) is available at *www.open-bio.org/bosc2002/*.

Biopathways: August 1-2 (9:00-17:00) *Westin Hotel*
The fourth BioPathways is organized by the BioPathways Consortium, an open forum to fostering computational approaches to the modelling, reconstruction, analysis, and simulation of biological networks. This year's meeting will include three plenary sessions, with respective focuses on: (1) continuous models for pathways representation, (2) pathways reconstruction, and (3) experiment design driven by pathways models ("systems biology" approaches). An industry session will feature presentations of applied work in industrial settings. Each session will include several long presentations (45 minutes), followed by a panel discussion. One of the aims of this year's meeting is to promote interaction between the physics and engineering communities, and the computer science and biology communities.

Text-Mining: August 2 (9:00-17:00) *Westin Hotel*
This text-mining meeting has two purposes. The first is to bring together researchers developing text data mining tools and related language processing methods to manage the information explosion in the biomedical field. This part of the meeting will include invited and contributed papers, with a focus on developing shared infrastructure (tools, corpora, ontologies) and challenge evaluations, in the style of the KDD Challenge Cups (KDD Cup 2002). The second part of the meeting will be a discussion focusing on the establishment of a formal SIG for text data mining.

Special Interest Group for Biological Simulation (SIGSIM02): August 3 (9:00-17:00) *Shaw Conference Centre*
The construction of computer-made cell models and the conduction of "*in silico* experiments" may become one of the most important paradigms of biology in this century. SIGSIM is a group of scientists whose interests are in simulation technologies, computer modeling of biological processes, metabolome analysis and systems biology. This year, SIGSIM will host SIGSIM02: Workshop on Computer Modeling of Cellular Processes. Workshop secretariat: *sigsim02@jtbcom.co.jp*

Bio-ontologies: August 8 (9:00-17:00) *Westin Hotel*
The fifth annual Bio-Ontologies meeting will be held the day after ISMB. Recent meetings have been well-attended and lively affairs. This year's theme is a Semantic Web of Bioinformatics Resources, mirroring the push by the W3C on the Semantic Web. With the current interest in bio-ontologies for marking up knowledge content of our resources, together with the interest in E-Science, our community is well placed to exploit the ideas of the Semantic Web. All bio-ontology activity should be able to fit within this theme. the meeting details and call for abstracts may be found at *img.cs.man.ac.uk/stevens/meeting02*. Additional information may be requested by emailing *robert.stevens@cs.man.ac.uk*.

Workshop on Education in Bioinformatics (WEB02): August 8 (9:00-17:00) *Westin Hotel*
The second annual WEB02 will cover topics in Bioinformatics Education including curriculum development, infrastructure and resource support and strategies for program initiation and development. There is also a new session on industry needs. In addition to short oral and poster presentation sessions, the workshop will attempt to define a curriculum for bioinformatics at the under-graduate and post-graduate levels. Abstracts are due June 21, 2002. WEB02 invites faculty, students, staff, administrators, and officials in government and industry to participate in this discussion. *surya.bic.nus.edu.sg/web02/*

ISMB 2003 DOWN UNDER

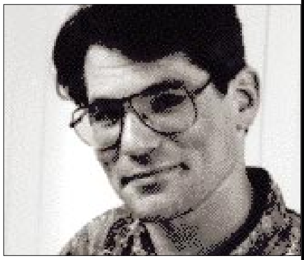
ISMB will venture beyond North America and Europe for the first time when ISMB 2003 convenes in Brisbane, Australia from June 29 to July 3, 2003.

The Institute for Molecular Bioscience, and the Advanced Computational Modelling Centre of the University of Queensland, will serve as local hosts. The venue for the 2003 conference and tutorials will be the Brisbane Conference and Exhibition Centre, Australia's largest purpose-built conference facility, adjacent to the fabulous South Bank parklands and a short walk or ferry-ride across the Brisbane River from the downtown hotel district. The Organizing Committee, co-chaired by Gene Myers (Program Committee) and Mark Ragan (Local Committee), is already hard at work to ensure that the conference will meet the highest scientific, technical and organizational standards and be great fun.

The organizers are excited by the opportunity to bring ISMB to the Asia-Pacific region: Involving new groups of participants from Australia, China, India, Korea, Japan, Malaysia, New Zealand, Singapore, Taiwan, Thailand, and other countries hitherto not fully represented at ISMB.

Brisbane, the capital of Queensland, is a cosmopolitan city of 1.6-1.8 million with three major universities and a growing biotechnology sector. Delegates may fly direct to Brisbane from all major Australian cities as well as Auckland, Bangkok, Brunei, Hong Kong, Jakarta, Kuala Lumpur, Manila, Osaka, Seoul, Singapore, Taipei and Tokyo. Late June/early July is mid-winter in Brisbane, with sunny warm days (average high 20°C = 68°F) and crisp cool nights (average low 10°C = 50°F). A favorable exchange rate will help deliver great value to participants.

World-class tourist destinations easily accessible from Brisbane include the Great Barrier Reef, the Gold Coast, Ayers Rock, and the great Australian outback. Sandy beaches, offshore islands, wet and dry tropical forests, mountains and World Heritage national parks lie within a 1-2 hour drive from downtown.



Gene Meyers
ISMB 2003 Co-Chair

Mark Ragan
ISMB 2003 Co-Chair

Delegates and exhibitors may wish to travel on to the XIX International Genetics Congress in Melbourne (July 6-12: *www.geneticscongress2003.com*) or the Fifth International Congress on Industrial and Applied Mathematics in Sydney (July 7-11: *www.austms.org.au/iciam2003*) immediately after ISMB 2003.

Monitor the ISMB 2003 website at *www.iscb.org/ismb2003* for updates and announcements.

ISMB 2003 ORGANIZING COMMITTEE

Gene Myers, *Celera Genomics* (Co-chair)

Mark Ragan, *Institute for Molecular Bioscience* (Co-chair)

Kevin Burrage, *Advanced Computational Modelling Centre, University of Queensland*

Antoine Danchin, *Pasteur Research Centre, Hong Kong University*

Terry Gaasterland, *The Rockefeller University*

Minoru Kanehisa, *Japanese Society for Bioinformatics, Kyoto University*

Tim Littlejohn, *Biolateral Pty Ltd.*

John Mattick, *Institute for Molecular Bioscience, University of Queensland*

Christos Ouzounis, *European Bioinformatics Institute*

Shoba Ranganathan, *Asia-Pacific BioNet, National University of Singapore*

David Wishart, *University of Alberta*

ISMB 2002

Job Fair

Top Companies! Hot Jobs! Live Interviews! Great Career Content!

The ISMB 2002 Job Fair is designed to benefit employers looking for top talent as well as students and professionals seeking a job. The Job Fair will be held on Sunday August 04 from 10:00 – 14:00 at the Shaw Conference Centre.

ISMB attracts the world's leading industry authorities in bioinformatics as well as students and professionals with exceptional talent, innovation, and future potential in the field.

The Job Fair at ISMB 2002 is designed to facilitate productive connections between company representatives and job seekers. Industry members will be able to meet individuals with competencies that are applicable to their organizations. In addition, rooms will be available for companies to interview potential candidates. Job seekers will have an unparalleled opportunity to meet industry members from leading companies who will all be in one place at one time.

How it all works…

Companies

Companies who sign up for the Job Fair will receive a listing in the conference program with their company name and contact, one six foot draped table to display company collateral materials and two chairs.

Participating companies will also have access to the on-line Job Fair to list their job openings on the ISMB 2002 website. This gives participating companies a link on the website that takes viewers directly to their respective website. The ISMB 2002 website receives up to 1000 hits per day and serves as an excellent resource to reach a highly skilled pool of potential employees.

Companies may also book time blocks at the conference for private interview rooms for any meetings they need to conduct including interviews.

Company representatives may contact candidates directly through the resume postings on ISMB's website *(www.ismb02.org/jobfair2.htm)* or onsite at the Job Fair.

The fee for corporate participation in the Job Fair is US$500. To sign up for the Job Fair visit: *www.ismb02.org/jobfair.htm*

Candidates

Prior to the conference, job seekers may post links to their resume on the ISMB 2002 website (*www.ismb02.org*). Potential employers are encouraged to contact candidates directly to schedule an interview. For resume posting instructions, please visit the ISMB 2002 resume submissions page *(www.ismb02.org/resumesub.htm)*.

Please contact employers directly using the job postings on the ISMB 2002 website *(www.ismb02.org/jobfair2.htm)*. Monitor the job postings page frequently, as new jobs will be added until the commencement of ISMB 2002. Please note: It will be possible to contact corporate representatives onsite at the Job Fair.

Job seekers should attend the Job Fair recruitment event on Sunday, August 4 from 10:00-14:00. Candidates—who are encouraged to bring multiple copies of their resumes—may informally meet with company representatives and sign up for interviews if appropriate. Job seekers may also have a chance to receive additional information about many leading companies in the field of bioinformatics.

There is no fee for candidates who wish to participate in the Job Fair.

For additional information, please contact the Job Fair coordinator, Karim Sayani *(karim@bioalberta.com)*.

LAST CALL FOR NOMINATIONS OF 2003 ISCB OFFICERS AND DIRECTORS

The terms of all ISCB officers and several ISCB directors will end in January 2003, and the Society is soliciting nominations for those positions. The Society is particularly interested in building board membership that represents the geographic diversity and interests of the membership, and seeks nominations from Africa, Asia, Europe and South America. New Officers and Directors will take office in January of 2003, and will serve for up to three years.

All ISCB Members are encouraged to put forward nominees for the President, Vice President, Treasurer, Secretary, and Director positions. Nominations should be sent by e-mail as soon as possible to *nominations@iscb.org*. See the Nominations page of ISCB's website *(www.iscb.org/nominations.shtml)* for further details regarding eligibility, job descriptions, and the nominations process.

ISMB 2002 KEYNOTE SPEAKERS: PIONEERS IN BIOINFORMATICS

ISMB 2002 will continue the tradition of presenting keynote speakers investigating biological questions with innovations in computational science.

Stephen Altschul is a major figure in the development of sequence searching techniques. He has written papers on the appropriate statistical approaches to evaluating sequence alignments. Altschul developed the immensely powerful and flexible sequence searching program BLAST as well as variations on the central idea of BLAST that have improved the sensitivity of the searching process: PHI-BLAST and PSI-BLAST. He is currently a Senior Investigator with the Computational Biology Branch of the National Center for Biotechnology Information (NCBI).

Michael Ashburner has been one of the pre eminent researchers in the study of *Drosophila melanogaster* throughout his career. With the advent of the *Drosophila* genome sequencing initiative, he developed FLYBASE, a powerful annotation platform that integrated new genome sequence data with the corpus of knowledge of genetic, developmental and physiological mechanisms amassed over the last century. Most recently he has been a pivotal player in the development of the Gene Ontology project. He is currently a professor in the Department of Genetics at Cambridge University and a Senior Researcher at the European Bioinformatics Institute (EBI).

Ford Doolittle has studied evolution from a molecular perspective for most of his scientific career. He has been studying evolutionary origins of prokaryotes and eukaryotes, and this includes wrestling with the role of lateral gene transfer between single-celled organisms in evolution and the problems that this lateral transfer raises for current methods of phylogenetic reconstruction. Doolittle is a professor of biochemistry at Dalhousie University and director of the Canadian Institute of Evolutionary Biology.

Terry Gaasterland is a leading figure in the field of automated genome annotation. While at the Argonne National Laboratory and the University of Chicago she developed the MAGPIE annotation system. Since moving to the Rockefeller University, where she is currently an assistant professor, she has initiated development of several other annotation tools. These include HERON, TANGO, EGRET and SANDPIPER, all based on logic-based queries for manipulating semantic information. She is applying these tools to microarray data, phylogenetic inference, and structural biology projects.

Barry Honig has developed many computational tools for studying and modeling protein three dimensional structure. His extensive theoretical treatments of molecular energetics and dynamics are providing new insights into the mechanisms of protein structure, protein-protein interactions, and protein-membrane interactions. As high-throughput structure prediction methods are being developed, Honig's work is at the leading edge of method development and investigating mechanisms of membrane targeting by peripheral proteins and the detailed dynamics of protein-protein association. He is a professor of biochemistry and molecular biophysics at Columbia University.

John Reinitz, associate professor at State University, New York (SUNY) Stonybrook, applies techniques of information theory to the systematic study of embryonic development in *Drosophila melanogaster*. His theoretical treatments of this complex phenomenon are based on experimental determination of the changing concentrations of maternally-derived signaling gene products as the hierarchy of determination develops in the syncytial blastoderm. His efforts have transformed the descriptive analyses of the patterns of individual gene expression into a well-defined, predictive model of information flow during the development of the fundamental body plan.

Isidore Rigoutsos is the manager of the Bioinformatics and Pattern Discovery group at IBM's Computational Biology Center. He developed the Teiresias algorithm, a generalized method for unsupervised pattern discovery. He and his collaborators have implemented this algorithm for a number of biological pattern identification problems and categorization problem covering most of the questions that are current in computational biology. This software initiative is a major part of the IBM BlueGene project in computational biology.

INVITED EDITORIAL

Anna Tramontano

Anna Tramontano, *ISCB Vice President*

I have the honor of being the first female Vice President of the ISCB as well as representing my European colleagues on the Society's Executive Committee. As such, I hope to succeed as efficiently and brilliantly as my predecessors in keeping the Society vital and forward-looking.

I first became interested in computational biology nearly twenty years ago, I took a post-doctoral research fellowship at the University of California, San Francisco's (UCSF) Department of Biochemistry and Biophysics, where I discovered molecular graphics. While at UCSF, my collaboration with Henry Dayringer and Robert Fletterick, yielded the first version of a popular molecular graphics package that is still widely used today. Later, I joined Arthur Lesk's group in the Biocomputing Programme at the European Molecular Biology Laboratory (EMBL) in Heidelberg. The Programme—coordinated by Chris Sander—set in motion the field of computational biology in Europe. Most active research groups in Europe today—as well as a few in other parts of the world—can be traced back to that period and to the many fruitful collaborations computational biologists initiated, over a beer, in the EMBL canteen!

I suppose I was witness to the adolescence of a science leaving infancy. Certainly *in silico* biology is a mature science now experiencing immense popularity. Sudden popularity in the movie business, as well as in science, carries risks. Growing interest in bioinformatics and computational biology may lead to an erosion of the terms caused by the temptation to "jump on the band wagon" for the sake of the resources that are becoming available.

In my view, the Society has a duty to play an active role in minimizing the negative effects of this new celebrity by setting rigorous scientific standards, by expanding our community with the active recruitment of young talented scientists, and by providing them with educational opportunities.

ISMB, the Society's annual meeting, represents the most effective tool for pursuing these goals, through the rigorous selection process for scientific contributions: the organization of tutorials, the visibility of the meeting, and the diversity of scientific interests. The success of the meeting continues to represent a precious and unique resource for the development of bioinformatics and computational biology worldwide.

I am extremely optimistic about the role regional groups can play in the ISCB. As an international society, we have the opportunity to face many situations with different needs and expectations. We need to muster the creativity, wisdom, and cooperation of everyone in the society to ensure we remain engaged, both geographically and scientifically. We must communicate and build strong bonds with local groups and ask for their guidance during these exciting times.

In the few months I have served as Vice President, I have discussed these issues with a very responsive and attentive board of directors. I intend to continue to support these causes and hope that the members of the Society will continue to help me achieve my goals.

ISCB STATEMENT ON BIOINFORMATICS SOFTWARE AVAILABILITY

I. INTRODUCTION

Conditions of bioinformatics software availability are extremely important to the field of bioinformatics. The ISCB, a professional society of 1300 bioinformatics scientists, has discerned significant confusion in recent months regarding the topic of software availability, and is disseminating this statement to clarify several issues regarding software availability, and to make recommendations on software availability policies for government agencies that fund bioinformatics research.

II. RECOMMENDATIONS

1. *The term "open source" has taken on many different meanings. This term creates confusion in discussions of software availability; therefore the term should be carefully qualified to indicate which variation of the open-source model is intended.*
2. *Government agencies that fund bioinformatics research should NOT REQUIRE that software produced with government research funds must be distributed under open-source license (particularly given the ambiguity in the meaning of that term). Because of the complexity inherent in software, no single distribution model is appropriate for all research projects. Government agencies should require clear statements of software availability in grant proposals.*
3. *As reviewers of bioinformatics grant applications, ISCB scientists have noted that these applications often contain confusing or unclear statements regarding the availability of software that will be developed under government grant funds. This statement contains several definitions of software availability that ISCB recommends for use in bioinformatics grant applications. ISCB recommends one of those definitions as a minimal requirement of software availability that funding agencies should require.*

III. ISCB LEVELS OF SOFTWARE AVAILABILITY

The International Society for Computational Biology (ISCB) provides the following definitions of software availability. It is ISCB's intent that these definitions be a standard reference. It is recommended that all software availability be defined in these terms (or specific stated variations thereof) and stated in all publications, grant applications, and other documents that describe software availability.

ISCB recommends that government funding agencies that support bioinformatics research, require a minimum of ISCB Level 0 Availability.

The levels of availability listed here are not meant to be exhaustive. Researchers may want to define variations to these levels, but ISCB strongly suggests that at least Level of Availability be maintained.

For all levels of availability, the licensee must clearly acknowledge the contributions of the author(s) of the original software in all redistributions.

ISCB Level 0 Availability:

a. *For Research Use: The software will be available free of charge, in binary form, on an "as is" basis for research purposes to educational institutions, non-profit research institutes, government research laboratories, and individuals, for non-exclusive use, without the right of the licensee to further redistribute the software.*

b. *For Commercial Use: The software will be available in binary form, on an "as is" basis to commercial institutions, possibly for a fee, for non-exclusive use, without the right of the licensee to redistribute the software.*

ISCB Level 1 Availability ("No fee"):

The software will be available free of charge to all institutions, in binary form, on an "as is basis", for non-exclusive use, without the right of the licensee to further redistribute the software.

ISCB Level 2 Availability ("No fee, source code for research use"):

Same as ISCB Level 1; in addition, source code is available for research use to educational institutions, non-profit research institutes, government research laboratories, and individuals, without the right to redistribute the source code.

ISCB Level 3 Availability ("No fee, source code to all"):

Same as ISCB Level 1; in addition, source code is available to commercial institutions.

ISCB Level 4 Availability ("No fee, unlimited redistribution, with source code"):

The software will be available free of charge to all institutions and individuals, in binary and source-code forms, on an "as is" basis, for non-exclusive use. The licensee may redistribute and/or resell the original software including the source code, and may redistribute and/or resell any modifications or derivative works created by the licensee. The licensee must clearly acknowledge the contributions of the author(s) of the original software in all redistributions.

This statement does not constitute, and should not be construed as, giving legal advice. Nothing in this statement is intended to constitute the giving of legal advice. The reader should consult with counsel before pursuing a course of action in reliance on information contained in this statement.

AFFILIATED REGIONAL GROUPS

Just as ISCB's global membership has increased, new relationships with affiliated regional groups have formed and old partnerships have strengthened. ISCB has started an Affiliated Regional Group Program to promote bioinformatics as a scientific discipline, and increase public and governmental recognition of its importance.

ISCB is pleased to announce the following members of the Affiliated Regional Group Program *(www.iscb.org/affiliates.shtml)*:

- Asia Pacific Bioinformatics Network *www.apbionet.org*
- Boston Area Molecular Biology Computer Types *xanadu.mgh.harvard.edu/bambct/bambct-intro.html*
- Bay Area Bioinformatics *www.bayareabioinformatics.org*
- Bioinformatics-India *www.bioinformatics-india.com*
- Biological Research Information Center of Korea *bric.postech.ac.kr/bricenglish/index.html*
- INBIOS-Bioinformatics Society of India *www.inbios.org*
- Italian Cooperation Group in Bioinformatics *cbm.bio.uniroma2.it/biocomp*
- Japanese Society for Bioinformatics *www.jsbi.org*
- Rocky Mountain Regional Center for Computational Biology *www.cudenver.edu/ccb*
- Israeli Society for Bioinformatics and Computational Biology (*forming*)

ISCB Affiliated Regional Group Program participants may benefit from the following:

- Cross-visibility within one another's web pages, conferences, journals, and bulletins
- Affiliated Regional Groups may request access to facilities at ISMB—ISCB's official conference—for regional meetings
- Appointment of an ISCB Board member as affiliate point of contact (POC) to consider regional matters relevant to ISCB
- Solicitation for nominations to ISCB's Board from Affiliated Regional Groups through the Society's regional POCs
- Eligibility for support of regional activities: Travel funds for a recognized scientist in the field to lecture at a regional meeting or workshop; travel fellowships for scientists from the region to travel to ISMB

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
AFFILIATED REGIONAL GROUP

The ISCB—through its Affiliated Regional Group Program—is hopeful this effort will strengthen the bioinformatics community by providing a locality for mutual support to advance common interests of bioinformaticians at large. Members of regional bioinformatics and computational biology groups who consider affiliation with ISCB to be potentially beneficial for their organizations, are encouraged to contact *admin@iscb.org* for further information.

ISCB STAFF TEAM

The ISCB has recently undergone major administrative and behind-the-scenes changes, such as the update of its website and overhaul of its membership database. The Society's newsletter has been revamped and an official history of the Society initiated as well as significant planning accomplished for the next few years of the Society's official conference, ISMB. Those efforts are the products of the ISCB staff *(group photo p2)*, under the guidance of ISCB President Phil Bourne.

Apart from the Society's full-time administrative officer, BJ Morrison McKay (introduced in newsletter 5.1), the ISCB is supported by a second full-time employee, Stephanie Hagstrom. An award-winning meeting planner, Hagstrom works for ISCB as the ISMB Conference Liaison, which includes overseeing nearly every aspect of organization and logistics for the Society's annual conference. When not working, she spends time with her family, is active in Meeting Professionals International, and serves on the board of directors for Mama's Kitchen, a San Diego organization that delivers food to individuals and families living with HIV/Aids.

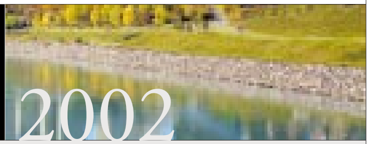
The rest of the ISCB staff serves the majority of the time for different departments within the San Diego Supercomputer Center (SDSC) and the National Partnership for Advanced Computational Infrastructure (NPACI).

Kim Baldridge, program director for SDSC's Integrative Computational Sciences program, oversees the ISCB staff. Additionally, Baldridge is deputy director of the NIH NCRR National Biomedical Computation Resource (NBCR) at SDSC and founded the Maria Goeppert-Mayer Annual Interdisciplinary Symposium.

(continued)

STUDENT TRAVEL FELLOWSHIPS

RECOMB 2002



This year, the ISCB provided travel awards for graduate students and postdoctoral researchers to attend the 2002 International Conference on Research in Computational Molecular Biology (RECOMB), held in Washington DC. Each was awarded a $500 travel fellowship to help cover the costs of attending the conference. The selection was based on geographic origin, field of study, and paper or poster presentation, though presenting a poster or paper was not a requirement for selection.

ISCB Travel Fellowship Recipients and Board Members *(clockwise from far left)*: Annette Höglund, Madan Babu Mohan, Hilary Booth, Dana Pe'er, Tomas Vinar, Sven Rahmann, Guang Song ,Ydo Wexler, Barbara Bryant, David Rocke, Phil Bourne (*not pictured:* Aik Choon Tan and Yujin Hoshida)

The winners included: Annette Höglund, a graduate student at Saarland University, Germany; M. Madan Babu, a graduate student at the University of Cambridge, UK; Hilary Booth, a postdoctoral fellow at the Australian National University; Dana Pe'er, a graduate student at Hebrew University, Israel; Tomas Vinar, a graduate student at the University of Waterloo, Canada; Sven Rahmann, a graduate student at the Max-Planck-Institut für Molekulare Genetik, Germany; Guang Song, a graduate student in the Computer Science Department at Texas A&M University, US; Claudia Rangel at Claremont Graduate University, US; Aik Choon Tan at the University of Glasgow, Scotland; Yujin Hoshida, a post-graduate student at the University of Tokyo, Japan; and Ydo Wexler a graduate student at the Technion, Israel.

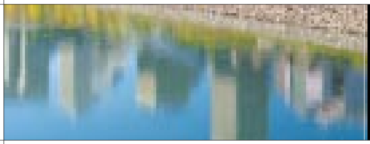
In addition to writing and editing articles and press materials for the ISCB, Cassie Ferguson works on SDSC's biweekly newsletter, *Online*, and the NPACI quarterly magazine, *EnVision*. A graduate of the University of California, Santa Cruz program in Science Communication, she prefers to spend her extra time in the outdoors with her family.

ISCB graphic designer and newsletter editor, Jennifer Matthews, produces web and print materials for several departments within SDSC as well as for the Scripps Institute of Oceanography's ROADNet project. Matthews also enjoys hiking and running with her husband and their Australian Shepherd.

Group leader of the web and database group in the High End Computing Program at SDSC, Josh Polterock, ISCB's webmaster, provides support for about 200 web applications, and database services to projects at SDSC and NPACI. When not tending to web servers and services, he spends time with his wife, Christine, and three kids, Hannah 7, Sam 6, and Sadie 2.

ISCB finance manager, Chris Smith, is program manager for SDSC'S Integrative Biosciences and Integrative Computational Sciences programs, and the NBCR. He also curates the CMS Molecular Biology Resource and tinkers in bioinformatics when time permits. When not in front of a computer, Smith collects power tools and has employed them on projects from home construction to crafting custom furniture.

Tracy Zhao who works as the ISCB database administrator, created a new database for the membership and implemented a new online payment for the ISCB. She also works as a programmer analyst for SDSC.



EVENTS AND OPPORTUNITIES OF INTEREST

DIMACS Special Focus on Computational Molecular Biology
DATE: September 2000-August 2003
UPCOMING EVENT: Protein Domains: Identification, Classification and Evolution
Dates: *February 27-28, 2003*; DIMACS Center, Rutgers, Piscataway, New Jersey, USA
URL: *dimacs.rutgers.edu/Workshops/index-compmolecbiol.html*

SHORT COURSE: **Bioinformatics: Methods and Techniques**
DATE: June 18-20, 2002
LOCATION: Stanford, Palo Alto, CA, USA
URL: *http://scpd.stanford.edu/scpd/courses/proEd/bioinf/default.asp?bioinformatics_iscb*
ABOUT: An introduction to fundamental problems in genomics and bioinformatics. Topics include DNA and protein sequence and structure analysis, structure prediction and the impact of new technologies such as mRNA expression arrays and proteomics techniques.
CONTACT: Jody Gladstein, 650-723-9041 *(scpd_proed@forsythe.stanford.edu)*

Bioinformatics
DATE: June 19-21, 2002
LOCATION: Boston, MA, USA
URL: *www.LifeScienceSolutions.com*
ABOUT: This information-intensive conference will bring together the industry's most forward-thinking computational biologists to examine diverse bioinformatics strategies and applications. Key components of this event include open-source industry collaboration and integration, computational proteomics, post-genomic bioinformatics and drug discovery. Focused pre-conference tutorials will offer hands-on experience with leading bioinformatics tools.
CONTACT: Ann Pendleton, 312.894.6418 *(conferences@marcusevansch.com)*

Bioinformatics and Genomics: Methods, Data, and Predictions
DATE: June 24-28, 2002
LOCATION: Laboratory for Information, SINGAPORE
URL: *sdmc.krdl.org.sg/cimm/BGMDP02*
ABOUT: The program on Post-Genome Knowledge Discovery will focus on the computational and statistical analysis of sequence and genetic data and the mathematical modeling of complex biological interactions, which are critical to the accurate annotation of genomic sequences, the study of the interplay between genes and proteins, and the study of the genetic variability of species.

NETTAB 2002 Second International Workshop on Agents in Bioinformatics
DATE: July 12-14, 2002
LOCATION: Bologna, ITALY
URLs: *www.nettab.org, www.nettab.org/2002/progr.html*
ABOUT: This workshop aims to bring together researchers working toward the vision of a genome analysis and annotation using agents-based systems. NETTAB2002 aims to strengthen the relationships within the bioinformatics community, to activate cooperation between bioinformatics and computer science communities, to collect the latest ideas, achievements and proposals in the application of agents and multi-agent systems to the bioinformatics area.

The Third International Conference on Bioinformatics of Genome Regulation and Structure (BGRS2002)
DATE: July 14-20, 2002
LOCATION: Novosibirsk, RUSSIA
URL: *www.bionet.nsc.ru/meeting/bgrs2002/index_local.html*
ABOUT: BGRS2002 will provide a forum for the accumulation, analysis, and recognition of genomic regulatory sequences. Experimental biologists are also encouraged to attend—BGRS2002 aims to be a stimulating event to facilitate an application of computational biology to experimental research.

SSGRR-2002: *Infrastructure for e-Business, e-Education, e-Science, and e-Medicine*
DATE: July 29-August 4, 2002
LOCATION: L'Aquila near Rome, ITALY
URLs: *www.ssgrr.it/en/ssgrr2002s/index.htm*
ABOUT: SSGRR decided to organize twice a year an international symposium in the general domain of Infrastructure for e-Business, e-Education, e-Science, and e-Medicine (in the widest sense: computer science and engineering, communications, and business administration), with the goal of getting together the leading world experts in the field, to present invited papers on their most important research contributions in the recent period.

CALL FOR SUBMISSIONS: **Discrete Dynamics in Nature and Society (DDNS) Special Issue: Complex Multi-Agent Interaction Dynamics**
DEADLINE August 31, 2002
URL: *www.tandf.co.uk/journals/titles/10260226.html*
ABOUT: DDNS's main field of interest is the use of nonlinear difference equations to model complex phenomena in natural and social systems. However, the rise in computer processing power, and the development of powerful parallel processing hardware and software, has made it possible to model many complex systems as the result of the interactions of discrete agents. This special issue of DDNS will focus exclusively upon this approach to system modeling. Papers will be considered on any and all topics, so long as the paper meets the parameters of using interactive multiple agent systems to generate or explain complex systems.

SHORT COURSE: **An Introduction to Bioinformatics: A Practical Approach**
DATE: September 2-3, 2002
LOCATION: University of Warwick, Coventry, UK
URL: *www.bio.warwick.ac.uk/shortcourses*
ABOUT: A course for those wishing to gain a practical understanding of the applications of bioinformatics
CONTACT: Dr. Charlotte Moonan, 024-7652-3540 *(Charlotte.Moonan@warwick.ac.uk)*

WABI 2002: 2nd Workshop on Algorithms in BioInformatics
DATE: September: 16-21, 2002
LOCATION: Faculty of Engineering, University of Rome "La Sapienza," ITALY
URL: *www.dis.uniroma1.it/%7Ealgo02/wabi02*

ABOUT: WABI2002 will cover research in algorithmic work in bioinformatics and computational biology. The emphasis is on discrete algorithms that address important problems in molecular biology, genomics and genetics that are founded on sound models, computationally efficient, and have been implemented and tested in simulations and on real datasets.

Second Virtual Conference on Genomics and Bioinformatics Sharing Knowledge with the World

DATE: September 24-26, 2002
LOCATION: Fargo, North Dakota, USA
URL: *www.ndsu.nodak.edu/virtual-genomics/upcom2.htm*
ABOUT: This conference will provide an environment to discuss information related to post-genomic era innovations. Genomic research has led to an explosive rate of data accumulation and a shift in the way biological research is conducted. This conference will feature high profile researchers and educators developing new applications in genomics and bioinformatics.

European Conference on Computational Biology 2002 (ECCB 2002)

DATE: October 6-9 2002
LOCATION: Saarbrücken, GERMANY
URL: *www.eccb2002.de*
ABOUT: The ECCB conference provides an opportunity to present cutting edge research in computational biology. This multi-disciplinary conference bridges computer science, molecular biology, biochemistry, pharmaceutics, and medicine by bringing together involved scientists from all over the world.
CONTACT: *ECCB.organizers@bioinf.uni-sb.de*

BioDigital 2002: International Trade Fair and Conference for Biotechnology, Bioinformatics and Microarrays

DATE: October 9-11, 2002
LOCATION: Messe Freiburg in Freiburg/Breisgau, GERMANY
URL: *www.biodigital.de*
ABOUT: Systems Biology, Protein Microarray, DNA Chips, Bioinformatics. The connection of trade fair and top-class conference of the BioDigital 2002 offers an interesting panel for science and business decision makers in Microarray technology and Bioinformatics.
CONTACT: +44-0-20-7017-5069; +44-0-20-7017-4822 *(fax)*

Invitation to the 3rd International Conference on Systems Biology: The Logic of Life

DATE: December 13-15, 2002
LOCATION: Karolinska Institutet, Stockholm, SWEDEN
URL: *www.icsb2002.org*
ABOUT: ICSB 2002 will feature experimental, computational and theoretical advances in the rapidly advancing fields of gene expression acquisition technologies, gene expression data analysis, functional analysis of biological control systems, proteinomics, modeling and analysis of kinetic networks, metabolomics, signal transduction, morphogenesis, and much more.

First Asia-Pacific Bioinformatics Conference Within Australia

DATE: February 4-7, 2003
LOCATION: Adelaide, AUSTRALIA
URL: *www.fit.qut.edu.au/~chenp/APBC2003*
ABOUT: Database management, artificial intelligence, data mining, and knowledge representation can provide key solutions to the challenges presented by biological data. Opportunities are emerging to integrate molecular biology components of bioinformatics with computational, physiological, morphological, taxonomic, and ecological components. Addressing this challenge will facilitate the way life science researches retrieve, analyze and visualize data and relationships in a collaborative work environment.
CONTACT: Dr. Phoebe Chen, +61-7-3864-1945; +61-7-3864-1969 *(fax) (p.chen@qut.edu.au)*

CALL FOR SUBMISSIONS: International Journal of Cooperative Information Systems

URL: *www.worldscinet.com/ijcis/mkt/guidelines.shtml*
ABOUT: This special issue's focus is Data Management and Modeling Support in Bioinformatics. Papers describing state-of-the research including, but not limited to, the following areas are solicited: Database integration and interoperability; Information Modeling, metadata and data sharing; Multidatabase indexing and multidatabase queries; Data semantic and control; Ontology design; Knowledge discovery and datamining; Algorithms for large scale and distributed biological databases

ADDITIONAL ITEMS

European Drive for Post-Genomic Research

In a drive to gear up research on genomics the European Commission has awarded $39.4 million to three large research projects. The funding is a prelude to the $2.2 billion earmarked for "genomics research for human health" in the next community research programme to be launched later this year. The projects on the genetics of twins, mouse genomics and structural proteomics are demonstrating the new way in which the Commission will fund research in the future: asking scientists from industry and academia to compose top teams from across Europe to conduct research at the cutting edge of science in a selected number of fields and giving them sufficient means to achieve critical mass and world-class excellence. This effort is part of the European Commission's commitment to invest more and better in the creation of knowledge and to build a coherent European Area for Research and Innovation.

American Heart Association (AHA)

The AHA supports research activities broadly related to cardiovascular function and disease, stroke, as well as basic science, clinical, bioengineering/biotechnology and public health problems. National Research Programs are offered bi-annually. Application deadlines: July 15, 2002; January 13, 2003 Information and forms are available at *www.americanheart.org/research.*

Israeli Society for Bioinformatics and Computational Biology

The newly formed Israeli Society for Bioinformatics and Computational Biology (ISBCB) has nominated their first president, Professor Hanah Margalit (Department of Molecular Genetics and Biotechnology, The Hebrew University), to a two year term. Founded at the 2002 Israeli Bioinformatics Annual Meeting, ISBCB is currently in the process of officially registering as a society with Israeli authorities.

To recommend a conference for inclusion in the ISCB Newsletter, please write to *admin@iscb.org*.

How are We Doing?

Please email ISCB staff at *admin@iscb.org* with any comments, questions, or concerns regarding the website *(www.iscb.org)*, this newsletter, or any other ISCB effort. The ISCB staff aims to meet the needs of ISCB's membership—member advice goes a long way toward helping the staff meet their objectives.

ISCB acknowedges the support from the National Biomedical Computation Resource, at the San Diego Supercomputer Center, at the University of California, San Diego, which provides the computational infrastructure for the ISCB web resource and underlying databases.

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