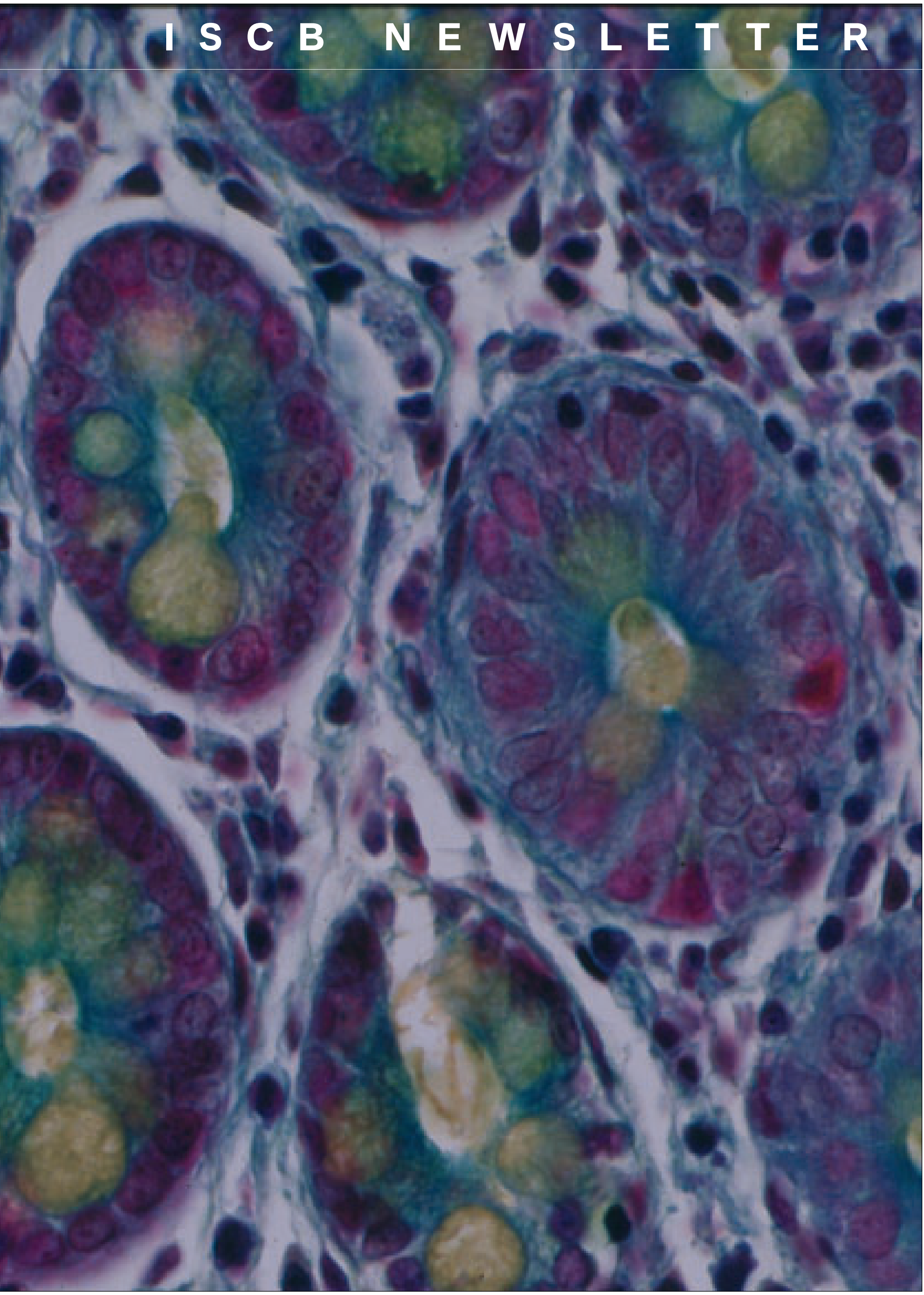
ISCB NEWSLETTER



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iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

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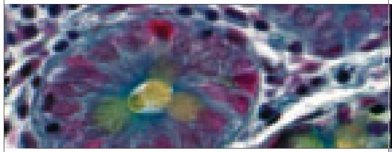


A NOTE FROM ISCB PRESIDENT

Michael Gribskov

If you made it to ISCB's annual conference, Intelligent Systems for Molecular Biology (ISMB 2003), held June 29 – July 3 in Brisbane, Australia, I am sure you agree it was a resounding scientific success. Throughout the conference I heard positive comments on the quality of the talks, logistics, networking opportunities, and the choice of Brisbane for ISCB's first conference in the Asia/Oceania region.

Deviating from our typical North American/European rotation enabled hundreds of participants from Australia, China, India, Korea, Japan, Malaysia, New Zealand, Singapore, Taiwan, Thailand, and others to come for the first time.Although our North American and European attendance was lower than in previous years, as an organization serving the needs of a worldwide membership, it is important to bring attention to burgeoning science centers, and Brisbane provided an ideal setting for accomplishing this goal.

Of course, ISCB could not produce a conference of this quality or size without the dedicated help of our volunteer organizing committees. Therefore, I would like to thank the individuals and organizations listed below, and the many student volunteers, who worked to ensure that ISMB met the highest scientific, technical, and organizational standards.

The ISMB 2003 Organizing Committee was co-chaired by Gene Myers, University of California Berkeley, and Mark Ragan, Institute for Molecular Bioscience, The University of Queensland, and included Kevin Burrage, Advanced Computational Modelling Centre, The University of Queensland; Antoine Danchin, Institut Pasteur, Paris; Terry Gaasterland, The Rockefeller University; Minoru Kanehisa, Japanese Society for Bioinformatics, Kyoto University; Tim Littlejohn, Biolateral Pty Ltd.; John Mattick, Institute for Molecular Bioscience, The University of Queensland; Christos Ouzounis, European Bioinformatics Institute; Shoba Ranganathan, Asia-Pacific BioNet and the National University of Singapore; David Wishart, University of Alberta.

The ISMB 2003 Local Organizing Committee was chaired by Mark Ragan and included Peter Adams, Tim Bailey, Jennifer Hallinan, Edith Hii, and Rohan Teasdale, all from the Institute for Molecular Bioscience, The University of Queensland, as well as Michelle Madden, Hotelier's International, a professional conference organizer contracted to help coordinate and execute conference logistics.

The ISMB 2003 Program Committee was chaired by Gene Myers and included Area Chairs Phil Bourne, San Diego Supercomputer Center, University of California, San Diego (Databases); Terry Gaasterland (AC Gene Expression); Frederique Galisson, Swiss Institute for Bioinformatics/University of Lausanne (Protein Function & Evolution); David Gilbert, City University, London (AI & Linguistics); Michael Gribskov, San Diego Supercomputer Center, University of California, San Diego (Alignments, Motifs, & HMMs); Gene Myers (Methods); Burkhard Rost, Columbia University (Protein Structure & Modelling); Alfonso Valencia, Centro Nacional de Biotecnologia (Protein Interactions & Text Analysis); Ralph Zimmer, Institute for Informatics, University of Munich (Gene Networds & Applications); and Stan Letovsky, Boston University (Networks & Pathways).

And finally, significant financial support came from our primary sponsors named in the ISMB 2003 recap article within this newsletter, as well as from our exhibitors Accelrys, BioLateral, Biomax Informatics AG, Cambridge University Press, Chemical Computing Group, Inc., CRC Press, Genvea Biosciences, Protein Data Bank, Springer-Verlag, The Blueprint Initiative, The MIT Press, VPAC, Western Desert Aboriginal Paintings, and Wiley.

ISMB 2003 CELEBRATES BIOINFORMATICS DOWN UNDER

ISMB marked its 11th year by venturing beyond North America and Europe to Brisbane, Australia from June 29 to July 3, 2003. The conference attracted 919 participants from 42 countries to its quality program of papers, posters, tutorials, special interest group meetings, and more. The Institute for Molecular Bioscience and the Advanced Computational Modelling Centre of the University of Queensland served as local hosts for the meeting, which was held at the Brisbane Conference and Exhibition Centre.

More than 500 participants took part in 15 tutorials on both established and cutting-edge topics relevant to the bioinformatics field, including "Bioethics for Bioinformaticists", "Molecular Modeling: building a 3D protein structure from its sequence", "Artificial Intelligence and Machine Learning Techniques for Bioinformatics", and "Data Warehousing in Molecular Biology". The Special Interest Group meetings also proved popular this year, with 98 participating in Bioinformatics Open Source Conference, 100 in Biopathways, 51 in Bio-Ontologies, 28 in WEB03, and 42 in Text Mining (BioLINK).

Once again, attendees had the opportunity to participate in the popular Orienteering Ice Breaker. The event, a tradition initiated at ISMB2002, involved finding control locations in a Brisbane city park using a map and a compass. Ironically, according to the ISMB website, the event is analogous to the NP-complete Prize Collecting Traveling Salesman problem, which has a respectable and fascinating literature, as well as mostly untapped applications in bioinformatics. ISMB concluded with a party at Dreamworld on the Gold Coast, where attendees enjoyed entertainment, wild rides, and wildlife.

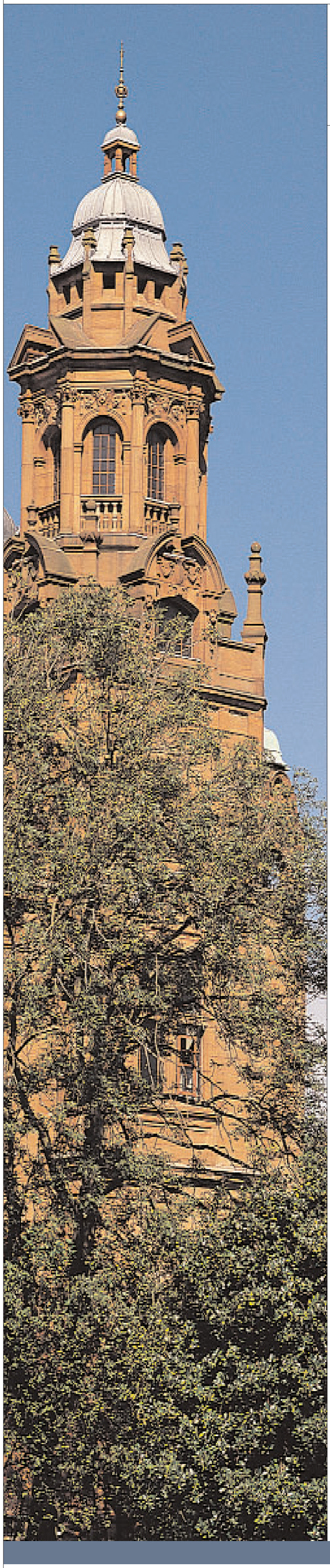
Notable speakers at ISMB 2003 included: Sydney Brenner, one of three recipients of the 2002 Nobel Prize in medicine and founder of the Molecular Sciences Institute and distinguished research professor, Salk Institute; David Haussler, Howard Hughes Medical Institute Investigator and professor of computer and information sciences, University of California, Santa Cruz; Yoshihide Hayashizaki, project director of Genome Exploration Research Group, Genomic Sciences Center, RIKEN; John Mattick, director of the Institute for Molecular Bioscience, University of Queensland; Ron Shamir, professor of computer science, Tel-Aviv University, and Michael Waterman, professor of mathematics, computer science and biological science, University of Southern California.

W. James Kent, the 2003 winner of the Overton Prize delivered the annual Overton Lecture. Kent is an assistant research scientist at the University of California, Santa Cruz. The prize, now in its third year, 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. The winner of the first-ever ISCB Senior Scientist Accomplishment Award was David Sankoff, Canada Research Chair in Mathematical Genomics at the University of Ottawa and a member of the Centre de Recherches Mathématiques at the Université de Montréal. The Senior Scientist Accomplishment Award recognizes members of the computational biology community who are more than 12 to 15 years post-degree and have made major contributions to the field of computational biology. (See *www.iscb.org/newsletter6-2/* for more information on Kent's and Sankoff's research and selection for these awards.)

Both industry and governmental sponsors provided invaluable support for ISMB 2003. Platinum Sponsors included: Hewlett-Packard, Queensland Government - Dept of Innovation and Information Economy, and Sun Microsystems, Inc. Gold Sponsors included: Apple Computer Australia, SGI, and The University of Queensland. Silver Sponsors included The Australian Partnership for Advanced Computing (APAC) and Queensland Parallel Supercomputing Foundation Ltd.

Travel fellowship support, which allows students and early-career scientists to attend ISMB, was provided by the United States Department of Energy, the United States National Institutes of Health, the United States National Science Foundation, and the ISCB.

IMAGES FROM THE TOP: *Orienteering participants calculate how many locations they can get to in a short allotment of time, David Sankoff takes home the ISCB Senior Scientist Accomplishment Award, Aboriginal dancers added a uniquely Australian cultural experience during the off-site dinner at Dreamworld, five recipients of the 2003 SGI Best Poster Award*



ON THE HIGH ROAD TO ISMB/ECCB 2004

When David Gilbert got up on stage at ISMB 2003 to give the audience a primer on next year's conference, few people, even among the organizers of next year's conference, were expecting him to remove his shirt. He did so to ensure that no one would be in any doubt as to the geographical location of ISMB/ECCB 2004—Glasgow, Scotland—by revealing a T-shirt emblazoned with a map of Scotland. If you missed this spectacle, David's presentation (without the striptease act) can be downloaded from the conference website at *www.iscb.org/ismbeccb2004*.

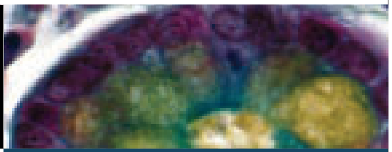
The UK is the ideal venue for ISMB/ECCB 2004: it has one of the largest and strongest bioinformatics communities in the world and it is home to the European Bioinformatics Institute, Europe's premier provider of bioinformatics resources. It also has a strong tradition in bioinformatics teaching, offering several masters and BSc courses. Scotland plays an active role in the UK's bioinformatics scene: it is home to a number of world-class organizations that are pushing the frontiers of biotechnology and bioinformatics, from eScience (the UK's National eScience Centre is based in Glasgow and Edinburgh) to the application of bioinformatics to agriculture and medicine (think Dolly the sheep and genome mapping projects for an entire farmyard). Bioinformatics has been identified as an area of key strategic interest in Scotland, and Scottish Enterprise, Scotland's main economic development agency, is promoting the development of biotechnology and bioinformatics in Scotland.

Apart from the state-of-the art Scottish Exhibition and Conference Centre, an unparalleled range of places to stay and its excellent international air links, Glasgow is undoubtedly one of Europe's most vibrant Cultural Capitals. It has some of the best arts venues, shopping, wining and dining in the UK, not to mention stunning views of the surrounding countryside. Around the city there are numerous reminders of Glasgow's impressive architectural heritage. The work of Charles Rennie Mackintosh, art deco architect and designer of world renown, can be seen throughout the city; this provided the inspiration for our conference logo.

Glaswegian culture will not be the only unique thing about next year's conference. As well as being the first time that ISMB is held jointly with ECCB, the European Conference on Computational Biology, we will be making a concerted effort to put the bio back into bioinformatics. Hot topics at ISMB/ECCB 2004 are likely to include genomics, evolution and phylogeny, transcriptomics, proteomics, structural biology, pathways, networks and systems, and applications of bioinformatics. The message from the programme committee is this: get collaborating with your friends in the wet lab and come to Glasgow to showcase the fruits of your labours.

As well as providing an exciting and innovative programme, we want to ensure that you get a proper Glaswegian welcome. Whisky tasting and Scottish dancing are likely to be part of the festivities; haggis and deep fried Mars bars are strictly optional. Look out for the call for papers in September or, better still, sign up to receive conference updates and news at *www.iscb.org/ismbeccb2004/prospects.php*.

SGI AWARDS



The ISMB 2003 program committee, chaired by Gene Myers, professor of electrical engineering and computer sciences at the University of California, Berkeley, chose the finalists for this year's SGI Best Paper and Best Student Paper awards. The winners in both categories were selected at ISMB 2003. This year's winners include:

- Best student paper: *Discovering Molecular Pathways from Protein Interaction and Gene Expression Data*. Eran Segal, Haidong Wang, and Daphne Koller.
- Best paper: *Discovery of Transcriptional Modules from DNA Sequence and Gene Expression*. Eran Segal, Roman Yelensky, and Daphne Koller.
- Best runner up paper: *A Probabilistic Method to Detect Regulatory Modules*. Saurabh Sinha, Erik van Nimwegen, and Eric Siggia.

Ten posters—from a pool of hundreds—were selected to receive 2003 SGI Poster honors. ISMB delegates selected the best poster winners. The winners selected were:

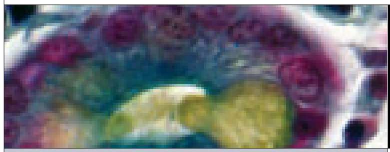
- *Domain-Domain Correlations in Yeast Protein Complexes*. Doron Betel and Christopher W.V. Hogue.
- *GOstat: Find Statistically Overrepresented Gene*. Tim Beissbarth and Terry Speed.
- *Efficiently Finding Regulatory Elements using Correlation with Gene Expression*. Hideo Bannai, Shunsuke Inenaga, Ayumi Shinohara, Masayuki Takeda, and Satoru Miyano.
- *Melbourne Brain Genome Project*. Seong-Seng Tan, Lavinia Hyde, Masters C, Gunnersen J, Kenshole B, Job C, Augustine C, Boon W-M, Brown M, and Scott HS.
- *Identification of Putative Transcription Factor Binding Sites Conserved Across Orthologous Human, Mouse and Rat Sequences*. Alex Gouth, Tim Beissbarth, Joelle Michaud, Catherine Carmichael, Matthew Ritchie, Gordon.
- *Identification of Putative Insulin Binding Motifs of the Insulin Receptor*. Steve Bottomley, Jessica Mitchell, Brian Plewright, and Erik Helmerhorst.
- *Prediction of a Full Length Gene from Partial Sequence*. Chung, Myungguen, Cho, Sooyoung, Ban, Hyojeong; Kim, Hyun, and Lee Youngseek.
- *PSORT-B: A Web-based Tool for Bacterial Subcellular Localization Prediction*. Jennifer L. Gardy, Cory A. Spencer, and Fiona S.L. Brinkman.
- *Genomics of Vertebrate Splicing Regulatory Elements*. Gene Yeo, Shawn Hoon, and Chris Burge.
- *A DNA-Based Theorem Proving by Resolution Refutation*. Ji-Yoon Park, In-Hee Lee, Young-Gyu Chai, and Byoung-Tak Zhang.

ISCB SPONSORSHIP OPPORTUNITIES

As ISCB extends its reach in terms of member relations, public affairs, conference management, student funding assistance to conferences, and many other exciting new initiatives, we must also diversify our revenue streams to reduce dependence on limited resources. In the past we have been very fortunate to feature high-level sponsors of ISMB, our annual conference. Now we are embarking on a concerted effort to develop corporate sponsorship programs that will jointly meet the needs of industry partners and those of the Society and its membership, beyond the limited life of each year's annual conference.

If the opportunity to become a sponsor of the ISCB appeals to you and/or your organization as one that fulfills a social responsibility goal toward international outreach for the Life Sciences community, we want to hear from you. Sponsorships are being customized to meet the unique goals of each of our current and future partners.

For additional information or to express interest in becoming a sponsor of the ISCB, please contact BJ Morrison McKay, Executive Officer, at *admin@iscb.org*



ISCB PRESIDENT-ELECT ELECTIONS PROCESS

From August 22 through September 5, 2003, all ISCB members will have the opportunity to vote for the next President of the Society by casting votes for the newly created position of President-Elect. The Board of Directors created this position earlier this year as the first step in an effort to develop a clear leadership path within the Society.

Current Officers (President Gribskov, Vice President Tramontano, Treasurer Rocke, and Secretary Bryant) were all elected last year to serve two-year terms that will expire on January 21, 2005. As Gribskov and Rocke are both running for President-Elect the winner will serve simultaneously in his current role through the expiration of his term. If a non-Officer runs in the future, the President-Elect would become an ISCB Officer and Executive Committee member for one year in a "training" role alongside the President before taking over the presidency for the following term.

A review of each of the President-Elect candidate statements is presented below. Full statements, including Curriculum Vitae and a synopsis of current research work, can be viewed at *www.iscb.org/candidate_list.php*. Beginning August 22 members will be able to cast votes on the ISCB website by logging in on the membership page at *www.iscb.org/login.php* and selecting President-Elect Election from the menu that presents on the left of the page.

CANDIDATE: Michael Gribskov, Ph.D.

Adjunct Associate Professor, University of California, San Diego

1. What do you think are the major issues facing ISCB over the next three years?

- Finances—ISCB is highly dependent on the ISMB meeting for operating funds. This puts the entire society at risk if the ISMB meeting is less successful than expected.
- Scientific leadership—ISCB needs to play a stronger role in organizing cutting edge meetings, book series, workshops, etc. that are of the highest quality.
- Improved structure of the society to better interact with members to accomplish scientific and policy goals.

2. How do you plan to address these issues? How should the society address these issues?

- The executive committee and board is currently working to diversify funding sources to lower our dependence on ISMB. Solutions include a corporate sponsorship program, an improved contract with OUP (publisher of the society journal, *Bioinformatics*), and belt tightening at ISCB.
- It is time to move beyond just ISMB and sponsor a wider suite of meetings that focus on the cutting edge of research. We should also consider an expanded tutorial program to improve the general standard of training. Other possible activities such as a book or text series are under consideration.
- A major accomplishment this year has been initiation of a process of strategic planning. Changes are being implemented now to improve the structure of ISCB.

3. What nonscientific expertise do you bring to the Board?

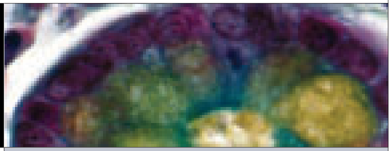
- Experience running a lab with an annual budget of ~$ 1M
- Experience on ISCB board of directors; 1 yr experience as ISCB VP; 1 yr experience as ISCB President
- Service on many advisory boards, government review panels, program committees, and editorial boards.

4. Apart from your research, what service have you performed for this field or ISCB so far?

- In the long term, I think the strategic planning process, in which we are now engaged, will have the greatest impact on the success of ISMB.
- Initiation of a successful corporate sponsorship program will be very important.

ROCKY 1

ISCB will sponsor the first Rocky Mountain Regional Bioinformatics Meeting ("Rocky 1") which will take place in Aspen, Colorado December 5-7, 2003. The meeting will bring together computational bioscientists from Montana, Idaho, Wyoming, Colorado, Utah, Nevada, Arizona, and New Mexico to share research results, build community, and get to know each other better. A mixture of invited lectures, discussions on topics of regional interest and short talks from many regional research groups will make up the scientific program. Informal community building opportunities include discounted lift tickets and a catered dinner at the top of Aspen Mountain for participants. For more information, see *www.iscb.org/rocky1* or contact *shagstrom@iscb.org*.



CANDIDATE: David Rocke, Ph.D
Professor, University of California, Davis

1. What do you think are the major issues facing ISCB over the next three years?

- The finances of ISCB are not yet on a firm footing. They are too dependent on a single meeting (ISMB) and the present revenues are not sufficient to sustain the needed growth of the society.
- The organization of ISCB needs some improvements to better meet the goals of the society.
- We need to continue to improve the ISCB sponsored publications. We need to explore the eventual establishment of additional high-quality publication outlets for our work.
- We should explore more extensive cooperation with other related professional societies, including joint sponsorship of meetings and possibly journals. These may include societies from both the biological side (such as our fellow FASEB societies) and from the computational/mathematical/statistical side such as ACM, IEEE, SIAM, and ASA.
- We should assist in developing curricula and publications to further education in computational biology and bioinformatics.

2. How do you plan to address these issues? How should the society address these issues?

- I believe that we are beginning as a Board of Directors (BOD) to address many of these issues. I think an important additional route to improvement is to gain information from our sister societies both in biology and in computation/mathematics/statistics. How are they financed? What services do they provide for members? How is the board and staff organized? How are committees appointed? We need to investigate more extensively the opinions of our members on what ISCB can do for them and for the discipline. We should conduct a carefully-planned, scientifically-designed survey of members and potential members (such as attendees at relevant meetings) to help in the already ongoing strategic planning effort.

3. What nonscientific expertise do you bring to the Board?

- Although I am now appointed in the College of Engineering and the School of Medicine at UC Davis, I spent 25 years teaching statistics and management science in schools of business. Through teaching, seminars, and some formal course work, I have acquired a working knowledge of the basic business disciplines, including finance, accounting, and management information systems. I now manage a research center with a $3 million budget, and have been Vice-Chair of my main department. I have also been Treasurer of ISCB for a year and a half, and have a good idea of the financial and organizational challenges we face.

4. Apart from your research, what service have you performed for this field or ISCB so far?

- I have been Treasurer of ISCB since January 2002. As a member of the Executive Committee of the BOD, I have been involved in all major decisions. Besides the budget, I am currently responsible for negotiating the renewal of the contract with Oxford University Press for the *Bioinformatics* Journal.

BEHIND THE SCENES AT ISCB

Many members have already had a chance to interact with Suzi Smith, who recently joined the ISCB staff in an administrative support role. Jumping right in to her new position, Suzi is responding to member inquiries, journal orders, and bookkeeping.

Suzi has many years of administrative experience, primarily in the banking and event planning industries. She is a California native, and was pleased to settle in San Diego after traveling the world with her husband during his 20 years of service in the US Navy. The next time you send mail to *admin@iscb.org*, don't be surprised if you receive a speedy reply from Suzi.

A less well-known member of the ISCB team is Lynn Fink, PhD. A recent graduate of University of California, San Diego, Lynn currently holds a postdoc position at the San Diego Supercomputer Center in Michael Gribskov's computational molecular biology lab.

In 2002 Lynn volunteered to serve on an ISCB committee, and we quickly enlisted her for programming assistance with the ISMB conference poster submissions. This effort resulted in a standardized database for the 2003 conference, which will serve for future years as well. Thank you, Lynn, for all of your great work!

STRATEGIC PLANNING

What will the future of bioinformatics hold? How will the needs of ISCB members and affiliates change as our science matures? Will we succeed in keeping pace with the growth of our community? This past February the ISCB board of directors began a strategic planning process to answer these questions and determine a clear path for the future of the Society.

John Pepin, a business consultant leading non-profit organizations through strategic planning and revenue diversification, was hired to facilitate the board through this process. As a Canadian who is based in the UK, he is able to offer a unique multinational perspective to our international organizational needs.

As a first step, a confidential questionnaire was sent to ISCB members and affiliates to gather information about expectations and needs. Presented as a series of 17 open-ended questions and 14 rating scales (i.e., “On a scale of 1 - 5 with 5 being the best…”), a few survey respondents were unhappy with the lack of multiple-choice answers that would have expedited the process. However, it was important for ISCB not to direct answers toward preconceived outcomes by limiting answers to lists of options. We thank the 250+ members and affiliates who completed the questionnaire, providing us with significant information to help direct the activities and issues of the ISCB in the months and years ahead.

The next steps in the process included confidential ISCB assessment interviews conducted by Pepin with leaders in our science, a series of teleconferences with members of the board, and a strategic planning retreat for a group of twelve ISCB leaders and staff. From all of this a framework of the strategic plan was developed. The results were shared with the full board of directors during a teleconference in mid-June, and a half-day strategic planning session was held during the annual board of directors meeting on June 29 in Brisbane, Australia.

Initial results of the surveys and board work identified ISCB’s top five strengths and weaknesses as:

STRENGTHS	WEAKNESSES
ISMB conference	Governance—needs more effective organization
Staff to do Society work	Financial dependence on ISMB
Bioinformatics as a rapidly growing field	Affiliate/collaborator /member relations are inconsistent
Journals offered by the Society	Perceived as U.S.-centric
Networking at the ISMB conference	Branding/recognition of ISCB is still underdeveloped

The plan, when finished, will lay the groundwork for capitalizing on our strengths, and addressing ways of improving upon each of the above weaknesses.

Another immediate outcome of the strategic planning effort is a slightly revised ISCB Mission Statement. Numerous survey respondents took issue with the reference to molecular biology in our original mission statement. Therefore, to avoid any perceived limitations, the statement now reads

ISCB MISSION

> *The International Society for Computational Biology is a scholarly society dedicated to advancing the scientific understanding of living systems through computation.*
>
> *The ISCB communicates the significance of our science to the larger scientific community, governments, and the public at large. The ISCB serves a global membership by advocating government and scientific policies, providing high quality publications and meetings, and through distribution of valuable information about training, education, employment and relevant news from related fields.*

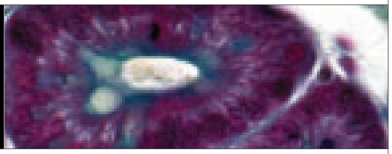
Additionally, the ISCB board of directors has created a Vision Statement for the first time in our history to help express what we aim to accomplish and become as an organization in the future.

ISCB VISION

> *The International Society for Computational Biology will measurably advance the worldwide awareness and understanding of the science of computational biology. As an authoritative society that represents the bioinformatics and computational biology communities, the ISCB will be the most respected and reliable international non-profit organization representing this community. Ultimately, membership in the society will be respected as an essential demonstration of personal commitment toward the advancement of computational biology.*

Following the planning session in Brisbane, the strategic plan is now taking shape to become a working document that the Society can use moving forward. It is being written in conjunction with a three-year business plan and budget to help set strategically based guidelines on how ISCB’s limited resources will be put to use, how to better organize the leadership of the Society, including a transparent leadership path, and how to increase our financial reserves so that we may add relevant member benefits and services in the years ahead. Upon completion and board approval, a copy of the plan will reside on the website for review by all members and visitors.

GOVERNMENT RELATIONS



by Dr. Barbara Bryant

ISCB joined FASEB (the Federation of American Societies for Experimental Biology) primarily in order to join voices with a group with access to U.S. lawmakers. The ISCB Government Relations Committee would like to hear from ISCB members about similar opportunities to access policy makers in other countries, and about the issues you think we ought to be addressing.

ISCB has set up a discussion area at *forums.iscb.org*, and we encourage you to visit that site and give us ideas and feedback. We are also in the process of setting up list serve email lists for more direct "discussion" of hot topics.

Here are a number of issues that FASEB's Public Affairs team has been addressing in the past few months:

U.S. Representative Martin O. Sabo (Democrat, Minnesota) drafted the "Public Access to Science Act," which would prohibit copyrighting of works funded by the U.S. government. The intent is to allow people to see scientific articles without having to pay large journal subscription fees. However, an unintended effect would be to eliminate the most common mechanism for protection, and subsequent commercialization, of software. FASEB's President, Robert D. Wells, has met with and written to Mr. Sabo on behalf of FASEB to caution against this new legislation, specifically stating, "Any significant changes to the existing system of scientific publication are likely to have serious and lasting consequences on the dissemination of new research knowledge. FASEB believes that it is vital that all stakeholders have a voice in the development of any new policies."

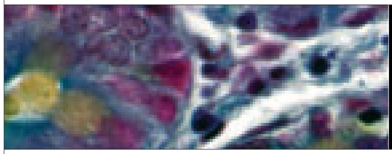
Most ISCB members support the idea of having good access to scientific literature, not only for us humans, but also for the digestion of our text-mining programs. The Public Library of Science (PLoS) approach (articles available free online to readers; authors pay a publishing fee) is an attractive alternative. However, some people I've spoken with are concerned about forcing such a business model on all publications (by means of the Sabo bill): What if it does not work for all journals? Would valuable news and review articles still get published? Would the quality of scientific literature be affected? They also point out that journals have been making great strides toward more open access lately; *Bioinformatics*, for example, is available free and at reduced prices for people in low per-capita income countries through non-profit institutions, and is released free to all one year after publication. Other ISCB members are avid proponents of the PLoS approach, and would like to see a wholesale jump to that model immediately. People generally would like to see more communication between the various parties in this debate, to achieve progress toward the shared goal of increased access to the results of scientific research and high quality publications.

FASEB will also be taking part in an NIH workshop on the topic of training and career development. There is particular concern about postdoctoral training, and its possible abuse by institutions that retain talented researchers at low pay in positions without advancement opportunities. Interested ISCB members are encouraged to provide their thoughts via our forums (*forums.iscb.org*), which will be communicated to the FASEB team involved.

FASEB carefully follows budgeting and spending of U.S. federal research dollars. They raised the alarm when research dollars were suddenly slated to be spent on procurement of anthrax vaccine. FASEB lobbies for increases in budgets for research; they were instrumental in the recent five-year doubling of the NIH budget, and are strong advocates for increases for NSF.

Another area that FASEB watches is the management and operation of the federal research agencies. When the VA suddenly canceled a number of promised grants, FASEB took action and continues to express concern about a shift away from peer review. FASEB objected to recent political scrutiny by congressmen of specific grants related to AIDS.

Please let us know of issues that ISCB might raise with the other FASEB member societies for consideration. As a new associate member of FASEB, ISCB can provide a strong voice for issues of critical importance to the growing field of bioinformatics.



SPECIAL INTEREST GROUPS

BioLINK Text Mining SIG

The third meeting of the Special Interest Group (SIG) for Text Mining was held in conjunction with ISMB in Australia this year, following the 2001 meeting in Copenhagen and the 2002 meeting in Edmonton. The Text Mining SIG has been organized by the BioLINK group *www.pdg.cnb.uam.es/BioLINK* with its main contributors Lynette Hirschman from MITRE (Bedford, MA) and Alfonso Valencia from the CNB (Madrid, Spain) together with this year's local organizers Christian Blaschke, Marc Light and Alexander Yeh. The SIG's main goal has been to foster communication in text mining and information extraction applied to biology and biomedicine. To this end, the BioLINK group holds regular open meetings to bring together researchers from the field to interchange ideas and share them with a wider community interested in the latest developments; in the past two meetings, the Text Mining SIG has included reports from related SIGs (e.g., Bio-Ontologies and BioPathways).

Despite the successes in other fields, Natural Language Processing (NLP) techniques were not introduced into biology until the late 90's. The field has been dominated by two, not necessarily convergent, approaches:

- Application oriented, where simple methods are used (possibly too simple) to address "real" biological problems;
- Tool oriented, where complex, state of the art NLP methods are used to address problems that are not always relevant to biologists.

During the SIG meeting it became apparent that three major bottlenecks hinder current development:

- The complex and non-standardized nomenclature of genes and proteins in the scientific literature. This makes it difficult to identify the basic content of a document, in particular, the entities mentioned.
- The non-existence of large, annotated standard corpora for training and evaluation of alternative methods.
- The lack of common standards and evaluation criteria that allow researchers to compare the performance of different methodologies.

To begin to address these problems, the BioLINK group is organizing a critical assessment of text mining methods later this year (see *www.pdg.cnb.uam.es/BioLink/BioCreative.eval.html*). The assessment is inspired by the CASP evaluations and will be carried out in collaboration with Swiss-Prot, HighWire Press, FlyBase and other groups. The tasks will include entity detection (gene and protein names) and the functional characterization of proteins by assignment of Gene Ontology terms, based on full-text documents.

Bio-Ontologies SIG

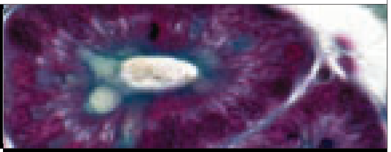
The annual one-day Bio-Ontologies Meeting has now been running for six years. The meeting consists of a series of half hour talks. These range in style from the fairly formal, and complete pieces of work, through works in progress, to the very informal, and discursive.

The theme of this year's meeting was "Ontologies and Text Analysis" The programme was strong this year, so that the tension between allowing time for the many excellent talks, discussion and questions from the floor was particularly keenly felt.

Although ontologies have been used for many years, the recent explosion of interest within bioinformatics can be explained straightforwardly in three words:- "The Gene Ontology" (*www.geneontology.org*). The success of GO continued to show at this year's meeting, with many talks relating directly or indirectly to GO.

Two main themes came out heavily this year (the call, program, abstracts and slides may be found at *www.man.ac.uk/~stevensr/meeting03/*). The first of these was the intended theme of the overlap between text and ontologies. This was the first time a theme in this meeting had been followed —indicating the close relationship of the two areas.

The second theme was the increase in bridges being built between formal ontologists and bioinformaticians. We welcome the willingness of many within the bio-ontology community to operate across domains to find solutions that work. We can see in the sixth annual Bio-Ontologies Meeting that the use of ontologies is moving out of a purely niche interest.



BioPathways SIG

The 5th BioPathways Consortium Meeting gathered 21 speakers, close to a hundred registered participants, and an undetermined number of visitors from neighboring SIGs.

The meeting featured two main scientific sessions, a session focused on databases and data exchange, and a contributed session on software tools. To foster depth of exchange, scientific sessions were structured as a series of long presentations, concluded by one hour of open discussion on the session theme.

The "Regulation and interactions on a systems scale" session revolved around a few key themes, such as the search for "modules" in biological networks, or the use of stochastic models and inference methods. The issues of reliability and validation of predictions were ubiquitous.

The "Function and evolution of metabolic networks" session illustrated well how the ongoing generation of measurements on a whole-cell scale is driving the need for models (static and dynamic), for network reconstruction methods, and for analytical approaches. A recurring theoretical theme was the use of comparative approaches.

The "Databases and Ontologies" session featured presentations on pathways exchange formats and languages by a fairly comprehensive selection of the existing groups (SBML, BioPax, CellML, OMG-LSR), as well as presentation on pathways databases, for which there is clearly an unfilled need.

Finally, the "Software Tools" session include presentations on a variety of pathways data management and visualization tools.

In summary, the meeting confirmed that the field of networks-related computational biology is more than ever in a fast-growth stage, with both frontier and depth expanding. While some theoretical subfields, such as network reconstruction from experimental data, are acquiring technical depth and generating predictions of increasing biological relevance, there is a clear trend towards a stronger coupling between theoretical and experimental approaches, leading to new open questions on both sides. Another noticeable trend is the strong revival of fields which had been perceived as fairly well understood and stable, such as metabolism, thanks both to the "systems-wide" perspective and to new theoretical tools.

More details on the meeting program can be found at *www.biopathways.org*.

OXFORD UNIVERSITY PRESS OFFERS FREE ONLINE JOURNAL ACCESS TO DEVELOPING COUNTRIES

The Oxford University Press is offering developing countries free or greatly reduced online access to many of its journals (initially until the end of 2004). This includes access to *Bioinformatics*, the ISCB's official journal.

The offer is being made in conjunction with the International Network for the Availability of Scientific Publications (INASP) and the World Health Organisation (WHO). This offer is only available for established not-for profit educational institutes.

More details, including a list of qualifying countries and participating journals can be found at *www3.oup.co.uk/jnls/devel/*.

RECOMB 2003

by Dr. Patricia Beziat

The “Seventh Annual International Conference on Research in Computational Molecular Biology—RECOMB 2003” was held in Berlin, Germany, from April 10-13. It brought together more than 500 scientists from 33 countries working in the field of bioinformatics and computational molecular biology. “This year's conference was attended by an higher-than-average amount of students and young researchers”, said Martin Vingron, local organizer of RECOMB 2003. “Thanks to ISCB and the European Commission, we were able to provide 107 Student Travel Fellowships, enabling them to come to Berlin to present their work to the community.”

The RECOMB 2003 program consisted of three components: the keynote lectures, the contributed talks and the poster session. Nine keynote speakers, each a leading expert of his/her field, allowed the audience a deep insight into a specific research area. A typical example was the lecture, “Biology and Bioinformatics on Halophilism,” by Dieter Oesterhelt. He took his audience to a journey into the world of halobacteria, extremely halophilic archaea living in habitats with extreme salt concentrations. Going through all the steps necessary to obtain the available biological data about one distinct halobacterium (data on microbiology, physiology, biochemistry and genetics), he led the audience to an understanding of what is necessary in order to model and simulate parts of cellular events of an organism and even a whole organism.

David Haussler gave an exciting lecture entitled “Computational Analysis of the Human and Other Mammalian Genomes”. He presented a broad overview of the key bioinformatic analysis problems presented by the working drafts for the human, mouse and rat genomes. In addition, he outlined some of his work combining hidden Markov models, used in bioinformatics to analyse DNA from a single species, with continuous time Markov models of molecular evolution, used to reconstruct evolutionary history of several species.

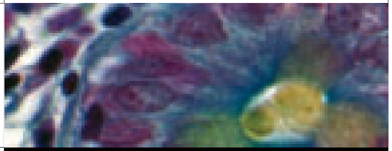
The second part of RECOMB 2003 consisted of contributed talks. The Program Committee, headed by Webb Miller, selected 35 papers out of 175 submitted for presentation at the meeting and inclusion in the Conference Proceedings. They were grouped in sessions dealing with expression data, networks, protein structure, sequence motifs, trees, sequences, proteomics, haplotypes and others. Amongst others, a talk by Derek Chiang about the theoretical analysis of the genomes of different yeast species has been one of the scientific highlights of RECOMB 2003.

ISCB Travel Fellowship Recipients (*clockwise from far left*): Sabine Berg, Silvio Tosatto, Tommy Kaplan, Matthias Futschik, Mathias Vandenbogaert, Michael Lappe, Tzvika Hartman

The talks were complemented by lively poster sessions. 183 extended poster abstracts outlined the broad spectrum of research in the field of Computational Molecular Biology and its medical applications. The abundance of different contributions enabled RECOMB 2003 to highlight developments in computational biology as well as important advances in experimental biology in the stimulating atmosphere of the conference.

RECOMB 2003 honored two young researchers (PhD students) for their excellent contributions to the conference. Gill Bejerano (Hebrew University, Israel) has been awarded the “RECOMB 2003 Best Paper by a Young Scientist Award” for his paper “Efficient exact p-Value Computation and Applications to Biosequence Analysis”. He devised a branch and bound approach to efficient exact p-value computation, and applied it to a likelihood ratio test in a frequency table setting. With two applications he briefly demonstrated his proposed method to be readily extensible to other tests and test statistics of interest. Andres Figueroa has been given the RECOMB 2003 Best Poster Award for his poster “Clustering Binary Fingerprint Vectors with Missing Values for DNA Array Data Analysis”.

In 2004, RECOMB will be held in San Diego from March 27-31, 2003. Dan Gusfield, Chair of the Program Committee, and ISCB Past President Philip Bourne, Head of the Local Organizing Committee, have already taken up their work, preparing for another RECOMB as challenging, vivid and stimulating as this year's conference.



BOOKS BY ISCB MEMBERS

Note: If you are an ISCB member with a new book and would like to see it in these pages, please email admin@iscb.org. In addition, reviews of books in computational biology and reading lists can be found in the publications section of the ISCB website.

This year, former ISCB President and current Board Member Philip Bourne of the University of California, San Diego, along with Helge Weissig of ActiveX in San Diego, edited ***Structural Bioinformatics***, the first textbook to be published in that field. The book is a collection of contributions from leading authorities. Written for molecular biologists, biochemists, biophysicists, and bioinformaticians in basic and clinical research, as well as undergraduate and graduate students in biology, medicine, and computer science, the book offers detailed coverage for practitioners while remaining accessible to the novice.

> *"This collection . . . is a must-read for all of us committed to understanding the interplay of structure and function . . . [T]he individual chapters outline the suite of major basic life science questions such as the status of efforts to predict protein structure and how proteins carry out cellular functions, and also the applied life science questions such as how structural bioinformatics can improve health care through accelerating drug discovery."*
>
> From the Foreword by John Wooley, associate vice chancellor for research at the University of California, San Diego.

As genomic and post-genomic innovations revolutionize the biological sciences, three-dimensional structural data continues to prove of vital importance to understanding function. ***Structural Bioinformatics*** represents an unprecedented, comprehensive account of the state of the discipline, providing an essential resource for students and practitioners.

Bourne and Weissig's authoritative text delivers a basic understanding of the theories, associated algorithms, resources, and tools used in structural bioinformatics, according to the publisher. Among other topics, the book covers: Fundamentals of protein structure X-ray crystallography Molecular visualization Structure classification of proteins (SCOP) Class, architecture, topology, and homology (CATH) classification Proteins as drug targets. Practicing researchers as well as students in biology, medicine, and computer science will find ***Structural Bioinformatics*** to be this field's premier resource.

> *Bourne, Philip E. and Weissig, Helge, eds.* Structural Bioinformatics. *New Jersey: Wiley-Liss, 2003.*

A second book that covers a wide range of issues in computational biology, ***Computational Biology and Genome Informatics***, was edited by 2003 ISCB Board Member Cathy Wu of Georgetown University Medical Center and the Bioinformatics National Biomedical Research Foundation; Jason Wang of the New Jersey Institute of Technology, and Paul P Wang of Duke University.

According to the publisher, the book contains articles written by experts on a wide range of topics that are associated with the analysis and management of biological information at the molecular level. It contains chapters on RNA and protein structure analysis, DNA computing, sequence mapping, genome comparison, gene expression data mining, metabolic network modeling, and phyloinformatics.

The important work of some representative researchers in bioinformatics is brought together for the first time in one volume. The topic is treated in depth and is related to, where applicable, other emerging technologies such as data mining and visualization. The goal of the book is to introduce readers to the principle techniques of bioinformatics in the hope that they will build on them to make new discoveries of their own.

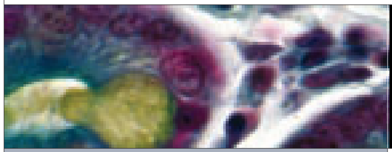
> *Wang, Jason T.L., Wu, Cathy H., Wang, Paul P., eds.* Computational Biology and Genome Informatics. *New Jersey: World Scientific Pub. Co, 2003.*

PSB 2004 REGISTRATION OPENS & ISCB TRAVEL FELLOWSHIPS OFFERED

Registration for the Pacific Symposium on Biocomputing (PSB), to be held January 6-10, 2004 at the Fairmont Orchid Hotel on the Big Island of Hawaii is now open at *psb.stanford.edu/*. Once again ISCB members are offered a $100 registration discount, and ISCB is offering a limited number of travel fellowships to member students and post docs who are presenting papers or posters.

As in the past, PSB 2004 will bring together top researchers from the US, the Asian Pacific nations and around the world to exchange current research in the theory and application of computational methods in problems of biological significance. PSB is a forum for the presentation of work in databases, algorithms, interfaces, visualization, modeling and other computational methods, as applied to biological problems, with emphasis on applications in data-rich areas of molecular biology.

ISCB student and postdoc members in need of travel funding assistance to attend PSB 2004 are encouraged to apply for one of the limited travel fellowships from ISCB. An application form is available at *www.iscb.org/ftravel_fellowship_form.php* and the deadline to apply is September 12, 2003. Announcement of awards will be made no later than October 1, 2003.



EVENTS AND OPPORTUNITIES OF INTEREST

NEWS & EVENTS FORUMS ON THE ISCB WEBSITE

You may now submit your bioinformatics conferences, events, and news directly to the ISCB website. Kudos to staff programmer Kyle Wright, who created the forms and supporting databases to enable the sharing of relevant news, conferences and events with all visitors to the site.

Upcoming conferences and events can be submitted at *www.iscb.org/events_post.php*, while news of a new product, publication, collaboration opportunity, fellowship program or any other information such as might be distributed in the form of a press release can be submitted at *www.iscb.org/news_post.php*. All submissions will be reviewed by ISCB staff to ensure appropriate content prior to posting to the conferences or news pages of the website. Events will remain posted on the site until five days after the start of the event, and news will remain for 90 days from the date of posting.

In addition, all visitors to our site are encouraged to link to the new ISCB Forums at *forums.iscb.org*. Numerous subject areas welcome your online input in an effort to address issues of importance and the diverse perspectives of members of our bioinformatics community. We look forward to your input soon!

Gordon Research Conference on Bioinformatics 2003: From Inference to Predictive Models
DATE: August 24-29, 2003
LOCATION: Queen's College, Oxford, UK
URL: *www.grc.org/programs/2003/bioinf.htm*

3rd ACM SIGKDD Workshop on Data Mining in Bioinformatics
DATE: August 27, 2003
LOCATION: Washington D.C., US
URL: *www.cs.rpi.edu/~zaki/BIOKDD03*

The Mathematics of Bioinformatics
DATE: August 27-29, 2003
LOCATION: Montreal, Quebec, CANADA
URL: *www.crm.umontreal.ca/Bio2003/*

3rd International Summer School on Computational Biology (ISSCB 2003)
DATE: August 31-September 5, 2003
LOCATION: Warsaw, POLAND
URL: *www.mimuw.edu.pl/isscb03/*

InCOB 2003
DATE: September 8-10, 2003
LOCATION: Penang, MALAYSIA
URL: *cgat.ukm.my/incob/*

3rd Annual Development, Evaluation, & Dissemination of Methods for the Analysis of Gene Expression by Microarrays
DATE: September 13-17, 2003
LOCATION: New Paltz, New York, USA
URL: *www.soph.uab.edu/statgenetics/Microarray/webnew/mrcnAnnualRetreat.asp*

7th European Conference on Artificial Life (ECAL-2003)
DATE: September 14-17, 2003
LOCATION: Dortmund, GERMANY
URL: *www.ecal2003.org*

WABI 2003: 3rd Workshop on Algorithms in Bioinformatics
DATE: September 15-20, 2003
LOCATION: Budapest, HUNGARY
URL: *wabi.biomath.mssm.edu/*

2003 IEEE International Workshop on Neural Networks for Signal Processing
DATE: September 17-19 2003
LOCATION: Toulouse, FRANCE
URL: *isp.imm.dtu.dk/nnsp2003/*

ECCB-JOBIM 2003
DATE: September 27-30, 2003
LOCATION: Paris, FRANCE
URL: *www.inra.fr/eccb2003/*

CALL FOR PARTICIPATION: ECCB Satellite Meeting: Modeling and Simulation of Biological Regulatory Processes
DATE: October 1, 2003
LOCATION: Paris, FRANCE
URL: *www.inra.fr/eccb2003/satellite2.html*

6th Annual Conference on Computational Genomics
DATE: October 8-11, 2003
LOCATION: Cambridge, Massachusetts, USA
URL: *www.jax.org/courses/tigr03.html*

German Conference on Bioinformatics
DATE: October 12-14, 2003
LOCATION: Neuherberg, GERMANY
URL: *www.gcb03.de.*

15th International Conference on Tools with Artificial Intelligence (ICTAI 2003)
DATE: November 3-5, 2003
LOCATION: Sacramento, California, USA
URL: *sierra.ecs.csus.edu:8080/*

BISTIC Symposium 2003
DATE: November 6-7, 2003
LOCATION: Bethesda, Maryland, USA
URL: *www.bisti.nih.gov/2003meeting/*

Atlanta Bioinformtics Conference
DATE: November 13-16, 2003
LOCATION: Atlanta, Georgia, USA
URL: *opal.biology.gatech.edu/GeneMark/conference/*

6th International Meeting On Single Nucleotide Polymorphism and Complex Genome Analysis (SNP2003)
DATE: November 20-23, 2003
LOCATION: Chantilly, Virginia, USA
URL: *snp2003.nci.nih.gov/snp2003/home.cfm*

II WOB 2003 - Second Brazilian Workshop on Bioinformatics
DATE: December 3-5, 2003
LOCATION: Macaé, RJ, BRAZIL
URL: *wob2003.inf.puc-rio.br*

Rocky 1
DATE: December 5-7, 2003
LOCATION: Aspen, Colorado, USA
URL: *www.iscb.org/rocky1*

PSB 2004
DATE: January 6-January 10, 2004
LOCATION: Big Island of Hawaii, Hawaii, USA
URL: *psb.stanford.edu/*

Bioinformatics Workshop Paper Presentation Competition
DATE: January 10-January 14, 2004
LOCATION: San Diego, California, USA
URL: *www.intl-pag.org/*

Hawaii International Conference on Sciences
DATE: January 15-January 18, 2004
LOCATION: Honolulu, Oahu, USA
URL: *www.hicss.hawaii.edu/*

2nd Asia-Pacific Bioinformatics Conference (APBC 2004)
DATE: January 18-22, 2004
LOCATION: Dunedin, NEW ZEALAND
URL: *www.fit.qut.edu.au/~chenp/APBC2004*

BIFI 2004
DATE: February 11-13, 2004
LOCATION: Zaragoza, SPAIN
URL: *bifi.unizar.es/zar2004/*

Proteomics: Sequence, Structure, Function
DATE: March 8-June 11, 2004
LOCATION: Los Angeles, California, USA
URL: *www.ipam.ucla.edu/programs/prot2004*

SAC 2004 -19th ACM Symposium on Applied Computing: Bioinformatics Track
DATE: March 14-17, 2004
LOCATION: Nicosia, CYPRUS
URL: *www.cs.iupui.edu/~bioin/*

RECOMB 2004
DATE: March 27-31, 2004
LOCATION: San Diego, California, USA
URL: *recomb04.sdsc.edu*

ISMB/ECCB 2004 (in conjunction with GPCVIII)
DATE: July 31-August 5, 2004
LOCATION: Glasgow, Scotland, UK
URL: *www.iscb.org/ismbeccb2004/*

ISMB 2005
DATE: TBD
LOCATION: Ann Arbor, Michigan, USA

ISMB 2006
DATE: August 4-11, 2006
LOCATION: Ceara, Fortaleza, BRAZIL

ADDITIONAL ITEMS

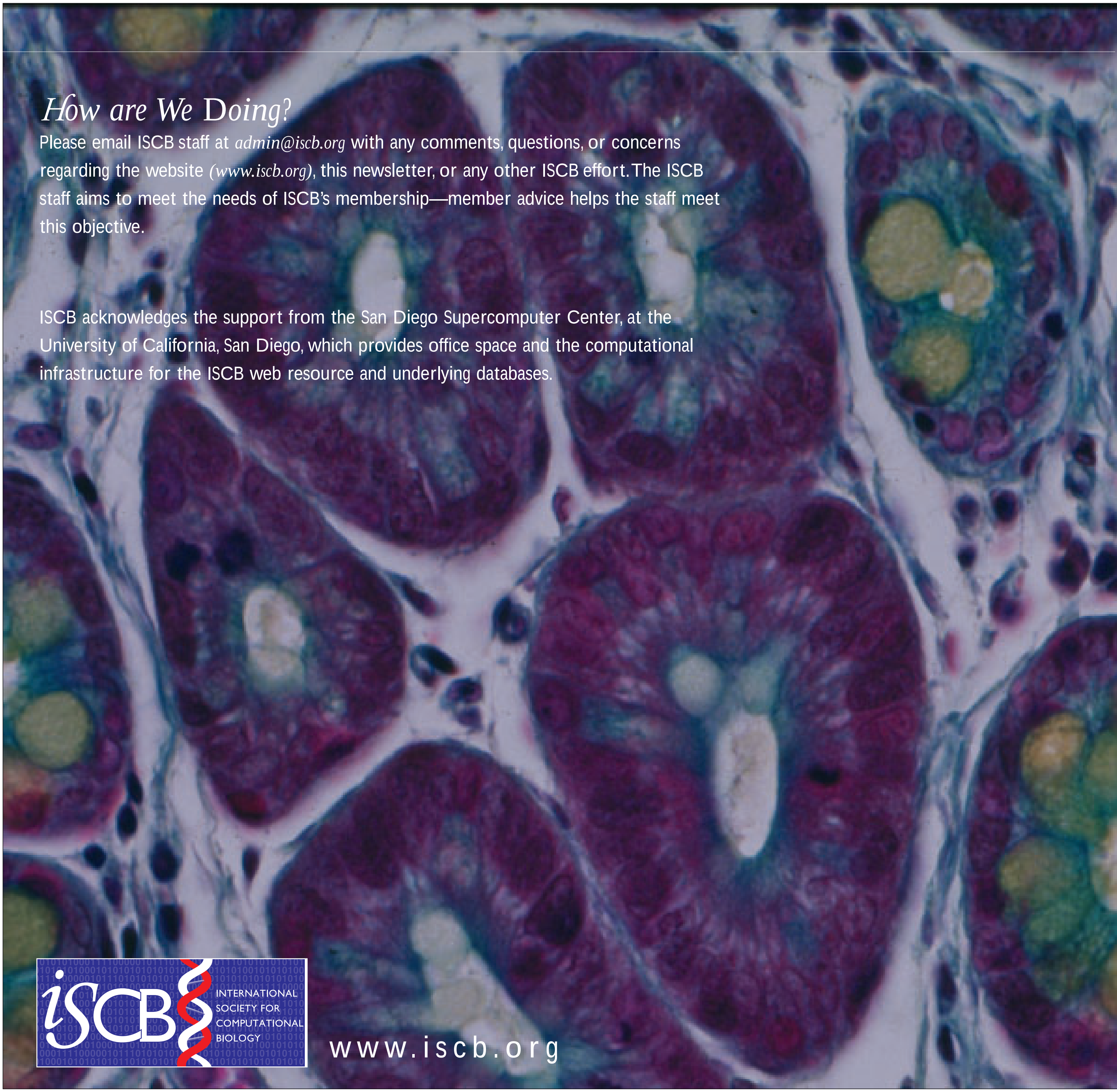
CALL FOR SUBMISSIONS: Bioinformatics India
URL: *www.bioinformaticscentre.org/journal/*
ABOUT: In an attempt to fill vacuum created by lack of comprehensive information on bioinformatics developments in India, the Bioinformatics Institute of India is launching first of its kind of journal dedicated solely to bioinformatics. BII is providing the platform for expression and is calling for research papers/ review articles/news clips to be published in this quarterly journal.

Forthcoming Titles from Chapman & Hall/CRC Press
URL: www.crcpress.com
ABOUT: Order the following titles online and receive a 10% discount—use discount code CHB20XXXX when ordering. *Statistical Analysis of Gene Expression Microarray Data*, Terry Speed; *Data Analysis Tools for DNA Microarrays*, Sorin Draghici; *Statistical Genomics and Bioinformatics, Second Edition*, Ben Hui Liu.

CALL FOR SUBMISSIONS: Statistical Applications in Genetics and Molecular Biology (SAGMB)
URL: *http://www.bepress.com/sagmb*
ABOUT: SAGMB publishes significant research on the application of statistical ideas to problems arising from computational biology. The focus of the papers should be on the relevant statistical issues but should contain a succinct description of the relevant biological problem being considered. The range of topics is wide and will include topics such as linkage mapping, association studies, gene finding and sequence alignment, protein structure prediction, design and analysis of microarray data, molecular evolution and phylogenetic trees, DNA topology, and data base search strategies.

Journal of Bioinformatics and Computational Biology (JBCB)
URL: *www.worldscinet.com/jbcb/jbcb.shtml*
ABOUT: The first issue is FREE online at: http://www.worldscinet.com/jbcb/jbcb.shtml idge National Labs, US) If you would like to receive a FREE printed copy for review, please complete the form at: *www.worldscinet.com/cgi-bin/printed_copy.cgi?jbcb.*
CONTACT: *limsoon@lit.a-star.edu.sg, mli@cs.ucsb.edu, jwooley@sdsc.edu*

CALL FOR SUBMISSIONS: Intl. Journal of Cooperative Information Systems
URL: *www.worldscinet.com/ijcis/mkt/guidelines.shtml*
ABOUT: 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



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 helps the staff meet this objective.

ISCB acknowledges the support from the San Diego Supercomputer Center, at the University of California, San Diego, which provides office space and the computational infrastructure for the ISCB web resource and underlying databases.

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

www.iscb.org

About the Cover Image

A visualization of a pre-malignant cellular phenotype in a colon cell line. The aberrant crypt foci are stained red using the CamaRx™ assay developed by Zetiq Technologies Ltd. for identifying cancerous cells.

Cover image provided by Hershel Safer.