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A NOTE FROM ISCB PRESIDENT

Phil Bourne

EXECUTIVE COMMITTEE

Philip E. Bourne, Ph.D., President Michael Gribskov, Ph.D., Vice President Anna Tramontano, Ph.D., Vice President David Rocke, Ph.D., Treasurer Barbara Bryant, Ph.D., Secretary

BOARD OF DIRECTORS Russ B. Altman, MD, Ph.D. Steven Brenner, Ph.D. Søren Brunak, Ph.D. Rita Casadio, Ph.D. Terry Gaasterland, Ph.D. Dietlind L. Gerloff, Ph.D. Roderic Guigo, Ph.D. Winston Hide, Ph.D. Lawrence Hunter, Ph.D. Minoru Kanehisa, D.Sc. Peter D. Karp, Ph.D. Toni Kazic, Ph.D. Teri E. Klein, Ph.D. Goran DS Neshich, Ph.D. Shoba Ranganathan, Ph.D. Burkhard Rost, Ph.D. Hershel M. Safer, Ph.D. Donna K. Slonim, Ph.D. David J. States, M.D., Ph.D. Gary D. Stormo, Ph.D. Masaru (Tommy) Tomita, Ph.D. Alfonso Valencia, Ph.D. Tandy Warnow, Ph.D.

Cathy H. Wu, Ph.D. **SOCIETY STAFF**

Mike Waterman, Ph.D.

Kim Baldridge, Ph.D., Staff Oversight Cassie Ferguson, Writer Stephanie Hagstrom, Conference Coordinator Jennifer Matthews, Design BJ Morrison McKay, Executive Officer Josh Polterock, Webmaster Chris Smith, Ph.D., Finance Tracy Zhao, Programming

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The ISCB Board of Directors meet by conference call every one to two months-depending on the amount of business to be discussed and once per year at the ISMB meeting. These are busy times for the Board as the Society evolves very rapidly. To give you a flavor of what happens, the following transpired at our recent meeting:

- Establishment of a Lifetime Achievement Award to be presented at the annual ISMB meeting.
- Establishment of a policy for Board member participation.
- Establishment of a small membership fee increase for next year.
- Suggest small changes to ISMB 2003's format.

Beyond these immediate changes a number of other initiatives are being discussed. We are contemplating an ISCB Book Series. Such a series would involve a series editor and a group of volume editors covering discrete areas within a bioinformatics graduate program. As one can imagine, this initiative is not something to be considered lightly. For the Society to stand behind such an effort, the Board must agree on the topic areas as well as recruit the best scientists in the field willing to commit to such an endeavor. There certainly is no shortage of publishers with an interest in taking on this project. I welcome comments on such an initiative.

We are also contemplating purchasing online access to back copies of ISMB Proceedings from 1993 to 2000 from The American Association for Artificial Intelligence (AAAI). The last two years have seen the Proceedings published as a supplement to Bioinformatics, available to members online. Whether this happens will likely depend on the cost to the Society—which is currently under negotiation. Again, I would like to hear from any members with thoughts on this matter.

To enhance our growing list of member benefits, the ISCB negotiated a special members' price for Comparative and Functional Genomics (CFG), published by John Wiley & Sons, Ltd. CFG covers research papers, reviews and features on all aspects of post-genomic research in man, animal models, plants, yeasts and bacteria. Topics of particular interest to ISCB members are the development and application of bioinformatics, evolutionary and comparative genomics, global profiling approaches (such as microarray and proteomics), large-scale mutagenesis and phenotyping, pharmacogenomics, and pharmacogenetics. For more information about CFG, visit

www.interscience.wiley.com/jpages/1531-6912/.

Finally, the Society has negotiated the availability of four pages per issue of Bioinformatics. In general terms, we propose to publish immutable information in those pages as opposed to the more transient information that appears in this newsletter. This will include the Society by-laws, including any modifications, annual cash flow, motions passed by the Board, and a notice for ISMB. Again, your thoughts on what should be published here are welcome. Paper alerts and book reviews are two topics that come to my mind.

In short, I welcome input on any Society, matters at admin@iscb.org.



IMAGE: ISCB President Phil Bourne demands R-E-S-P-E-C-T.

TENTH ANNUAL ISMB DRAWS RECORD ATTENDANCE

The ISCB's official annual meeting, Intelligent Systems for Molecular Biology 2002 (ISMB), capped four days of scientific presentations and exhibits by recognizing outstanding achievements and contributions to the field of computational biology. With over 1500 attendees, 500 posters, and 50 podium presenters, the conference, held in Edmonton, Alberta, Canada from August 3rd to the 7th, 2002, was the largest held to date.

"Judging by all the positive comments and the overflowing audiences for presentations, ISMB 2002 was a great success," said ISCB president Phil Bourne. "This year's meeting added to the foundation of ISMB as the organizers of next year's conference begin planning for ISMB 2003 in Brisbane."

Attendees had a chance to hear talks by key figures in computational biology, to view hundreds of scientific posters, to attend software demos, and to participate in a number of Special Interest Group meetings and Birds of a Feather sessions. Along with the scientific presentations and the exchange of ideas, conference attendees were treated to a festive evening at Fort Edmonton, where the crowd toured the historic buildings, feasted on barbeque, and danced for hours.

On the last day of the conference, the ISCB awarded the Overton Prize to David Baker, associate professor at the University of Washington and Howard Hughes Medical Institute Investigator. The SGI Best Paper Award was given to Pier Luigi Martelli of the University of Bologna, and ten posters won the SGI Best Poster Award (co-authors included Piero Fariselli, Anders Krogh, and Rita Casadio). The ISCB also provided a record 103 travel fellowships to graduate students and postdoctoral researchers through contributions from several sponsors and government agencies.

ISMB 2002 highlighted the work of many outstanding researchers in such diverse areas as: machine learning, pattern recognition, knowledge representation, databases, combinatorics, stochastic modeling, string and graph algorithms, linguistic methods, robotics, constraint satisfaction, and parallel computation. Biological areas of interest include: protein structure, protein function, genomics, proteomics, molecular sequence analysis, evolution and phylogenetics, molecular interactions, molecular structure, gene expression, metabolic pathways, regulatory networks, developmental control, and systems biology.

According to ISMB 2002 Conference Chair David Wishart, 90 people took part in reviewing 207 papers for the program, and accepted 50. Over 60 volunteers helped to keep the conference running smoothly.

ISCB conference liaison Stephanie Hagstrom said, "I would like to thank the Platinum Sponsors of ISMB 2002, Hewlett Packard and IBM, and our Gold and silver sponsors. The conference would not be possible without the support of those companies."

In addition to serving as a forum for computational science, the ISCB held its annual public membership meeting and a meeting of the Board of Directors, where several new Directors were elected. The Board voted on a number of other issues, including the promotion of the Society's Administrative Officer to the position of Executive Officer.

Prospective attendees of ISMB 2003, to be held in Brisbane, Australia, from June 29 to July 3 can learn more about next year's conference at www.iscb.org/ismb2003/index.shtml.











IMAGES FROM THE TOP: Barbara Bryant, ISCB secretary, leads the orienteering activity. David Wishart, ISMB 2002 chair, opens the plenary sessions. Pier Luigi Martelli, winner of the ISMB Best Paper by SGI discusses his research. Dietlind Gerloff, ISMB board member, comments to a speaker. Delegates dance at the ISMB Banquet held at Fort Edmonton.

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OVERTON PRIZE 2002

The winner of this year's Overton Prize, David Baker, associate professor at the University of Washington and Howard Hughes Medical Institute Investigator, delivered the Overton Lecture on the last day of ISMB 2002. In the keynote talk, titled "Predication and design of protein structures and protein-protein interactions," Baker thanked the ISCB, "for this great honor." He then reviewed his research as well as explaining the contributions of his colleagues. Baker said, "It's an exciting time because we can create new molecules that do all kinds of interesting things."

Larry Hunter, the founder of the ISCB and current Board member, introduced Baker. "David's contributions to the field are many and excellent," he said. Hunter mentioned the CASP4 competition and said, "Thanks on behalf of the bioinformatics community for unraveling one of our most interesting problems."

The ISCB Awards
Committee unanimously selected Baker to receive the Overton Prize for his work in applying computational science to drug design, genetics, and health care, and, in particular, the Rosetta algorithm, which predicts protein structure.

ISCB WELCOMES

The ISCB welcomes six new members to its board of directors. Steven Brenner, Rita Casadio, Roderic Guigo, Goran Neshich, Shoba Ranganathan, and Burkhard Rost were voted in during an annual Board meeting, held August 5, 2002, in conjunction with ISMB 2002. The new Board members were elected based on nominations gathered from the membership. The new members were elected to three-year terms as four other members completed their service to the Society.

"I am pleased to welcome the new Board members. They demonstrate the depth, scientifically and geographically, of the Society as a whole, and will particularly enhance the voice of the Society in their regions while providing an international representation on the Board of Directors," said ISCB President Phil Bourne.

Steven E. Brenner, Ph.D., is assistant



professor and leader of a computational genomics research group at the University of California, Berkeley. His research interests

include computational approaches for structural genomics and sequence analysis, and the use of both of these to infer-molecular function. Brenner was educated and trained at Harvard University, the MRC Laboratory of Molecular Biology and Cambridge University, and Stanford University. More about his research group may be found at *compbio.berkeley.edu*.



Rita Casadio, Ph.D., is a professor of biophysics and group leader of the biocomputing unit at the Interdepartmental Centre for Biotechnological Researches at the University of Bologna, Italy. Casadio has worked on biophysics in laboratories both in the US and Germany. Her current research focuses on theoretical and experimental membrane and protein biophysics. Presently she is interested in computer modeling of relevant biological processes, such as protein folding. This she applies to her research on the application of neural networks to the prediction of secondary structure of proteins from their residue sequences. More about her research may be found at www.biocomp.unibo.it.

Roderic Guigo, Ph.D., is a researcher at the



Institut Municipal d'Investigació Mèdica, an Associate Professor at the Universitat Pompeu Fabra, and coordinator of the Bioinformatics

Program at the newly created Center for Genomic Regultaion in Barcelona. Guigo obtained his Ph.D. in 1988 from the Universitat de Barcelona where he worked at the Department of Statistics with advisor, Jordi Ocaña. Guigo conducted postdoctoral research as a fellow with Temple F. Smith at Harvard's Molecular Biology Computer Research Resource. Ongoing work with Smith includes several sequence analysis projects. Guigo continued his postdoctoral research with Los Alamos National Laboratory's Theoretical Biology and Biophysics Group where he worked on genome analysis with James W. Fickett. Following this, Guigo returned to the Universitat de Barcelona where he worked in the Department of Statistics. More about his research may be found at www1.imim.es/main/research.html.

Six New Board Members

Goran Neshich, Ph.D., is a structural bioin-



formatics group leader at the Brazilian Enterprise for Research in Agriculture (EMBRAPA), Informatica

Agropeciam, Compines, Brazil. Neshich started his work in structural bioinformatics while studying structure and function relationship of the photosynthetic reaction center during his graduate work done with Don DeVault at the University of Illinois at Urbana-Champaign. He conducted his postdoctoral research with Barry Honig at Columbia University. Neshich is the principal author of STING and the STING Millennium Suite, a popular software application for presentation of macromolecular interactions, structure analysis, and visualization. STING is accessible from the Protien Data Bank (PDB), www.pdb.org. He is continuing to develop tools for comprehensive presentation of physical-chemical properties of proteins (Protein Dossier) and applying those to generate structure/function descriptors. His latest initiative is developing the Protein Dossier to be suitable for presentation of results obtained and used in drug and drug target identification and chemogenomics. More about his research may be found at www.cbi.cnptia.embrapa.br.

Shoba Ranganathan, Ph.D., is an associate



professor of biochemistry and biological sciences at the National University of Singapore, Singapore, Malaysia.

Ranganathan's research focuses on: protein

structure comparison, prediction and modeling and function prediction; creation and mining of boutique databases for computational biology and immunology; alternate splice variants and intron-exon evolution; comparative genomics and organism-based transcription regulation; and developing Grid computing applications in bioinformatics. Ranganathan has served as the Vice President of the Asia Pacific Bioinformatics Network (APBioNet) since January 2000; and as the Secretary of S* Life Science Informatics Alliance since July 2000. More about her research may be found at *surya.bic.nus.edu.sg/shoba*.

Burkhard Rost, Ph.D., is an associate profes-



sor of biochemistry and molecular biophysics, Columbia University, New York, USA. Rost's research focuses on the prediction of protein structure

and function by combining means from simple statistics to artificial intelligence and evolutionary information. His group is currently also working on the following projects: to improve and extend the EValuation of Automatic protein structure prediction (EVA) server to continuously evaluate structure prediction; to improve methods to predict secondary structure and solvent accessibility; to build a database of predictions for entire genomes; and to predict structural domains from sequence. More generally, his group attempts to shift focus from predicting structure to predicting function. More about his research may be found at *cubic.bioc.columbia.edu*.

The ISCB Board of Directors consists of 30 members who lead committees on awards, conferences, education, finance, nominations, and publications.

2003 REGISTRATION NOW OPEN

Sign up now for year 2003 membership and avoid interruptions to online and hardcopy journal subscriptions. The ISCB aims to meet the demands of its growing membership by opening 2003's membership registration for new and renewing members two months earlier than in the past. Beginning October 6, 2002, membership registrations will be recorded for the coming year, rather than the few remaining months of this year. As ISCB membership follows the calendar year—January 1-December 31—it is important to sign up before January to take full advantage of membership features and benefits throughout 2003.

To register or renew for 2003, visit www.iscb.org/membership. All current and past members can login using previously assigned membership numbers and email addresses registered with ISCB. Members will find 2003 membership pricing and journal subscription rates on the registration page. Once registration has been completed, members will be able to re-login and print a receipt for their records.

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ANNUAL OPEN MEMBERSHIP MEETING

On August 6, 2002 the ISCB held its annual public members meeting to review the state of the Society as well as to offer members a chance to voice their concerns and to make suggestions for the upcoming year. ISCB President Phil Bourne presented a summary of the past year's accomplishments and possible future directions for the Society, then opened the floor to the membership.

Among the first issues discussed was the number of people who chose not to join the ISCB when registering for ISMB—despite significant cost savings for the registrant. Several members mentioned that many companies and grants will not reimburse for professional society memberships. However, others mentioned that the registration form could be improved to emphasize that registering for ISMB as a member is a benefit that pays for itself.

Another topic discussed at length was the format of future ISMB meetings, whether or not to hold parallel sessions extending the poster sessions, and the degree to which SIGs should be incorporated into the meet-

ing. In a show of hands, the majority of participants in the membership meeting indicated a preference for parallel sessions.

However, ISCB Founder and current Board member Larry Hunter said, "As the AI community split, their meeting ran mostly parallel sessions. Eventually the community diverged and the conference and journal split up—much to the detriment to the field. We need to be careful about this."

Several people spoke about the importance of software demonstrations to ISMB and mentioned that they would like to see them more closely integrated into the overall program. Terry Gaasterland, Board member and researcher at the Rockefeller University, suggested that demos be reviewed. "Anything that we're going to be spending time on should be reviewed somehow," she said.

One suggestion that was seconded by several members was the idea of providing a five to ten minute slot for researchers with the best poster to make a presentation. Another member mentioned the possibility of recording sessions or providing video on demand.

Bourne brought up the topic of removing the special or "S" designation of papers accepted for the ISMB issue of *Bioinformatics*. He said that researchers may be hesitant to submit their best work for the conference since papers published with the "S" designation tend to carry less academic weight than regular papers. However, the process for refereeing papers would have to be brought up to a level that is as rigorous for regular papers, a sentiment echoed by several other members, said Bourne.

Among the more controversial issues discussed was the procedure for issuing society positions such as the open source statement released earlier this year. In general, the speakers wanted to change the procedure for making statements. In a sentiment echoed by several other members, Rick Lathrop of the University of California, Irvine, said, "If we are going to issue a statement about an emotionally charged topic in the name of the membership, please poll the membership; use the mailing list."

APPLICATION DEADLINE NOVEMBER 1, 2002: ISMB 2004 AND 2005

Organizing Committee Requirements

The ISCB Conference Committee will be responsible for reviewing submissions from potential Organizing Committees to host the ISMB conference. The general qualifications and considerations for selecting an Organizing Committee to host the Annual ISMB conference are listed below.

- 1. Organizing Committee Chair or Co-chairs must be senior in the bioinformatics field.
- Organizing Committee Chair or Co-chairs must have experience with chairing or participating on an organizing committee for a scientific conference.
- 3. At least two Organizing Committee Members must have participated in past ISMBs.

- 4. All Organizing Committee Members must be members of the ISCB.
- Organizing Committee must consist of members who have scientific credibility in the bioinformatics field and include international and gender diversity.
- 6. Organizing Committee should have adequate support from the Local Organizing Committee to successfully organize the arrangements for the conference either through their own staff, student volunteers or by hiring an outside professional meeting planning company.
- 7. Suggested conference location must have adequate conference facilities to meet the requirements of the conference. Facility must have

- high-speed Internet to be considered and a meeting room to accommodate up to 1800 people for lectures.
- 8. Several Organizing Committee Members must be located in the same region as the conference location to manage the Local Organizing Committee arrangements.

Proposal selection will be based on the best proposal with consideration for geographical distribution of the conference. For additional submission specifics and historical data, see: www.iscb.org/word-docs/RFP2004_2005.doc.

ISMB 2003: G'DAY FROM DOWN UNDER!

Judging from the reception at the ISMB 2003 display booth in Edmonton, people had better start polishing those papers and consulting the better half on travel plans! To give delegates a taste of Australia, the ISMB 2003 Brisbane organizers brought along 1000 stuffed koalas—almost all of which had been adopted enmasse by the end of the first day. Why settle for the toy when one may experience the ridgy-didge (Aussie slang for original/genuine)? ISMB 2003 will be the perfect opportunity to combine serious science with a bit of relaxation with family or colleagues.

For biologists, Australia is nirvana—recognized internationally as one of only twelve mega-biodiverse countries (plenty of which is on display around Brisbane). From the local committee's perspective, one of the key long-term benefits of bioinformatics in Queensland will be to manage and explore data from molecular bioprospecting. The co-host for ISMB 2003, the Institute for Molecular Bioscience at the University of Queensland, has recently spunoff several companies with both in vitro and in silico platform technologies that link natural products (such as those in cone-shell snail venom) to pharmaceutical development. In silico analysis is a lot safer and saner than chasing new antibiotics in reptile blood, but for the vicarious crocodile hunters, Steve Irwin's Australia Zoo is just an hour's drive north. The local organizing team has also heard rumors from certain SIG groups of a field trip in "Mining marine biodata—an applied approach" out on the Great Barrier Reef.

Queensland is known as the "Sunshine State" for good reason. Brisbane's winter (the northern-hemisphere summer) is the sunniest time of all. ISMB 2003 organizers found arrival in the Alberta "summer" rather chillier than the

accustomed wintertime in the Brisbane subtropics (where an exceptionally cold night might drop to 7°C/45°F). Just across the road from the convention centre where ISMB 2003 will be held is South Bank Beach (see picture) with nearby child-minding facilities. South Bank was built on the 1988 World Expo site and is host to many restaurants, pubs and alfresco cafes (a la Tivoli Gardens in Copenhagen). Despite the common joke of the Aussie seven-course lunch (meat-pie and sixpack of beer), Brisbane is a sophisticated cosmopolitan city, noted for its fusion cooking style that combines Western cuisine with Eastern and local ingredients.

ISMB gets bigger and better every year, and the ISMB 2003 organizers have every intention of ensuring that the trend continues. Organizers are already engaging the ISCB's regional affiliates, and delegates may look forward to productive interactions with the rapidly growing bioinformatics communities in Japan, Korea, China and elsewhere in Southeast Asia. Parallel sessions will be introduced, in a limited way, for the first time. Gene Myers and his Program Committee expect to see high-quality presentations in diverse areas. The Call for Papers will be open at the website (www.iscb.org/ismb2003) by early October. We look forward to your papers, and to greeting you in Brisbane next year!

ISMB 2003 Key Dates

December 3, 2002 Tutorial Proposals Due January 2, 2003 Close Paper Submission March 3, 2003 Registration Opens April 24, 2003 Close Poster Submission

IMAGE: Brisbane's Southbank Beach—Courtesy of Brisbane Tourism @





CAPRI AND ECCB TRAVEL FELLOWSHIPS

ISCB had provided travel awards for graduate students and postdoctoral researchers to attend both the Critical Assessment of PRediction of Interactions (CAPRI) Evaluation Workshop (capri.ebi.ac.uk/EvaluationMeeting.html) as well as the European Conference on Computational Biology (ECCB: www.zbi.uni-saarland.de/ECCB2002).

CAPRI Fellowship recipients:

- Juan Fernandez Recio, The Scripps Research Institute
- Jeffrey J. Gray, Johns Hopkins Univ.
- Engelbert Mephu Nguifo, Université d'Artois
- Zhiping Weng, Boston Univ.

ECCB Fellowship recipients:

- · Ming Chen, Univ. of Bielefeld
- Kim Hei Jin, Pohang Univ. of Science & Technology
- Bin Hu, Keio Univ.
- Laszlo Kajan, Univ. of Montreal
- Sivakumar Kannan, Univ.of Montreal
- Jeane Cecília Bezerra de Melo, Univ. of Pernambuco, Recife, Brazil
- B.V.L.S.Prasad, Indian Institute of Science
- Einat Sitbon, Weizmann Institute of Science
- Mallika Veeramalai, Univ. of Glasgow
- Markus Wistrand, Sweden Center for Genomics and Bioinformatics

ISMB 2002

ISCB is pleased to announce the winners of this year's ISMB Best Paper and Best Poster Awards by SGI.

Pier Luigi Martelli took home best paper honors for "A sequence profile based HMM for predicting and discriminating beta barrel membrane proteins." Co-authors included: Piero Fariselli, Anders Krogh, and Rita Casadio.

Prior to ISMB, Martelli was selected as one of three finalists in the best paper category. It was determined—by a subset of the senior review committee—that Martelli should receive the award for best paper based on his written paper and oral presentation at ISMB.

Ten posters—from a pool of over 500—were selected to receive Best Poster honors. ISMB delegates selected the best poster winners. The winners selected were:

- Using Structure and Sequence Information for Predicting Transcription Factor Binding Sites.
 Tommy Kaplan, Nir Friedman and Hanah Margalit. The Hebrew University, Jerusalem.
- Automatic Classification of Protein Structures
 Using Gauss Integrals. Peter Røgen and Boris
 Fain. Department of Mathematics,
 Technical University of Denmark, Denmark
 and Department of Structural Biology,
 Stanford University.
- Mauve: Multiple Genome Alignments. Aaron
 Darling, Bob Mau, Frederick R. Blattner
 and Nicole T. Perna. Departments of
 Computer Science, Animal Health,
 Biomedical Sciences, Oncology and
 Genetics, University of Wisconsin-Madison.
 The first two authors contributed equally to
 this work.

SGI Awards

- Finding Biological Themes in z-derived Gene Lists with EASE: the Expression Analysis Systematic Explorer. Douglas A. Hosack and Richard A. Lempicki. Laboratory of Immunopathogenesis and Bioinformatics, SAIC Frederick.
- From RegulonDB to a Multigenomic

 Microbial Database of Operon Organization
 and Gene Regulation. Salgado H, SanchezSolano F, Diaz-Peredo E, Gama-Castro S,
 Garcia-Alonso D, Perez-Rueda E, JimenezJacinto V, Medrano-Soto A, MorenoHagelsieb G and Collado-Vides J. Nitrogen
 Fixation Research Center, Av. Universidad,
 Cuernavaca, Morelos.
- Modeling Genetic Regulatory Networks Using Dynamic Bayesian Networks. Y. Zeng, R. Khan, J. Garcia-Frias and G. Gao.
 Department of Electrical and Computer Engineering, University of Delaware.
- Expert-system based annotation strategies using GenDB, an open source genome annotation system. Alice McHardy, Jan Kleinluetzum and Folker Meyer. Center for Genome Research, Bielefeld University
- G-language Genome Analysis Environment.
 Kazuharu Arakawa, Koya Mori, and Masaru Tomita. Institute for Advanced Biosciences, Keio University, Department of Environmental Information and Graduate School of Media and Governance.
- A High Throughput Pipeline for Validating Novel Splice Variants Discovered Using Whole-Genome Junction Arrays. Patrick Loerch, Chris Armour, Phil-Garrett-Engele, Ralph Santos, Zhengyan Kan, Jason Johnson and Daniel Shoemaker. Rosetta Inpharmatics.
- Atomic Reconstruction of Metabolism.
 Masanori Arita. Computational Biology
 Research Center, Koto-ku Aomi, Tokyo.

BOURNE RECEIVES SUN CONVERGENGE AWARD

Sun Microsystems has acknowledged the scientific leadership of San Diego Supercomputer Center's (SDSC) Director of Integrative Biosciences and ISCB President, Phil Bourne, presenting him with the Convergence Award at BioFusion 2002, an event held at the Old Globe Theater in San Diego, California, on June 24, 2002.

The Sun Microsystems Convergence Award recognizes a scientific leader who has fostered the integration of information technology with the life sciences, with the ultimate goal of improving global public health.

"Phil Bourne's leadership continues to have a dramatic impact on facilitating the IT convergence into the advancement of Life Sciences," said Howard Asher, director, life sciences industry solutions worldwide at Sun Microsystems. "It is because of Phil Bourne's contributions that Sun Microsystems has honored him with the Convergence Award."

"SDSC is proud to see Phil recognized for his contributions to the biology community in San Diego and around the world," said SDSC Director Fran Berman. "Thanks to Phil and our world-class team of computational biologists, SDSC has been able to make unique contributions to biology and bioinformatics and to foster breakthroughs in scientific discovery for biology and health care."

Bourne, a computational biologist for nearly two decades, is considered a leader in the world's bioinformatics community. Along with his research projects at SDSC, Bourne serves as a professor of pharmacology at the University of California at San Diego, and an adjunct professor at the Burnham Institute and the Keck Graduate Institute.

Bourne has headed up a long roster of projects, including serving as co-director of the Protein Data Bank and a principle investigator of the Systematic Protein Annotation and Modeling project, funded by the National Institutes for Health.

The award was one of several life science and achievement prizes presented at BioFusion 2002, an event sponsored by the T Sector Magazine and BIOCOM to honor life science executives and leaders in the California life science sectors.

BJ MORRISON MCKAY: EXECUTIVE OFFICER

The ISCB Board of Directors voted to appoint the Society's first Executive Officer, BJ Morrison McKay, at the board meeting held in conjunction with ISMB. Previously, McKay served as the Society's Administrative Officer.

"BJ is extremely competent, and has made enormous contributions to ISCB since joining us earlier this year," stated ISCB President, Phil Bourne. He cited her excellence in managing a move of the Society from Stanford to offices based at the San Diego Supercomputer Center at the University of California, San Diego, as well as the management and association experience she brings to the role.

As Executive Officer, McKay will focus on forging strategic partnerships with industry and special interest groups to bring additional resources and benefits to members and affiliated regional groups worldwide. McKay will also liaise between the Executive Committee, Board of Directors, and Society members, to create and provide a record of institutional memory for future reference.

To reach McKay, please write to admin@iscb.org.





EVENTS AND OPPORTUNITIES OF INTEREST

DIMACS Special Focus on Computational Molecular Biology

DATE: September 2000-August 2003 UPCOMING: Protein Domains: Identification, Classification and Evolution Dates: *February 27-28, 2003,* DIMACS Center, New Jersey, USA URL: *dimacs.rutgers.edu/Workshops/ index-compmolecbiol.html*

European Conference on Computational Biology 2002 (ECCB 2002)

DATE: October 6-9 2002 LOCATION: Saarbrücken, GERMANY URL: www.eccb2002.de

ABOUT: Provides an opportunity to present cutting edge research in computational biology. 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-II, 2002 LOCATION: Freiburg/ Breisgau, GERMANY URL: www.biodigital.de ABOUT: Tade fair and top-class conference for science and business decision makers in Microarray technology and Bioinformatics. CONTACT: +44-0-20-7017-5069; +44-0-20-7017-4822 (fax)

WORKSHOP: Computer Graphics and Visualization Techniques for Medical Applications — University of Colorado

DATE: October 18, 2002

URL: www.cudenver.edu/ccb/workshops.html
ABOUT: Designed to acquaint researchers in
medicine and bioinformatics with new computer
graphics, visualization and interactive techniques.

COPE '02: IZKF Muenster Workshop on Comparative Analysis of Protein Evolution

DATE: October 24-26, 2002
LOCATION: Muenster, GERMANY
URL: www.izkf.uni-muenster.de/cope2002
ABOUT: Designed to bring together researchers from biomedicine with an interest in specific protein families, and researchers from bioinformatics who analyze the evolution of proteins.

CALL FOR PAPERS: **3rd IEEE Symposium on Bioinformatics and Bioengineering**

DATE: October 28, 2002 LOCATION: Washington DC Area, USA SUBMISSION DEADLINE: March 10-12, 2003 URL: www.cs.msstate.edu/~bibe

ABOUT: The BIBE Symposium provides a common platform for the cross fertilization of ideas to help shape knowledge and scientific achievements by bridging bioinformatics and bioengineering through an interactive forum.

CALL FOR PAPERS: *Journal of Parallel & Distributed Computing,* Issue on High-Performance Computational Biology

MANUSCRIPT DEADLINE: November 15, 2002 URL: www.academicpress.com/

www/journal/pc/pcifa.htm

ABOUT: Aimed to provide a forum for the publication of important research contributions in developing high-performance computing solutions to problems arising from molecular biology. CONTACT: Editors: Srinivas Aluru — aluru@iastate.edu; David A. Bader — dbader@eece.unm.edu

Standards and Ontologies for Functional Genomics (SOFG)

DATE: November 17-20, 2002
LOCATION: Hinxton, UK
URL: www.wellcome.ac.uk/hinxton/sofg
ABOUT: MGED-supported conference to bring
together the scientists who are developing standards and ontologies for describing highthroughput functional genomics experiments
and those who are using these new tools. .
CONTACT: +44 -0-1223-495002; +44 -0-1223495023 (fax); nicky.clarkson@hinxton.wellcome.ac.uk

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

DATE: December 13-15, 2002 LOCATION: Stockholm, SWEDEN URL: www.icsb2002.org ABOUT: Experimental, computational and theoretical advances in the 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 transduc-

tion, and morphogenesis.

First Asia-Pacific Bioinformatics Conference Within Australia

DATE: February 4-7, 2003
LOCATION: Adelaide, AUSTRALIA
URL: www.fit.qut.edu.au/~chenp/APBC2003
ABOUT: 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: +61-7-3864-1945; +61-7-3864-1969 (fax); p.chen@qut.edu.au

New Zealand Bioinformatics Conference

DATE: February 13-14, 2003 LOCATION: Wellington, NEW ZEALAND

URL: *bioconf.otago.ac.nz*ABOUT: This conference boasts something for everyone in bioinformatics. Workshops will cater to biologists and computer scientists. We will follow up with a series of seminars related to the areas of microarray analysis, phylogenetics

ACM Symposium on Applied Computing — Bioinformatics Track

and protein structure and function prediction.

DATE: March 9-12, 2003
LOCATION: Melbourne, Florida, USA
URL: www.cs.iupui.edu/~bioin/
ABOUT: The biomedical information science
and technology initiative report identifies the
need for computational tools to meet important
challenges in biomedical research. This track will
address research issues related to any area of
bioinformatics.

BioThailand 2003

DATE: July 17-20, 2003
LOCATION: Bangkok, THAILAND
URL: biothailand2003.biotec.or.th
ABOUT: The National Center for Genetic
Engineering and Biotechnology will organize
BioThailand 2003: Technology for Life featuring
scientific meetings, trade show and the showcase
of Thai biotechnology innovations.
CONTACT: 66-2564-6700; 66-2564-6701 to 5
(fax); biothailand2003@biotec.or.th

ADDITIONAL ITEMS

New Distance Learning Professional Masters Program in Biomedical Informatics

URL: smi-web.stanford.edu/academics/
ABOUT: The Biomedical Informatics training program at Stanford University will offer a professional Masters degree beginning Spring 2003. The professional MS program is designed so students may remain fully employed while studying for their degree. Students accepted into the program may enroll part-time with up to 5 years to complete the program. It is possible to fulfill the requirements for the degree on-line through courses delivered by the Stanford Center for Professional Development.

DIMACS — Celera Genomics Graduate Student Award in Computational Biology

URL: dimacs.rutgers.edu/SpecialYears/2000_2003
ABOUT: Nominations requested for a graduate student award as part of the DIMACS Special Focus on Computational Molecular Biology.
CONTACT: +1-732-445-5928;

+I-732-445-5932 (fax); center@dimacs.rutgers.edu

Oxford University launches part-time MSc in Bioinformatics

DATE: October 2002

URL: www.conted.ox.ac.uk/bioinformatics
ABOUT: Oxford University will launch a new,
part-time M.Sc. in Bioinformatics October 2002
for those with a mathematical background
and/or biological knowledge. The program is
designed for individuals in full time employment
in industry.

CONTACT: bioinf@conted.ox.ac.uk

Announcing Cluster Analysis of Gene Expression Dynamics (CAGED)

URL: chip.org/caged

ABOUT: Computer program for cluster analysis of gene expression data collected through microarray experiments. CAGED implements a Bayesian clustering method designed to handle temporal experiments and subsuming standard independent experiments as a special case.

New Graduate Program at the University of Alabama: Specialization in Bioinformatics

URL: www.cis.uab.edu

ABOUT: Jointly administered by computer science faculty and biomedical research faculty in the UAB Medical Center. In addition to the computer science graduate admission require-

ments, the specialization requires an approved background in molecular biology.

OUP Offers Free Online Trial of Human Molecular Genetics

URL: hmg.oupjournals.org/

University of Colorado Center for Computational Biology introduces its Certificate in Computational Biology

URL: www.uchsc.edu/sm/pmb/bioi/

ABOUT: CU Center for Computational Biology begins the program fall 2002. It feeds into two new computational biology options for the MS degree: computer science and applied mathematics which feed into the School of Medicine Ph.D. in analytical health sciences/bioinformatics.

American Heart Association (AHA)

URL: www.americanheart.org/research

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 biannually. Application deadline: January 13, 2003.

Bioinformatics Training Program for Health Research

URL: www.bioinformatics.bc.ca
ABOUT: Trans-disciplinary program (offering learning streams leading toward certificate, MS, or PhD) designed and taught by leading researchers and their institutions in British Columbia and the Pacific Northwest.

CALL FOR SUBMISSIONS: Intl. Journal of

CONTACT: +1-604-707-5965; nstewart@bcgsc.ca

Cooperative Information Systems

URL: www.worldscinet.com/ijcis/mkt/guidelines.shtml

ABOUT: This issue focuses 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

To recommend a news item be included in the ISCB Newsletter, please write to admin@iscb.org.

ISCB members receive a 10% discount when they register by November 8, 2002 for the following events:

Data Analysis and Visualization: New York City - December 3-5, 2002

This event focuses on approaches and strategies in determination of gene expression—integrating advancements in microarray and visualization technologies with applications ranging from the research lab to the clinic. Benefit from keynotes, case studies and interactive discussion with leading industry and research organizations.

Register: www.melifesciences.com/ISCB5.htm email: conferences@marcusevansch.com

Executive IT Life Science: New York City - December 3-5, 2002

The 2nd semi-annual forum designed to address the IT challenges of the life-sciences industry, and allow senior executives the opportunity to discuss, strategize and offer solutions to the ever-changing IT landscape in the pharmaceutical and biotech markets.

Register: www.melifesciences.com/ISCB3.htm email: conferences@marcusevansch.com

Bioinformatics in Systems Biology: New York City - December 3-5, 2002

This event focuses on applying bioinformatics to the study of biology as an integrated system—Maximizing the technological advances to integrate, analyze, and manage data from the complex systems responsible for all biological functions.

Register: www.melifesciences.com/ISCB4.htm email: conferences@marcusevansch.com

Knowledge Management for R&D: New York City - December 3-5, 2002

This event focuses on knowledge management platforms and strategies, essential to enhancing R&D. Workshops, case studies and panel sessions will uncover the answers to leveraging collaborative knowledge distribution to ensure intelligent drug discovery and design.

Register: www.melifesciences.com/ISCB1.htm email: conferences@marcusevansch.com

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