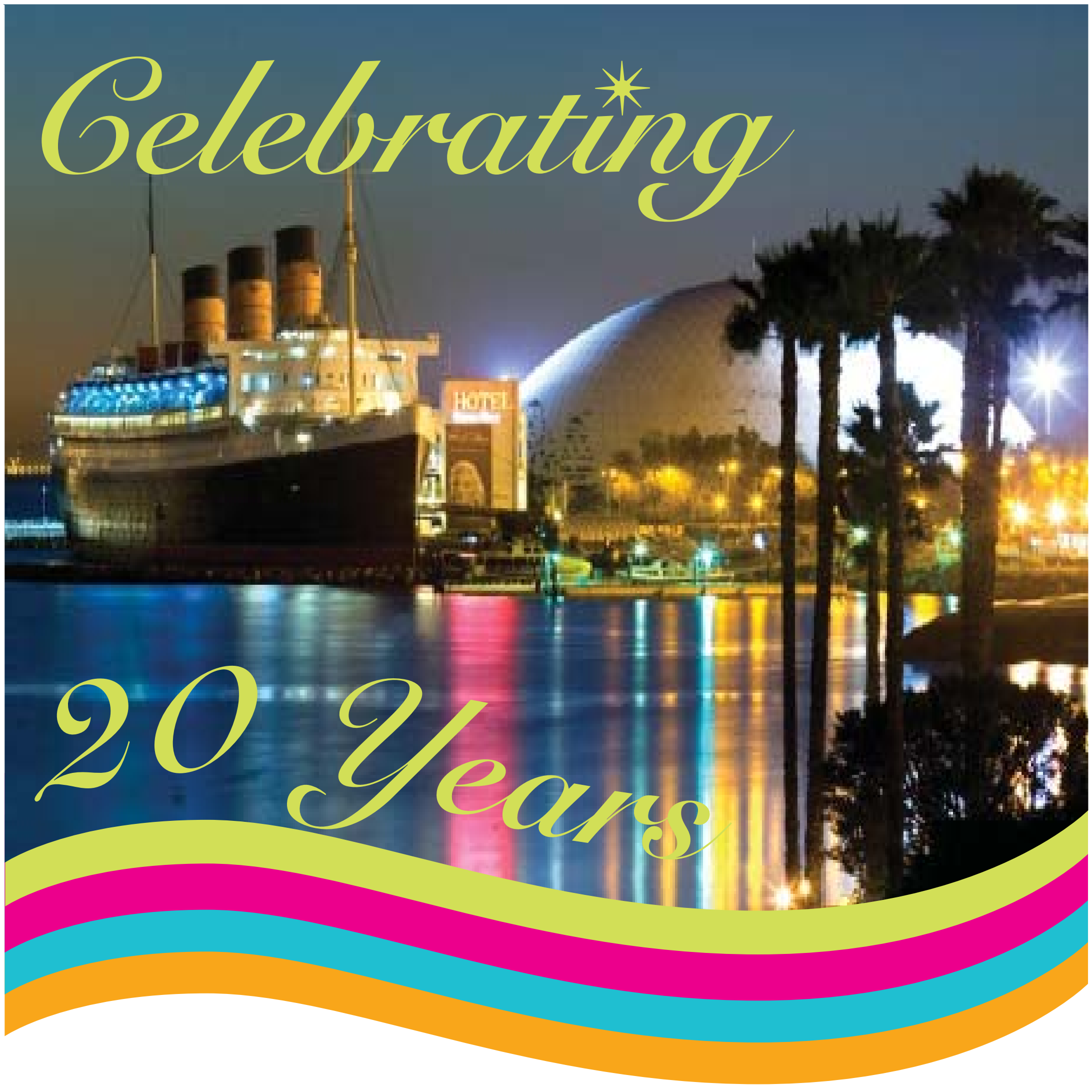
ISCB NEWSLETTER

ISMB 2012 FOCUS ISSUE



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INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

A LETTER TO ISCB MEMBERS & COLLEAGUES

CELEBRATING MANY MILESTONES TOGETHER

Burkhard Rost
President

BJ Morrison McKay
Executive Officer

A milestone is one of a series of numbered markers placed along a road… Milestones are placed to provide reference points… (Wikipedia). This year ISCB is reaching and celebrating many milestones on its path to continued growth. Each of these milestones marks an advance in our field as well as in biomedical sciences. Each advance contributed to the good of life. We could all be proud to be part of that!

5, 10, 20, 50, and even 100 years… These are the milestones we are celebrating throughout 2012. For such a young society in a field that was full of new and massive challenges just a few short years ago, we are pleased that bioinformatics and computational biology have achieved a level of incontrovertible recognition for building essential tools that advance biological research, and we salute the longevity of the following conferences and institutions:

5 Years In 2012 ISCB held the Fifth Annual Conference on Semantics in Healthcare and Life Sciences (CSHALS). This meeting is the result of a proposal brought to ISCB by members Eric Neumann and Ted Slater, and remains the only meeting ISCB organizes that focuses on a single, specialized topic, and that features applications specific to hospitals and pharmaceutical research and development. Since its inception CSHALS has been held in Cambridge, Massachusetts, USA, but the idea of rotating with a European location or starting a European version of this event is open for consideration. If this interests you and you would like to get involved please let us know – new initiatives can only move forward with support from our community and the commitment of volunteers to lead the way.

10 Years The Rocky Mountain Bioinformatics Conference (Rocky), held every year in Snowmass/Aspen, Colorado, USA, was started ten years ago during an ISCB Board of Directors meeting. At that point ISCB revenue was derived completely from ISMB. Larry Hunter, a founder of both ISMB and ISCB and ISCB's first president, suggested during this meeting a first step toward diversify with a small ISCB meeting in Colorado. Originally conceived of as a regional meeting, Rocky drew an international attendance from the beginning, and has grown to welcome over 150 people annually from around the world. The meeting is well known for offering lengthy networking breaks in the middle of the day, but the real beauty of Rocky is that virtually everybody who wishes to present their research can do so either as a 7-10 minute flash presentation, or as a poster. A lot of science is presented at this 2 ½-day meeting, and is balanced by substantial networking on the slopes or in town during the mid-day breaks.

20 Years ISMB is celebrating its 20th anniversary this year in Long Beach, California, USA. In its very first year ISMB drew 200 people to Bethesda, Maryland, USA, for a gathering of researchers applying artificial intelligence to the study of molecular biology. Although the scientific foundation of the meeting remains true to its original core concept, the ISMB of today bears little resemblance to that of 20 years ago. By the fifth ISMB in Halkidiki, Greece, during which the ISCB was founded as a professional society to serve our community, the collective total number of talks barely exceeded 200. At the 20th ISMB in Long Beach, more than 200 talks will be presented.

This jump in participation was caused by moving from a single papers track (through 2003), to parallel papers tracks thereafter, to the truly multi-track meeting format introduced at ISMB/ECCB in Vienna (2007). Tracks have their own "life" and "identity" and we have experimented over the years with how to optimally define those tracks. Last year at the ISMB/ECCB in Vienna (our second meeting in that city), we introduced the Oral Poster Presentations - short talks selected from among the best poster submissions. In Long Beach we have even more of this due to an overwhelmingly positive reaction. This year, we dare another leap: we combine the Proceedings and Highlight tracks during the presentation (they remain separate entities for the task of reviewing). The rationale was to avoid too much overlap and "running around." We will need your feedback on how you liked this novelty. Now that we have hopefully managed the worst overlaps, we can consider coordinating even the topics during the smaller tracks, namely Late Breaking Research, Oral Poster Presentations, and Technology. This will be another challenge that we hope to approach for next year's ISMB/ECCB in Berlin, Germany.

At our 20th Anniversary ISMB, we have made many efforts to present exceptional science and have also planned presentations and social events facilitating this milestone celebration. We hope that you will be joining in all of the fun this week in Long Beach.

50 Years The U.S. Congress authorized establishment of the National Institute of General Medical Sciences (NIGMS) in 1962, making this its 50th anniversary year. From the start the NIGMS mission has been to conduct and support research and training in the general or basic medical sciences. Within NIGMS there are six divisions, and although the Division of Biomedical Technology, Bioinformatics, and Computational Biology may prominently feature among PIs within our discipline, our community members and conference attendees

(continued)

certainly interact with all the NIGMS divisions. In recognition of this Golden Jubilee we are offering two Special Sessions organized by NIGMS in Long Beach.

100 Years This year the Federation of American Societies for Experimental Biology (FASEB) celebrates its centennial and recently partnered with NIGMS for joint celebrations in Washington DC. At just 15 years old, ISCB has a long way to go until our own centennial, but we are inspired by FASEB's long history of accomplishments in the promotion of the scientific agenda in the U.S., and can learn much from their governance model as they successfully work on behalf of the shared interests of 26 different professional societies.

Arguably, the association with FASEB has been one reason for another important recent achievement of ISCB, namely the publication of strong stances for open access, spearheaded by Rick Lathrop chairing the ISCB Public Affairs and Policy Committee (R Lathrop et al. (2011) *Bioinformatics* 27:291-4; R Lathrop et al. (2011) *PLoS Comput Biol* 7:e1002014). This strong endorsement of open access was also the basis of two letters that ISCB sent this year to the members of the U.S. Congress to express our strong support in favor of open access to scientific literature resulting from research that is publicly funded. Rick Lathrop directed this initiative, and you can read about both of these actions in this newsletter and then take action of your own using the text of ISCB's letter as your template.

Global society Also this past year ISCB has finally realized the last important leap toward the realization of another dream, namely that of becoming a society that routinely organizes meetings in both the Northern and the Southern hemispheres, and one on each of five continents (North America, Europe, South America, Africa, and Asia) at least every two years. The last important step was the organization of ISCB-Asia/InCoB in December 2011 in Kuala Lumpur, Malaysia. Sheila Nathan chaired this first ISCB-Asia as a joint meeting with the 10th anniversary InCoB meeting organized by APBioNet (Asia-Pacific Bioinformatics Network). ISCB Board member Paul Horton chairs the second ISCB-Asia in December 2012 on the BGI campus in Shenzhen, China.

Just four months ago the second ISCB-Latin America was a resounding success – with 240 participants - in Santiago, Chile, under the leadership of ISCB member Francisco Melo, who chaired the conference brilliantly. The next event in that series will be held in 2014 as a joint meeting with the Brazilian Association for Bioinformatics and Computational Biology's 10th anniversary X-Meeting (due to this collaboration ISCB-Latin America 2014 has been moved to October instead of its regular window in mid-March). ISCB-Africa is already moving well through the planning process for our third conference organized together with ASBCB, the African Society for Bioinformatics and Computational Biology, being held next March and chaired by Alia Benkahla in Tunis, Tunisia. Each of these new "ISCB-x meetings" has the goal of bringing the international and local scientific communities together for shared investigation and collaboration. We salute the conference chairs named above, each of who has put so much energy into creating a truly amazing meeting. Please be sure to join us as many of these upcoming events as your schedule allows!

Throughout this newsletter you will find other ISCB announcements and profiles: the ISCB 2012 prize winners Ziv Bar-Joseph (ISCB Overton Award) and Gunnar von Heijne (ISCB Senior Scientist Award); the seven new ISCB Fellows (Bonnie Berger, Peter Karp, Jill Mesirov, Pavel Pevzner, Ron Shamir, Martin Vingron, Gunnar von Heijne); and Stacy Slagor as the newest full-time addition to our professional staff.

For the second time, you can vote for ISCB officers (members of the ISCB Executive Committee) and Student Council Leaders at ISMB. The election starts online on July 3rd and concludes both online and in person in Long Beach through the end of ISMB on July 17th.

In 2012, ISCB is passing a series of milestones that mark so many achievements. This is a moment in time to be proud of being part of such a dynamic and exciting young professional society. ISCB continues to be small. This means, we are nothing without your active contribution. Becoming and staying a member is an important first step. We all need more from you. Thanks for contributing to our growing community. May we share many milestones ahead!

BJ Morrison McKay
Executive Officer

Burkhard Rost
President

OFFICER AND STUDENT COUNCIL ELECTIONS – THE CHOICE IS YOURS

By Dietlind Gerloff and Anna Tramontano,
ISCB Nominations Committee Co-Chairs

Following last year's revised process for President-Elect elections, which started online approximately two weeks before ISMB/ECCB in Vienna, and then continued online and in-person during the conference, we are now once again in the midst of our annual elections. This year the pool of candidates is much larger, as it includes the ISCB Officer positions of Vice President, Treasurer, and Secretary, plus the Student Council leadership positions of Chair, Vice-Chair, Treasurer, Secretary, and Representative to the ISCB Board of Directors. All members are highly encouraged to participate in the process by casting their online ballots from the privacy of their homes or research labs/offices, or, if attending ISMB 2012 in Long Beach, by visiting the "voting booth" adjacent to the ISCB booth in the exhibition area. The online voting site opened on July 3rd, and can be accessed at www.iscb.org/elections until the close of ISMB 2012 on July 17th. Members simply login to the elections site and vote for their candidates of choice. The voting booth is intended to make the activity of voting as inviting and easy as possible, and each voter will walk away with a sense that they participated in an important aspect of their ISCB membership by helping to select our future leaders.

The Officer election results require ratification by the ISCB Board of Directors, as per the Society's bylaws. This year we will do this through a special process in August (the Board does not typically meet in August), with the final outcome announced via the ISCB home page shortly thereafter. Be sure to visit www.iscb.org by the end of August to see if your chosen candidates have won. Most importantly, we thank you in advance for your participation!


ECCB'12 Computational Biology

9-12 September 2012,
Congress Center Basel, Switzerland

For program details and registration please visit:
www.eccb12.org

By Torsten Schwede, ECCB'12 chair, SIB Swiss Institute of Bioinformatics & Biozentrum University of Basel, Switzerland

ECCB'12 - the European Conference on Computational Biology - is the key European computational biology event in 2012 uniting scientists working in a broad range of disciplines, including bioinformatics, computational biology, medicine, and systems biology. ECCB'12 will take place 9.-12. September 2012 at the Congress Center Basel, Switzerland. Registration is open now at http://eccb12.org - early registration rates apply until 1. August 2012. ECCB'12 will be organized in association with the 10th [BC]2 Basel Computational Biology conference - the annual scientific symposium of the SIB Swiss Institute of Bioinformatics.

The scientific program for ECCB'12 is highly competitive: among hundreds of submitted manuscripts, 48 were selected by peer review for oral presentation and publication in a special proceedings issue in Bioinformatics. Because of the stringent selection, we look forward to an exciting program. One the highlights of ECCB are keynotes by internationally well known experts. ECCB'12 features an outstanding line-up of speakers: The opening keynote will be given by Nobel laureate Aaron Ciechanover (Technion, Israel Institute of Technology), followed by the EMBO Lecture by Søren Brunak, (Technical University of Denmark), and keynotes by Barry Honig (Columbia University, New York), Laurent Keller (University of Lausanne), Gene Myers (MPI of Molecular Cell Biology and Genetics, Dresden) and Mihaela Zavolan (Biozentrum University of Basel & SIB).

The conference schedule includes plenty of time for discussions and networking during breaks and poster sessions. Don't miss this opportunity to present your own research as a poster to the conference participants!

Traditionally, workshops, tutorials and satellite meetings are organized during the weekend preceding ECCB. On Saturday (8. September) UniProt celebrates its 10th anniversary with a satellite symposium on "Bioinformatics Research Infrastructure for the Life Sciences". The European ISCB Student Council Symposium provides a platform for PhD students and postdocs in the field of computational biology for scientific and social networking. ECCB'12 features a broad spectrum of pre-conference workshops and tutorials to get an interesting perspective on the cutting edge of a research field:

- 6th International Workshop on Machine Learning in Systems Biology (MLSB)
- Annotation, Interpretation and Management of Mutations (AIMM)
- Computational Proteomics: From Mass Spectrometry to Protein Complexes
- Bioinformatics Training for Life Scientists: Showcases and Challenges from Tutors' Perspectives
- Imaging Analysis and Computational Modeling for Cancer and its Therapy
- Detecting Transcription Factor Binding Sites with ChIP-Seq Data and Predicting Damaging Cis-Regulatory Variations
- Applications of Bio-Ontologies in Large-Scale Data-Driven Science: A Practical Introduction
- Protein Evolution: From Sequence to Structure to Function
- GWAS: Statistics and Bioinformatics to Analyse Genotype to Phenotype Relationships from Molecular Traits to Disease Phenotypes
- Inferring Genetic Diversity from Next-Generation Sequencing Data: Computational Methods and Biomedical Applications
- Reads to Biological Patterns: End-to-End Differential Expression Analysis of RNA Sequencing Data Using Bioconductor
- Editing Wikipedia for Scientists

Situated in Switzerland at the heart of Europe, Basel is one of the continent's most convenient locations for events. The Congress Center Basel is in the city centre and easy to get to, while the Old Town, the shopping districts and the city's many museums and parks are within easy walking distance.

Don't forget to register by 1. August at http://eccb12.org to secure the early registration rates. We are looking forward to welcoming you for an exciting ECCB'12 in Switzerland!

MEET THE ISCB FELLOWS CLASS OF 2012

The ISCB Fellows program honors members that have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. The process established for electing Fellows includes a call for nominations to our member community. After the 2012 nominations deadline, the Fellows Selection Committee, which includes all Fellows together with the current ISCB Board of Directors, elected six new Fellows. During the 2009 inaugural year of the program, ISCB committed to also automatically conferring Fellows status on all winners of the ISCB Accomplishment by a Senior Scientist Award. Therefore, seven new Fellows now join their 17 colleagues from previous years.

The outcome of this year's election is presented with tremendous pride. Each of these very accomplished researchers has made exceptional contributions to ISCB's mission to advance the scientific understanding of living systems through computation. Please join us in congratulating our new ISCB Fellows Class of 2012.


Bonnie Berger
Massachusetts Institute of Technology, USA

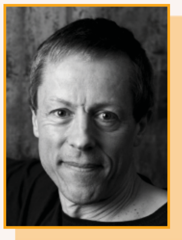

Peter Karp
SRI International, USA


Jill Mesirov
The Broad Institute of MIT
and Harvard, USA


Pavel Pevzner
University of California,
San Diego, USA


Ron Shamir
Tel Aviv University, Israel


Martin Vingron
Max Planck Institute for Molecular
Genetics, Germany


Gunnar von Heijne
2012 ISCB Accomplishment by a
Senior Scientist Award Winner
Stockholm University, Sweden

ISCB Student Council 8 Symposium 2012

by Alexander Goncearenco, Student Council Symposium 2012 Chair and Olga Botvinnik, Student Council Symposium 2012 Co-Chair

The ISCB Student Council Symposium (http://symposium.iscbsc.org) is a forum for graduate students, post docs, and new researchers in the fields of computational biology and bioinformatics to present their work to an international audience and develop valuable skills in an open, friendly and supportive environment. Organized and orchestrated by student volunteers from all over the world, this Symposium is designed to enable students attending ISMB to network with their peers and participate in a global exchange of ideas and scientific knowledge.

This year, the Student Council Symposium will showcase 10 student speakers and more than 50 student poster presentations on broad range of scientific subjects — from comparative genomics and evolution to the bioinformatics of health and disease. In addition, we are honored to have Dr. Jonathan Eisen (University of California Davis), Dr. Robin Dowell (University of Colorado at Boulder), and Dr. Matthew Hibbs (University of Maine at The Jackson Laboratory) as keynote speakers. Their talks promise to be thought-provoking and inspiring to all computational biologists. With the help of our generous sponsors and Student Council volunteer peer reviewers, we awarded 7 travel fellowships for symposium delegates. Congratulations to all fellowship recipients!

The organizing committee and volunteer staff look forward to seeing you in Long Beach! If you're not able to attend our Symposium, please stop by the ISCB Student Council Booth during ISMB or visit our website at www.iscbsc.org and learn more about how you can get involved.

2012 ISCB OVERTON PRIZE: ZIV BAR-JOSEPH

By Justin Mullins, Freelance Science Writer, London, United Kingdom

Ziv Bar-Joseph loves to run. He rises early and hits the streets and trails around Pittsburgh where he lives, often in training for a long-distance race. This dedication has paid off. He has the enviable distinction of having run a sub-three hour marathon, a feat achieved by few amateurs. "Running is very important to me," he says.

But it is not just in his running that Bar-Joseph shows a willingness to go the distance. As a computer scientist and computational biologist at Carnegie Mellon University in Pittsburgh, Bar-Joseph shows a similar dedication as head of the Systems Biology Group at the School of Computer Science. "We have all been impressed by the novelty of the approaches he has developed," says Alfonso Valencia, chair of the ISCB Awards Committee.

Bar-Joseph gained a PhD in computer science from the Massachusetts Institute of Technology between 1999 and 2003. That time turned out to be hugely significant, not least because computational biology was undergoing a revolution. "For the first time, we were getting sequences for large species. First, the fly, then humans. It was very inspiring," he says.

Initially, Bar-Joseph knew little about computational biology but took a class to better understand the significance of these advances and the problems they posed. "It seemed to me that these types of problems were well-suited for the machine learning tools I had experience with," he says.

One of the key problems was how to compare sequences either within species or between them. Various researchers had developed methods to do this using a branch of computer science called combinatorics, which essentially counts the number of similar patterns.

But while this works well when comparing two sequences, it's not so good for comparing seven or eight sequences. It doesn't scale. Consequently, researchers began to experiment with probabilistic approaches that focus on the statistical properties of the patterns. In particular, computational biologists had significant successes with a statistical approach called a hidden Markov model. That attracted Bar-Joseph who had studied this model.

He also recognised that other earlier studies, attempting to reconstruct networks in cells, were significantly limited: the data was a snapshot of a complex dynamic system but they treated it as if it were static.

Clearly, biological systems change. "One thing I've been involved in is introducing dynamics into the algorithms so that they can cope with the way things change in time. That requires different tools," he says.

The approach has paid off when it comes to understanding regulatory networks and explaining how proteins control each other. For example, yeast has about 6,000 proteins. Of these, some 250 are control proteins and each of these, on average, controls 100 or so other proteins. However, each control protein is itself controlled by a handful of other proteins.

Understanding a system like this is a tricky business. The static data can tell you what proteins control other proteins, but that doesn't tell you when and under what conditions because that requires more experiments.

Other types of data are more temporal and can reveal how protein levels change over time. "The question we asked was whether we can use this temporal data to try and recover the underlying network dynamics," he says. "We came up with methods to integrate these datasets in order to reconstruct the set of events over time and these have since been used in various other systems too."

Photo courtesy of Carnegie Mellon University.

Bar-Joseph has learnt to work closely with biologists who test the results. "If the algorithm predicts that 'a' controls 'b', for example, you can do the experiment to test whether that's true." That's important because the patterns that the algorithms reveal must be biologically relevant.

To better understand the challenges that experimentalists face, Bar-Joseph spent a sabbatical working in a wet lab doing exactly this kind of work. That taught him some valuable lessons. For example, wet lab work is not just a question of validating the model. "The results from the lab feed back into the model and enhance it. It's a two-way street," he says.

Others have been impressed with Bar-Joseph's approach to experimental work. "Ziv is an example of somebody coming from the theoretical side of things and completely embracing the experimental approach," says Burkhard Rost, president of the ISCB. "It's stunning how he is able to handle such a diverse set of technical methods."

This process of feedback from biology to computer science has become an important theme in Bar-Joseph's work. One of his recent successes is in explaining the way fruit flies develop bristles on their foreheads. These bristles are like aircraft sensors, measuring temperature, wind speed, and so on. To work well, they need to be spaced in a very precise way.

The bristles grow from cells but clearly only a small subset of cells. The cells do not know how many neighbours they have or the local density of bristles nearby. So what determines which cells grow into bristles and the spacing between them?

Bar-Joseph quickly realised that this was similar to a problem that computer scientists have wrestled with for 30 years. This is the problem of determining the subset of computers in a network that control all the others. When each computer in the network is connected to one computer in this subset (but no two in the subset are connected to each other), this subset is called maximally independent.

Finding maximally independent sets is hard, particularly in large distributed networks. Computer scientists do it by assuming that every computer knows who all its neighbours are.

Bar-Joseph realised that the fruit fly cells that eventually become bristles form a maximally independent set—they are connected to all other cells but not to each other. However, they do not know who their neighbours are and so must solve this problem in a different way. His breakthrough was to work out how they did it and develop an algorithm that does the same thing while assuming no knowledge of the neighbours. "It takes a bit longer but that's the trade-off," he says.

This may have important applications for wireless sensor networks that researchers are using to monitor everything from ocean conditions to volcanic eruptions. "We only published at the beginning of 2011 so we don't know if it will penetrate the commercial world," he says.

Valencia is also impressed by Bar-Joseph's broader contribution to the computational biology community. "He is a member of the editorial board for the journal *Bionformatics*, so clearly his contributions go beyond this theoretical and experimental work," says Valencia. "That's very good for a young scientist."

The future holds many promising problems for Bar-Joseph too. He is particularly interested in studying how pathogens interact with cells, how the proteins from flu viruses interact with cell proteins, for example. "If we can reconstruct the networks of interactions then we might be able to determine intervention points that will guide us to therapeutics," he says.

He also wants to study the interaction networks in different species. Many of the genes in humans and mouse are similar, but drugs that work well in mouse often don't work in humans because the pathways, levels, and interactions are different. "We want to get more insight into this," he says.

That's clearly a long game. These are problems that will require dedication, talent, and endurance to solve. Exactly the kind of qualities you might find in a marathon runner.

This article is excerpted from the May 2012 issue of PLoS Computational Biology. To link to the full journal article please visit www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1002535

2012 ISCB SR. SCIENTIST AWARD:GUNNAR VON HEIJNE

By Justin Mullins, Freelance Science Writer, London, United Kingdom

Perhaps it all began with the French lessons. As a a young PhD student in theoretical physics at the Royal Institute of Technology (KTH) in Stockholm, Gunnar von Heijne decided, on whim, to brush up on his rusty, schoolboy French. He took a few lessons and also subscribed to the French popular science magazine *La Recherche*.

Flicking through its pages, he came across a short article on protein secretion and the signal hypothesis, the mechanism that describes the way secretory proteins cross a membrane.

At the time, the late-1970s, very little was known about this process, but some ideas were beginning to emerge. For example, it was thought that a so-called signal peptide—a short chain of amino acids—at the end of the protein carried the signal that determined how the proteins are transported out of the cell.

The article confused him, however. It showed a diagram of a hydrophobic signal peptide squeezing through the similarly hydrophobic membrane. "That didn't make sense to me. The hydrophobic peptide ought to become anchored in the membrane," he says.

The puzzle piqued his interest. He solved it by calculating the energetics of a polypeptide chain passing through lipid bilayer, which he published in 1979. This work by a theoretician created ripples in a field dominated by experimentalists.

And so began the career for which he now receives the Accomplishment by a Senior Scientist Award from the International Society for Computational Biology (ISCB). "Gunnar is one of the big stars of our field," says Burkhard Rost, president of the ISCB. "He is one of the few who completely change the field using computational methods." Polypeptide energetics was only the start, however.

By the early 1980s, molecular biologists had begun to determine the sequence of amino acids in the signal peptides from different proteins. However, little had been done to study the properties of signal peptide sequences as a group.

von Heijne changed this. He began comparing the sequences, looking for recurring patterns that might help to identify them. "I looked at 20 to 30 signal peptides. Once you did that, some clear patterns emerged that had not been seen before," he says.

He found that small, uncharged amino acids tended to occupy certain positions in signal peptide chains, the -3 and -1 positions. It is at this site that the signal peptide is later cleaved from the protein once it has passed through a biomembrane. This pattern has since become known as the (-3, -1)–rule.

"Nowadays you would say this was a very trivial bioinformatics study," he says modestly. However, this was an important discovery and von Heijne's paper has since become one of the most highly cited in the field.

He then used the newly discovered patterns to make predictions about proteins. For example, it became possible to create an algorithm that would take a protein sequence and predict whether it had a signal peptide at the end.

Initially, that was not very useful. When molecular biologists sequenced a gene or messenger RNA, they generally knew what they were working on; whether it would have a signal peptide on the end or not.

But that changed when sequencing became faster and biologists started to sequence things they didn't know much about. "The algorithms have continually improved and are now extremely useful," he says.

Secretory proteins have to move across a lipid bilayer through a molecular machine called a translocon. The signal peptide guides the ribosome that makes the protein, towards the translocon. This triggers the opening of this protein-conducting channel through the membrane.

But other types of protein only make the journey partway, becoming embedded half in and half out of the membrane. These so-called membrane proteins use the same translocon machinery as the secretory proteins. "So it was a natural step to start looking at these membrane proteins next," says von Heijne.

The part of the protein that ends up in the membrane is very different to the parts outside exposed to water. This transmembrane section must be much more hydrophobic. So the trick to predicting which parts of a protein become embedded in the membrane is to look for the segments that are most hydrophobic.

Once you know the transmembrane segments, an interesting problem is to determine how the protein becomes woven into the membrane. For example, if it has four hydrophobic sections, there are two ways in which it can be arranged in the membrane: with the termini pointing either in or out. But which orientation should the protein take?

"We discovered a very simple principle that determines this," he says. The regions that connect the transmembrane segments contain positively charged amino acids, which give them an electric potential. The simple principle is that the segments with the greatest number of positive charges end up inside the membrane, an idea that has since become known as the "positive inside rule".

"This is very important work and provides some of the best data on membrane proteins," says Alfonso Valencia, chair of the ISCB awards committee.

In the late 1980s, von Heijne began to realise that he could gain significant insight into these and other problems by doing experiments rather than just theory work. So he set up his own lab. "I trained as a chemist so I wasn't a complete novice in a wet lab," he says.

This first idea was to see whether it was possible to make proteins that inserted "upside-down" into the membrane. He could show that by changing the location of the positively charged amino acids in a protein, it is possible to make it take up the opposite orientation.


Photo by Max Brouwers.

This link between his theoretical and practical work has been important for him. Bioinformatics studies often throw up patterns that may or may not have biological relevance. "The only way to determine whether they are important is to do the experiments," he says.

"It's hard to overstate the significance of von Heijne's work. Membranes and transmembrane proteins are the gates and gatekeepers to our cells; they determine what gets in and what stays out," explains Rost. "That's why around two-thirds of drugs target membrane proteins."

Understanding the structure of transmembrane proteins provides crucial insight into how cells work and is also useful for future drug development. "That's why the methods developed by Gunnar are so important," says Rost.

To continue his work, von Heijne set up the Stockholm Bioinformatics Centre at the beginning of the millennium. And today, von Heijne runs the Centre for Biomembrane Research in Stockholm, where he has brought together computational, modelling, and experimental groups. Few places can boast the same breadth of experience under one roof.

Throughout this time, von Heijne has maintained an impressive work–life balance as a scientist, a husband, and a father. He says that's been possible, at least in part, because he was working in a new field with few competitors. "I never felt stressed that we'd be scooped. I work hard but not crazily."

Others clearly admire his positive approach, which he combines with a relaxed attitude. "He also looks ten years younger than he has any right to!" says one envious colleague.

For a while in the 1980s, he spent half his time working as a science journalist for the Swedish National Radio. "You decide on Monday what you broadcast on Friday so there is immediate feedback, which has a good pulse to it," he says.

But for von Heijne, doing science is more satisfying than reporting it. "Radio stories have a short half life; they're on air, then they're gone," he says. "The rewards in science are greater and longer lasting." It's surprising how far schoolboy French can take you.

This article is excerpted from the May 2012 issue of PLoS Computational Biology. To link to the full journal article please visit www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1002535

21st Annual International Conference on Intelligent Systems for Molecular Biology

12th European Conference on Computational Biology

berlin

2013 ISMB ECCB

CONFERENCE JULY 21–23

SIGS & TUTORIALS JULY 19–20

MARK YOUR CALENDAR!

CONFERENCE CO-CHAIRS

Burkhard Rost, *Technical University Munich, Germany*

Anna Tramontano, *University of Rome, Italy*

Martin Vingron, *Max Planck Institute for Molecular Genetics, Berlin, Germany*

KEYNOTE SPEAKERS

Gil Ast, *Sackler Medical School, Tel Aviv University, Israel*

Carole Goble, *University of Manchester, United Kingdom*

ADDITIONAL KEYNOTES

2013 ISCB Fellows Keynote

2013 ISCB Overton Prize

2013 ISCB Accomplishment by a Senior Scientist Award

www.iscb.org/ismbeccb2013

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

An Official Conference of the International Society for Computational Biology

NEWS FROM ISCB STUDENT COUNCIL

By Geoff Macintyre (SC Chair) and Thomas Abeel (SC representative to the ISCB Board of Directors)

The ISCB Student Council is now in its eighth year of operation. Over the years the Student Council and its extended Regional Student Group network has grown to over 2000 students across 20 countries. The purpose of the Student Council (SC) is to provide activities and support for the next generation computational biologists. We achieve this goal by organizing and supporting scientific events, networking opportunities, soft-skills training, educational resources, and other career development activities for computational biology students throughout the world. If you would like to learn more about the SC and how it operates please continue reading. Additional information can be found at www.iscbsc.org.

Who are the Student Council?
The Student Council is a volunteer organisation run entirely by students for students. The ISCB provides ongoing financial support allowing the SC to continue to grow and expand. In addition, the SC raises valuable funds from sponsors to assist in initiatives such as travel fellowships for the SC Symposium. An elected Executive Team consisting of a Chair, Vice-Chair, Secretary and Treasurer oversees the operations of the Student Council. The 2012 elections are currently taking place, www.iscbsc.org/content/elections. All members are invited to cast their vote during ISMB.

Beyond the Executive Team, the SC is made up of a series of organisational Committees including: The Education and Internship Committee, Outreach and Volunteer Committee, Web Committee, Fundraising Committee, RSG Committee, and SC Symposium Committee. The efforts of all Executive Team and Committee members ensures that SC events and initiatives run smoothly and the SC continues to be successful. The SC is always looking for motivated and enthusiastic students to join SC Committees. Volunteers gain invaluable experience by being part of the operations of an international organisation. Time volunteering for the SC also creates networking opportunities with the broader computational biology community. All of this assists students in their future career prospects. For more information about joining the SC, visit www.iscbsc.org

Student Council Initiatives
The longstanding premier event of the SC is the Student Council Symposium held in conjunction with ISMB. In past years the symposium has regularly attracted over 100 delegates with high quality poster and oral presentation submissions. A number of high-profile, eminent scientists have delivered keynote presentations and this year is no exception with Dr. Robin Dowell, Dr. Matthew Hibbs, and Dr. Jonathan Eisen on the program at http://symposium.iscbsc.org/

> ***As a volunteer for the Student Council I had the opportunity to interact with scientists from all over the world and to create a network that I can rely on when it comes to finding collaborators for a project or identifying new career opportunities. These connections have opened many doors for me that otherwise would have been closed.***
>
> *- Nils Gehlenborg, past SC Chair and Volunteer, currently a Research Associate at Harvard Medical School.*

More recently, the SC has started a new symposium series under the brand of European Student Council Symposium (ESCS) that is organized in conjunction with the European Conference on Computational Biology (ECCB). While this is still a very young event series, it is growing rapidly, with the number of submission doubling over the first two editions. Check http://escs.iscbsc.org/ for more details.

Over the past two years the SC has been running an Internship Program to create opportunities for students from developing nations to gain experience in an established lab. Four students have been awarded internships at the Schneider and Rost labs during this time with great feedback from the students and group leaders involved. Many group leaders around the world have since shown interest in the program and we are currently reviewing applications for internships in Germany and Australia. For more information visit www.iscbsc.org/content/internships-0

Recently, the SC has been working closely with the founder of the Arts and Science Exhibition, Dr. Milana Frenkel-Morgenstern, to reorganize the Arts and Science Exhibition. While there were no submissions accepted this year, there will be an exhibition of past years winners at ISMB 2012. Watch for announcements on submissions for next year.

The SC Regional Student Group (RSGs) initiative aims to promote interaction among students pursuing research in the field of bioinformatics and computational biology. Student groups in different regions around the world can apply for affiliation with the ISCB SC, which provides them access to guidelines on running students events, a global student support network, and funds to run events. In the past year we have seen the addition of three new RSGs from Turkey, Italy and Argentina. There are over 20 active RSGs across the world. For more information on how to participate, visit www.iscbsc.org/content/regional-student-groups

SC Activities @ ISMB

- **ISCB Student Council Symposium:** A full day of student presentations, keynote lectures and student poster session. Friday July 13
- **Student Council Booth:** Come find out what all the fuss is about. Visit the SC Booth in exhibit hall B during ISMB
- **Career session:** Want to find the perfect job? Join our panel of experts for a discussion of all things careers. Monday July 16, 5:30-6:30pm
- **Job posting board:** Located next to the SC booth, you can come advertise your position or search for a job. We provide a service for connecting job seekers with job advertisers at ISMB. Go to the SC Booth to find out more.
- **Student Council Social event:** Come socialise with fellow students at the official SC Social event @ ISMB event, July 15, 8-10pm, Gladstone's Long Beach, 330 South Pine Avenue.
- **Student Council Social HQ:** Each evening SC members will be gathering in an informal setting to sit back and continue discussions. Come visit the SC Booth to find out more. HQ will be located at the same place as the social event: Gladstone's Long Beach
- **ISMB party:** Want to kick back after a couple of hard days at the conference? Join the official ISMB party, Monday July 16, 9pm. Tickets are available at the SC booth.

You can read more about the ISCB Student Council at the SC website (www.iscbsc.org)--or look us up on Facebook, LinkedIn, and Twitter. Of course, the best way to find out about the Student Council is to talk to our members. If you have a few minutes between sessions or if you're feeling lost in the crowds, stop by the ISCB Student Council booth. We'll show you how we're making a difference in the computational biology student community.

FASEB UPDATES

By Jennifer Hobin, Director of Science Policy and Jennifer Zeitzer, Director of Legislative Relations, FASEB Office of Public Affairs

2012 marks the 100th anniversary of the Federation of American Societies for Experimental Biology (FASEB), and we have had many occasions throughout the year to celebrate this centennial together with our member societies and partners in advocacy. Since its beginning, FASEB has engaged in advocacy on behalf of scientists, including members of ISCB, which joined the Federation in 2003. More and more, FASEB has focused its attention on scientific issues with far-reaching global impacts, significantly increasing its relevance to international societies like ISCB. The following is an overview of the initiatives FASEB has led on behalf of the biomedical research community in just this last year, although much of this work represents ongoing advocacy efforts over the past several years if not decades.

Despite Congress' efforts to cut federal spending, the final fiscal year (FY) 2012 budget provided $30.64 billion for the U.S. National Institutes of Health (NIH) – a $240 million (0.08 percent) increase above the FY 2011 level. But while NIH fared well in 2012, President Obama's 2013 budget proposal requested no increase for NIH. Furthermore, the Joint Committee on Deficit Reduction's failure to produce a deficit reduction plan could trigger immediate cuts (i.e., "sequestration") for all federal agencies in January 2013. A FASEB analysis predicts that this could result in a $2.8 billion (11.1 percent) cut to NIH. To educate lawmakers about the devastating impact of further budget cuts, FASEB sent letters and submitted testimony to the Appropriations Committees urging Congress to sustain the investment in NIH. FASEB board members participated in 70 meetings with Congressional offices during the Federation's Capitol Hill Day in May, and an e-action alert generated several thousand emails to Senate offices in June. The House and Senate Appropriations Committees are expected to consider the FY 2013 NIH funding bills in late June, but Congress is likely to defer final action until after the November elections.

While increased funding for science is a priority, FASEB also recognizes the importance of making the best use of available resources. To that end, FASEB advised NIH to reallocate funding to provide more money for individual investigator-initiated research project grants, examine the value added from additional funding going to well-funded investigators, phase in limits to the percentage of salary charged to grants, and reduce overhead charges that erode research funding. FASEB also recommended easing burdensome administrative requirements by eliminating effort reporting, improving human subjects and animal care and use regulations, and reducing the number of regulatory compliance courses investigators are required to take.

Research training is also a FASEB policy priority. The Federation provided input to NIH on how it could improve training and increase diversity in the research workforce, organized a career development workshop to help postdocs transition to independent positions, and has been developing an interactive, web resource to help trainees identify career opportunities.

In addition, FASEB's report, *Engaging Basic Scientists in Translational Research: Identifying Opportunities, Overcoming Obstacles*, provided recommendations as to how research institutions, funders, professional societies, and publishers could facilitate the participation of basic scientists in translational research. FASEB also provided input to NIH on positioing the Clinical and Translational Science Award program to advance therapeutics development.

One hundred years ago the founders of FASEB could not have guessed at the research topics that investigators are addressing today. Yet, the need to advocate for the benefit of scientists remains a constant theme that has transcended the test of time. We now look forward to what may lie ahead in the next 100 years!

INTRODUCING STACY SLAGOR

You may notice a new face at ISMB now that Stacy Slagor is leading ISCB's fundraising efforts as Director of Corporate Relations and Development. In 2011, while consulting on a fundraising feasibility project for the Society, Stacy joined us for ISMB/ECCB in Vienna to interview several of our volunteer leaders, sponsors, and exhibitors. This year, we are pleased to introduce her as a full-time member of our professional staff - the first new full-time position for ISCB in over ten years. "You see, we were so convinced by the expertise and skills Stacy demonstrated while working as our consultant that we could not have been more delighted when she accepted our offer to work exclusively for ISCB on a full-time basis," said BJ Morrison McKay, ISCB's Executive Officer.

In her new role Stacy brings over 17 years of experience in successfully building partnerships with universities, non-profits, industry and government. She has previously worked as a corporate relations executive at the University of California, San Diego and at the University of Rochester in New York, and was running her own fundraising consultancy when she came to the attention of ISCB nearly two years ago.

Based in San Diego, California, Stacy has embraced her new responsibilities by helping to structure a Fundraising Committee, reaching out to many of our conference sponsors and exhibitors, and working to develop new giving opportunities for corporations, foundations and individuals. To be most effective she needs to go where our members and supporters go, so you might spot her at other conferences you attend throughout the year, such as ECCB, CSHALS, and the Bio-IT World Conference & Expo, to name a few.

Stacy can be contacted at stacy.slagor@iscb.org and +1-858-630-5339, or on Twitter @StacySlagor.

PLoS COMPUTATIONAL BIOLOGY OVERVIEW

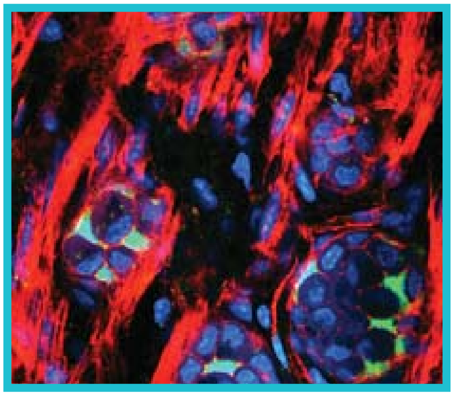
By Rosemary Dickin, Editorial Manager, PLoS Computational Biology

2011-2012 has seen steady growth for *PLoS Computational Biology*, with submissions up 22% since last year, and an average of 36 new Research Articles published each month. While the publication of the highest quality research remains the journal's main focus, *PLoS Computational Biology* also aims to move beyond the boundaries of traditional publishing and to engage our readership.

Our latest initiative, **Topic Pages**, makes full use of PLoS' open access license to bridge the gap between traditional journal articles and Wikipedia. "Circular permutation in proteins" (1), a review-style article with an innovative twist, was published in March 2012. The article had been drafted and openly reviewed in a wiki setting and, upon publication, a copy was placed on Wikipedia to undergo the usual edits seen in any other article on the site. The PLoS article remains the 'version of record' while Wikipedia gains high-quality content; more information about this project can be found in (2).

Our Education section has continued to flourish, in part because of the journal's relationship with the ISCB. Last year we introduced a collection, **Bioinformatics: Starting Early**, which takes the notion of biology as a computational science into high schools. 2012 will also see the conclusion of our series of mini-reviews, **Editors' Outlook**. Launched last summer, this collection broaches subjects from genome organization to experimental neuroscience. They speak to the breadth of our field and editorial board, and collectively will form a vision from our many expert editors of what is being, and will be, accomplished in the coming years.

PLoS Computational Biology is grateful for the contributions made by many members of the community – including 146 Guest Editors and 1985 reviewers in 2011 (3). To accommodate the increasing number of submissions to the journal we have introduced several new additions to the Editorial Board in the last 12 months: Associate Editors Marcel Salathé, Teresa Przytycka and Niko Beerenwinkel, and Topic Pages Editor Daniel Mietchen. Douglas Lauffenburger and Konrad Körding also took on more senior roles at the journal as Deputy Editors.



Stem cells in small intestinal crypts. Image Credit: Paul Appleton, doi:10.1371/journal.pcbi.1002515

PLoS Computational Biology is a 'Community Journal'; we value your ideas and comments, so please don't hesitate to get in touch in person at ISMB or via ploscompbiol@plos.org any time.

Examples of Highly Downloaded Articles 2011-2012

- Cytoskeletal Signaling: Is Memory Encoded in Microtubule Lattices by CaMKII Phosphorylation? Craddock TJA, Tuszynski JA, Hameroff S (2012) *PLoS Comput Biol* 8(3): e1002421. doi:10.1371/journal.pcbi.1002421
- Most Random Gene Expression Signatures Are Significantly Associated with Breast Cancer Outcome. Venet D, Dumont JE, Detours V (2011) *PLoS Comput Biol* 7(10): e1002240. doi:10.1371/journal.pcbi.1002240
- Using Electronic Patient Records to Discover Disease Correlations and Stratify Patient Cohorts. Roque FS, Jensen PB, Schmock H, Dalgaard M, Andreatta M, et al. (2011) *PLoS Comput Biol* 7(8): e1002141. doi:10.1371/journal.pcbi.1002141
- Effect of Promoter Architecture on the Cell-to-Cell Variability in Gene Expression. Sanchez A, Garcia HG, Jones D, Phillips R, Kondev J (2011) *PLoS Comput Biol* 7(3): e1001100. doi:10.1371/journal.pcbi.1001100

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1. Circular Permutation in Proteins. **Bliven S, Prlić A.** 2012, *PLoS Comput Biol*, 8(3) e1002445. doi:10.1371/journal.pcbi.1002445, p. 8(3): e1002445. doi:10.1371/journal.pcbi.1002445.

2. *Topic Pages: PLoS Computational Biology Meets Wikipedia*. **Wodak SJ, Mietchen D, Collings AM, Russell RB, Bourne PE**. 2012, *PLoS Comput Biol*, 8(3): e1002446. doi:10.1371/journal.pcbi.1002446.

An Australian desert ant deciding which way is home. Image Credit: Antoine Wystrach doi:10.1371/journal.pcbi.1002336

A REPORT OF THE CURRICULUM TASK FORCE

By Lonnie R. Welch, Ohio University
Russell Schwartz , Carnegie Mellon University
Fran Lewitter, Whitehead Institute and ISCB Education Committee Chair

The International Society for Computational Biology (ISCB) Education Committee (EduComm) promotes worldwide education and training in computational biology and bioinformatics and serves as a resource and advisor to organizations interested in developing educational programs.

The topic of curricula for bioinformatics programs has long been of interest to ISCB and EduComm. Dr. Russ Altman, a founding board member and past president of ISCB, has been associated with one of the first bioinformatics degree programs (at Stanford University) and wrote an article on this topic [1]. Dr. Shoba Ranganathan, as chair of EduComm a decade ago, began organizing a yearly Workshop on Education in Bioinformatics (WEB) at Intelligent Systems for Molecular Biology (ISMB) meetings that generated exchange of information and many productive discussions. Curriculum development was one aspect of bioinformatics education covered in these sessions [2].

The field of bioinformatics has grown in the past decade. There are many such degree granting programs around the world at the bachelor's, master's, and PhD levels. This article provides a status report of the EduComm's ongoing endeavor to identify a set of core curricular guidelines for bioinformatics education at all levels. As a pilot project, the Curriculum Task Force of the EduComm conducted a survey in the spring of 2011. This initial survey was sent to members of the EduComm, consisting of 50 individuals from various regions of the world, and to the EMBnet community, representing 79 people from more than 30 countries. The response rate was 33%, with 41 individuals completing the survey.Analysis of the survey produced an initial set of recommendations to be used as a discussion point from which to launch a larger effort to develop a working bioinformatics curriculum. With increased input from the larger community, the EduComm will continue to refine its results. Individuals who are interested in contributing to this initiative are encouraged to contact the Chairs of the ISCB EduComm.

The purposes of this article are to further disseminate the survey results and to solicit participation in the initiative. The initial survey results are summarized, the preliminary working curriculum is defined, and the next steps of the EduComm Curriculum Task Force are outlined.

Survey Results

Responses were received from 41 individuals in 20 countries (covering five continents). This is a small but diverse group of respondents representing a wide array of professional positions, including scientist, professor (all ranks), director of bioinformatics, technician, engineer, postdoctoral researcher, teaching assistant, and lecturer. The levels of students taught by the respondents ranged from secondary thru PhD.

Topics suggested by survey respondents for inclusion in a bioinformatics curriculum fit into two primary areas, *(1) computation, mathematics, and statistics and (2) biology and chemistry*. An initial working bioinformatics curriculum was constructed by selecting topics suggested by at least ten respondents (i.e., more than 25% of the survey respondents), resulting in five topics in each of the two primary areas. This initial working curriculum is shown in Table 1.

Analysis and Next Steps

The results of our survey were presented at the Third RECOMB Satellite Conference on Bioinformatics Education (RECOMB-BE) [3]. Several observations and suggestions were offered during the discussion that followed the presentation. It was noted that the survey did not provide a list of possible topics from which to choose. This was intentional, to avoid introducing biases that would affect the answers. The unrestricted nature of the questions resulted in a wide array of topics being suggested. Responses that addressed similar concepts were grouped together to identify general topics.

COMPUTATION, MATHEMATICS, AND STATISTICS	BIOLOGY AND CHEMISTRY
Programming/scripting/ software engineering (36)	Cellular and molecular biology (21)
Statistics/probability (31)	Genomics (12)
Databases (24)	Basic biology (11)
Algorithm design/data structures/ computation theory (20)	Evolutionary biology (10)
Machine learning (13)	Genetics (10)

Table 1. The initial working bioinformatics curriculum.

The initial working curriculum does not completely represent the breadth of suggested topics. For example, it does not contain anything explicitly related to medicine, structural biology, or biochemistry. A small minority of the respondents suggested these topics; thus, they are not reflected in the consensus. (Additional grouping could be performed in order to increase the coverage of the responses.) In addition, due to the diversity of suggestions, the topic categories above tend to be general areas rather than contents of specific courses. Furthermore, due to the use of the word topic in the survey, respondents suggested only content areas, not issues of process, which appear frequently in descriptions of desired program outcomes. Specific examples of missing items include (1) scientific communication, (2) lifelong learning, and (3) professional behavior (including ethics).

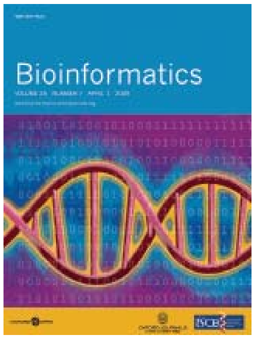
It was also suggested that ISMB's topic areas be considered as a general framework for a bioinformatics curriculum. The most recent ISMB topic areas are as follows:

- Applied Bioinformatics
- Bioimaging & Data Visualization
- Databases & Ontologies
- Disease Models & Epidemiology
- Evolution & Comparative Genomics
- Gene Regulation & Transcriptomics
- Mass Spectrometry & Proteomics
- Population Genomics
- Protein Interactions & Molecular Networks
- Protein Structure & Function
- Sequence Analysis
- Text Mining

This initial working curriculum is only intended to prompt discussion and to inspire the generation of more specific recommendations for refined curricula for bioinformatics. It provides useful guidelines for those seeking to determine core topics for a bioinformatics program (it is not intended to be used as a standard for accreditation purposes). The EduComm is currently (a) summarizing curricula from existing bioinformatics programs, (b) surveying directors of bioinformatics core facilities and biological researchers to identify the skills needed for people they hire, and (c) reviewing bioinformatics career opportunities to determine skill sets required by current employers of bioinformaticians. The new survey results may be used to propose curricular guidelines.

Continued on page 13

BIOINFORMATICS JOURNAL UPDATE



2012 is set to be an important transition year for *Bioinformatics*. After an 8 year term, Executive Editor Alex Bateman has decided to step down from his journal role at the end of 2012. Working together Alex and Alfonso Valencia have achieved a tremendous amount on behalf of *Bioinformatics* during this time – we and the journal will miss him. We are busy working to appoint Alex's successor to lead the journal alongside Alfonso from 2013 – look out for news later in the year.

Once again we received around 2000 submissions in 2011 – the efforts of around 3000 reviewers and our editorial team led us to accept ~30% of these, with an average time from submission to first decision of 30 days. We were very pleased to welcome Michael Brudno to the Associate Editor team last November, and more recently Inanc Birol has joined the team bringing further expertise in genome sequencing and analysis. We would like thank David Rocke and John Quackenbush for their hard work as Associate Editors for the journal over many years, and we are delighted that they have both joined the Editorial Board.

In 2012 we're continuing our sponsorship of the high-throughput sequencing (HiTSeq) SIG at the ISMB. Look out for our latest special collection of sequencing papers distributed at the meeting. Last year's award winners for the best papers at this event were:

- Andrew McPherson 'Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data'
- Christian Rödelsperger and Peter N. Robinson 'Identity-By-Descent Filtering of Exome Sequence data for Disease-Gene Identification in Autosomal Recessive Disorders'

We'll be publishing further conference sections in the future, including of course the 2012 ISMB and ECCB proceedings.

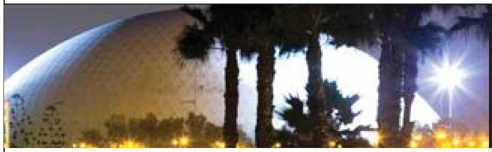
Bioinformatics challenges for personalized medicine	Guy Haskin Fernald Emidio Capriotti Roxana Daneshjou Konrad J. Karczewski Russ B. Altman	http://bioinformatics.oxfordjournals.org/content/27/13/1741.full
On the organization of bioinformatics core services in biology-based research institutes	Olli Kallioniemi Lodewyk Wessels Alfonso Valencia	http://bioinformatics.oxfordjournals.org/content/27/10/1345.full
Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling	Paweł P. Łabaj Germán G. Leparc Bryan E. Linggi Lye Meng Markillie H. Steven Wiley David P. Kreil	http://bioinformatics.oxfordjournals.org/content/27/13/i383.full
A pipeline for RNA-seq data processing and quality assessment	Angela Goncalves Andrew Tikhonov Alvis Brazma Misha Kapushesky	http://bioinformatics.oxfordjournals.org/content/27/6/867.full
On the organization of bioinformatics core services in biology-based research institutes	Yong Lin, Jian Li Hui Shen Lei Zhang Christopher J. Papasian Hong-Wen Deng	http://bioinformatics.oxfordjournals.org/content/27/15/2031.full

In case you missed them, above are the top 5 accessed articles published in the journal in 2011. At the time of writing the 2011 impact factors have not been announced but based on our own citation analysis we are hoping to see *Bioinformatics'* impact factor increase this year.

As ever, we welcome any comments or feedback on any aspect of the journal - please do not hesitate to get in touch with us (bioinformatics.editorialoffice@oup.com).

With best wishes,

The *Bioinformatics* Editorial team



Curriculum Task Force Report continued from page 11

The ISCB EduComm (www.iscb.org/iscb-leadership-a-staff-/1172) invites participation from the worldwide community of computational biologists and bioinformaticians.

Please join us for the Birds of a Feather (BoF) session, entitled Curriculum Guidelines for Bioinformatics and Computational Biology (An Open Forum of the Curriculum Task Force of the ISCB Education Committee), which will be held on July 16, 2012 at the ISMB meeting (www.iscb.org/ismb2012-program/birds-of-a-feather). At the BoF session, the Curriculum Task Force of the ISCB Education Committee will hold an open forum to discuss bioinformatics curriculum guidelines. Participants will consider curricular implications of the task force's surveys of career opportunities, hiring practices of bioinformatics core facility directors, and existing curricula. The forum seeks input from all interested individuals.

Additionally, we are seeking input via a blog. To read a more detailed report of the survey and to post your comments, please visit the blog site at http://bioinfocurriculum.blogspot.com/.

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1. Altman RB (1998) A curriculum for bioinformatics: the time is ripe. *Bioinformatics* 14: 549-550.

2. Ranganathan S (2005) Bioinformatics education--perspectives and challenges. *PLoS Comput Biol* 1: e52. doi:10.1371/journal.pcbi.0010052

3. Welch L, Schwartz R, Lewitter F (2011) *Report from the ISCB Education Committee*: a draft curriculum for bioinformatics [abstract] presented at the third annual RECOMB Conference on Bioinformatics Education (RECOMB-BE), an ISMB/ECCB 2011 satellite meeting, July 2011, Vienna, Austria.

This article is excerpted from the June 2012 issue of PLoS Computational Biology. To link to the full journal article please visit www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1002570

NIGMS CELEBRATES 50 YEARS

What is NIGMS?

Established in 1962, The National Institute of General Medical Sciences (NIGMS) is one of 27 separate Institutes and Centers of the National Institutes of Health (NIH) in the U.S. Department of Health and Human Services. For 50 years NIGMS has supported basic research and training to help increase our understanding of living systems and to lay the foundation for advances in disease diagnosis, treatment and prevention.

Currently NIGMS funds approximately 4,700 research grants and supports over 4,300 trainees (26% of all trainees receiving assistance from NIH). Furthermore, by 2010, NIGMS had already funded the Nobel Prize-winning research of 74 scientists.

50th Anniversary!

On May 16th the NIGMS' 50th anniversary was honored by the Federation of American Societies for Experimental Biology (FASEB) at a joint celebration on Capitol Hill in Washington, DC, hosted by FASEB as part of their yearlong centennial celebration. The event was attended by over 200 people, including ISCB board member Judith Blake, members of the U.S. Congress, NIH Director Dr. Francis Collins, Acting NIGMS Director Dr. Judith Greenberg, NIGMS alumni, science reporters, representatives from research advocacy organizations and patient groups, and many more. Presentations highlighted advances in biomedical research that have been achieved over the last 50 - 100 years as a result of the federal government's investment in NIGMS and basic research, and three Nobel Laureates reflected on the impact that early funding from NIGMS had on their careers.

During its 50th anniversary year NIGMS is supporting special lectures, symposia, and sessions at the annual meetings of ten scientific societies, and poster awards at another six. At ISMB be sure to attend the special session "Celebrating Science Together: ISMB 20 Years and NIGMS 50th Anniversary Special Session," July 16th, from 2:30-4:25 p.m. The session has been organized by Steven Brenner, University of California, Berkeley, and includes presentations by notable NIGMS-funded researchers, with a special presentation by Peter Lyster, program director for the NIGMS Division of Biomedical Technology, Bioinformatics, and Computational Biology.

NIGMS is also hosting the following anniversary activities:

- DeWitt Stetten, Jr., 50th Anniversary Symposium at NIH on October 17th (see www.nigms.nih.gov/News/Meetings/Stetten_2012.htm)
- Cell Day 2012, an interactive Web chatroom about the cell for middle and high school students on November 2nd (see http://publications.nigms.nih.gov/cellday2012/)
- NIGMS 50th Anniversary Personal Reflections – an invitation to share stories about what support from the Institute has meant to your research (see www.nigms.nih.gov/About/50Anniversary/PersonalReflections.htm).

NIGMS Fun Facts:

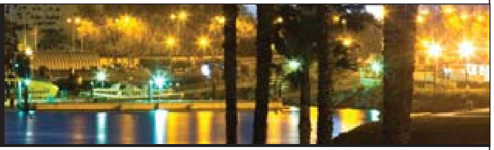
In 1962 the average R01 (an investigator initiated research grant) was 22,810 USD (actual dollars, not adjusted for inflation). The average R01 is today 343,847 USD.

In 1974 NIGMS was the first NIH institute to have a female director, and she later served as acting director of NIH – twice! The National Research Service Award Program also bears her name. Who was she? Dr. Ruth Kirschstein served as NIGMS director from 1974 to 1993, and as acting director of NIH in 1993 and again from 2000-2002. Read all about her at www.nlm.nih.gov/locallegends/Biographies/Kirschstein_Ruth.html

In 2011 NIGMS received its 100,000th grant application. Then director Jeremy Berg announced on the NIGMS Feedback Loop blog, "We just reached a milestone—our 100,000th grant application. Interestingly, it's for a K99/R00 (Pathway to Independence) award. This program enables promising postdoctoral scientists to receive mentored—and later independent—research support. Given our strong commitment to research training, mentoring and workforce development, it's somehow fitting that this application is for a program that addresses these needs." The full post is available at https://loop.nigms.nih.gov/index.php/2011/02/25/milestone-grant-application/

If you knew these three fun facts you really know your NIGMS! The director position for this Institute is open once again – perhaps you should apply!

ISCB CONTINUES TO ADVOCATE FOR OPEN ACCESS



By BJ Morrison McKay, ISCB Executive Officer

The effort to preserve open access to scientific literature funded with public funds has become a never-ending challenge. The ISCB Public Affairs and Policies Committee has closely followed this issue, and busily advocated on behalf of open access. The ISCB Public Policy Statement on Open Access to Scientific and Technical Literature was released in October, 2010, and reported in full in the ISCB Newsletter - Summer 2011. This past December the Research Works Act (H.R. 3699) was introduced in the U.S. House of Representatives, but eventually withdrawn by the bill's sponsors before gaining a companion bill in the Senate or moving through the Congressional hearing process. That bill would have prohibited federal agencies from requiring, as a condition of their research grant funding, that the public be guaranteed online access to the products of research funded by public tax dollars. Shortly before the withdrawal, ISCB sent a letter signed by Richard Lathrop-ISCB Public Affairs and Policies Committee Chair, Scott Markel-ISCB Publications Committee Chair, and Burkhard Rost-ISCB President to every member of the House encouraging them to vote against the bill, and pointing to our own policy statement as a guiding principle on open access.

More recently, the Federal Research Public Access Act (FRPPA; H.R. 4004 and S. 2096) was re-introduced to both chambers of Congress (the House and the Senate), after previous attempts at this legislation in 2006 and 2010. These companion bills would require federal research funding agencies, as a condition of their research grant funding, to develop policies that ensure the public is guaranteed online access to the products of research funded by public tax dollars. Naturally, ISCB has taken a stand in favor of these bills, and sent personalized letters of support to all members of Congress, plus each of their Chief's of Staff and Legislative Assistants for the respective committees reviewing these bills.

Below is the full text of the letter sent in support of FRPPA. We encourage all members in the U.S. to adapt this letter for sending a personalized version to your own members of Congress to ensure the protection of open access to scientific results. Additionally, if you are not in the U.S. and ever have news of regulations being introduced in your country that would prohibit or restrict open access in any way, please let us know at info@iscb.org. This issue is not confined to the U.S., and as an international society we are committed to advocating on behalf of open access in all corners of the world.

ISCB Letter to all members of the U.S. Congress, sent June 4, 2012:

On behalf of the International Society for Computational Biology (ISCB), we strongly encourage you to sign on as a co-sponsor of H.R. 4004 / S. 2096, the "Federal Research Public Access Act (FRPAA)," introduced on February 9 and referred to the House Committee on Oversight and Government Reform / Senate Committee on Homeland Security and Government Affairs. This bill would require federal research funding agencies, as a condition of their research grant funding, to develop policies that ensure the public is guaranteed online access to the products of research funded by public tax dollars.

This bill will empower American taxpayers in accessing the results of the crucial scientific research they funded. By supporting the growing trend for cooperation and collaboration made possible by the open and rapid sharing of information and research results, this bill will improve our ability to exploit scientific discoveries, promote critical advances in life-saving scientific research, and accelerate the pace of innovation in all scientific disciplines.

Most critically, this bill would propagate the highly successful National Institutes of Health (NIH) Public Access Policy to other agencies. The NIH Public Access Policy now gives millions of Americans public access to vital health care information from the NIH's PubMed Central database. Under the current policy, more than 90,000 new biomedical manuscripts are deposited for public accessibility each year, allowing researchers, physicians, healthcare professionals, taxpayers, and families to access and use this critical health-related information in a timely manner.

This bill would make such a collection the rule, rather than the exception, for federal agencies. It affects not only the results of biomedical research produced by the NIH, but also scientific research from all other federal agencies. Access to critical information, paid for with taxpayers' money and addressing vital areas such as energy, public safety, the environment, and hundreds more, would be significantly extended by this legislation --- greatly to the benefit of the lives and well-being of the public, which funded the research in the first place.

In October, 2010, ISCB published a public policy statement on "Open Access to Scientific and Technical Research Literature" (www.iscb.org/iscb-policy-statements/literature_open_access). This policy statement embraced Open Access even beyond the current NIH policy. The vision of individualized medicine offers many reasons for hope and a brighter future. Achieving such important goals poses immense challenges for the discipline of computational biology. No single research institution is ready for a challenge of this magnitude, so we have learned to join forces and to share scientific results and information. The objective of ISCB's statement on Open Access is to increase the availability of scientific results and developments in our field well beyond what is currently accomplished by the NIH. An excerpt from this statement:

> *The International Society for Computational Biology strongly advocates free, open, public, online: (i) access by person or machine to the publicly-funded archival scientific and technical research literature; and (ii) computational reuse, integration, and distillation of that literature into higher-order knowledge elements.*

We strongly urge you to require all federal research funding agencies to ensure timely, public access to the results of research funded with taxpayer dollars. Please become a co-sponsor and support H.R. 4004 / S. 2096.

Sincerely,

Scott Markel, Ph.D.
Chair of ISCB Publication Committee

Richard Lathrop, Ph.D.
Chair of ISCB Public Affairs & Policies Committee

Burkhard Rost, Ph.D.
ISCB President

GLBIO 2012 HIGHLIGHTS

By Stacy Slagor, ISCB Director of Corporate Relations and Development

Over 320 attended the 2nd Annual Great Lakes Bioinformatics Conference (GLBIO) that was held May 15-17, 2012, at the University of Michigan. Eight U.S. states and two Canadian provinces comprise the North American Great Lakes region, and this conference series aims to advance the computational approaches to biology within the region. Held for five years as the OCCBIO of the Ohio Bioinformatics Consortium, the meeting was rebranded in 2011 and adopted as the newest official conference of the International Society for Computational Biology. GLBIO, like OCCBIO before it, provides an interdisciplinary forum for students, faculty and researchers in academic, industry, nonprofit, and government labs to present, learn and discuss across a broad spectrum of bioinformatics topics.

Conference co-chairs Lonnie Welch (Ohio University) and Jim Cavalcoli (University of Michigan) continued the tradition started last year by organizing a group hike through the hills of the Nichols Arboretum adjacent to the University's Ann Arbor campus. Future collaborations were sparked as conference-goers got to know one another over discussions of the upcoming sessions while enjoying the inviting trails and sunny, summerlike skies.

Nine tutorials were presented on a range of topics, including high throughput sequencing, cancer 'omics, RNA 3D structure prediction, and supercomputing for bioinformatics. Russell Schwartz, Carnegie Mellon University, provided the opening keynote, *Learning Population Histories from Genome Variation Data*. Mercedes Pascual, University of Michigan, presented a keynote titled, *Pathogen Diversity from an Ecological Perspective*, and Michael Lynch, Indiana University, delivered a keynote about the *Mutation, Drift, and the Evolution of Subcellular Features*. A banquet was held at the University of Michigan Museum of Art, where Howard Cash, President and CEO of Gene Codes Corporation, shared his insight into developing DNA sequencing software with a keynote entitled, *Designing Bioinformatics for the Wetware: Usability Challenges with Massive Amounts of Data*.

Program Committee co-chairs Laura Brown (Michigan Technical University), Margit Burmeister (University of Michigan), and Elodie Ghedin (University of Pittsburgh), coordinated the selection of 38 oral presentations on topics of bioimaging, computational proteomics, disease models and epidemiology, gene regulations and transcriptomics, metagenomics, protein structure and function, population genomics, and sequence analysis. Also presented was a special session on undergraduate and graduate bioinformatics education, and the Ohio Bioinformatics Consortium held a career development session for their members and funders. A lively exhibition that included 17 sponsors, six additional exhibitors, and 75 posters furthered the conference goal of fostering collaborative relationships and networking opportunities while exposing attendees to many new ideas.

Within the last year the Great Lakes Bioinformatics Consortium (GLBC) has reorganized and regained official affiliate status with ISCB. Together, the GLBC and ISCB are now looking ahead to GLBIO 2013, which will be co-hosted by Carnegie Mellon University and the University of Pittsburgh, with conference sessions at Carnegie Mellon. Mark your calendar today to join us May 14-16, 2013 in Pittsburgh. We hope to see you there!

CALL FOR PROPOSALS TO ORGANIZE ISCB-ASIA 2013

By Paul Horton, Chair
Janet Kelso, Co-Chair
ISCB Conferences Committee

ISCB is pleased to announce this Call for Proposals for individuals or groups interested in hosting the next open ISCB-Asia conference, slated for the third quarter of 2013, to co-organize this meeting with ISCB anywhere in the Asia region. The proposal deadline is the 1st of August, 2012. If you are not personally interested but know of someone else who could do an excellent job of organizing this event, please feel free to forward this mail. An overview of ISCB, its expansion into regionally-based international meetings, and the details of the proposal requirements are all specified below.

ISCB-Asia 2013 Meeting

The aim of the International Society for Computational Biology (ISCB) is to serve the worldwide computational biology community by addressing scientific policies, providing access to high quality publications, organising meetings, and serving as a portal to information about training, education, employment and news from related fields. ISCB currently has over 3000 members from more than 70 countries around the world. Among its many activities ISCB hosts annual meetings, including ISMB, the world's longest running and largest international bioinformatics conference (held jointly with ECCB every other year in Europe), as well as a series of smaller, newer meetings. ISCB also has affiliations in place with several other significant meetings in the field, such as PSB and RECOMB.

In an extension to its meeting activities, ISCB is participating in the organization of regional meetings in locations where ISMB has not been held. In 2009 and 2011 joint ISCB-Africa meetings were held in collaboration with the African Society for Bioinformatics and Computational Biology (ASBCB), and the 2013 meeting is now being planned for Tunis, Tunisia; in 2010 and 2012 ISCB-Latin America was held in Uruguay and Chile, respectively; the first ISCB-Asia was held jointly with InCoB 2011 in Malaysia, and the 2012 meeting is now being planned for China (Shenzhen). With the aim of continuing these successful regional meetings, ISCB is now soliciting applications for the co-organization of our next meeting in Asia for 2013.

A requirement that ISCB-Asia become permanently affiliated to an existing meeting or society is not intended. Having co-organised the ISCB-Asia meeting with the Asia-Pacific Bioinformatics Network in 2011 and with BGI in 2012, ISCB now looks to continue expanding its network of affiliations by seeking proposals from other existing societies or conferences in the Asia region, or by working with a group that has a similar interest in organising a new bioinformatics community meeting in Asia.

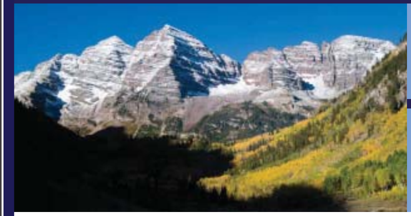
Proposals should be submitted via email to asia-rfp@iscb.org by 1 August 2012.

The full call for proposals can be downloaded at www.iscb.org/iscb-news-items/1408-2012-may17-first-call-presentations-iscb-asia-sccg2012

ISCB COMMUNITY CONFERENCES & x-MEETINGS

ROCKY 2012

10th Annual Rocky Mountain Bioinformatics Conference



December 6 – 8, 2012
Aspen/Snowmass
Colorado

Rocky is an official conference of the International Society for Computational Biology

While keynote speakers highlight the major advances and future directions of our science, the flash presentation and posters that make up the majority of the meeting enable all attendees to present at this small/mid-size meeting that puts an emphasis on networking and building new collaborations.

www.iscb.org/rocky2012

CSHALS 2013

Conference on Semantics in Healthcare and Life Sciences

February 27 – March 1, 2013
Cambridge/Boston, USA

CSHALS is the premier annual event focused on the use of semantic technologies in the pharmaceutical industry, including hospitals/healthcare institutions and academic research labs.

www.iscb.org/cshals2013

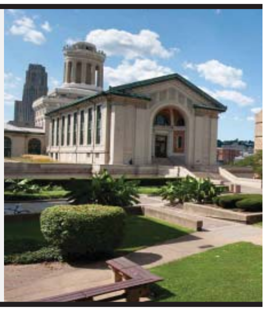
An official conference of the International Society for Computational Biology.

GLBIO 2013

Hosted by Carnegie Mellon University and the University of Pittsburgh

Great Lakes Bioinformatics Conference

May 14–16, 2013 Pittsburgh, PA



The 3rd GLBIO provides an interdisciplinary forum for the discussion of research findings and methods. An important goal is to foster long term collaborative relationships and networking opportunities among the institutions and corporations of the North American Great Lakes states and provinces.

www.iscb.org/glbio2013

An official conference of the International Society for Computational Biology.

ISCB-Asia/SCCG 2012

Dameisha Beach
Shenzhen, China
December 17-19, 2012

http://www.iscb.org/iscb-asia2012

We invite you to attend ISCB-Asia/SCCG 2012, co-hosted by the International Society for Computational Biology and BGI. Just minutes from Hong Kong, Shenzhen is a vibrant city and the site of one of the world's largest sequencing centers.

Our conference presents a unique opportunity to present and absorb cutting edge research in computational biology including NGS data analysis, cloud and workflow platforms for bioinformatics, cancer genomics, metagenomics, machine learning, protein bioinformatics and open problems in computational biology.

KEY DATES

Paper/oral submit deadline:
30 July 2012

Poster submit deadline:
30 July 2012

Early registration deadline:
12 November 2012

华大基因 BGI

An official conference of the International Society for Computational Biology

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ISCB Africa ASBCB

March 13 - 15, 2013
Tunis, Tunisia

Workshops11 – 12th March

www.iscb.org/iscbafrica2013

ISCB and its regional affiliate, the African Society for Bioinformatics and Computational Biology (ASBCB), are teaming up for the third time to jointly host the ISCB Africa ASBCB 2013 Conference, March 13-15, in Tunis, Tunisia.

This meeting will feature an exceptional slate of keynote speakers and provide a forum for the dissemination of the latest bioinformatics research being conducted around the world on issues particularly relevant to Africa.

An Official Conference of the International Society for Computational Biology and the African Society for Bioinformatics and Computational Biology

UPCOMING CONFERENCES AND EVENTS

ISCB CO-SPONSORED & AFFILIATED EVENTS

2012 Brazilian Symposium on Bioinformatics
(BSB 2012)
Brazil - MS - Campo Grande
Hosted By: Federal University of Mato Grosso do Sul, Campo Grande, Brazil
Aug 15, 2012 - Aug 17, 2012
ISCB Member Discount: 14%
http://bsb2012.facom.ufms.br/

RECOMB-BE: Satellite Conference on Bioinformatics Education
Russia - St. Petersburg
Hosted By: Algorithmic Biology Lab at St. Petersburg Academic University
Aug 26, 2012 - Aug 26, 2012
http://bioinf.spbau.ru/be2012

RECOMB-AB: Satellite Conference on Open Problems in Algorithmic Biology
Russia - St. Petersburg
Hosted By: Algorithmic Biology Lab at St. Petersburg Academic University
Aug 27, 2012 - Aug 29, 2012
http://bioinf.spbau.ru/ab2012/

ECCB12 – 11th European Conference on Computational Biology
Switzerland - Basel
Hosted By: Swiss Institute of Bioinformatics & Biozentrum University of Basel
Sep 09, 2012 - Sep 12, 2012
ISCB Member Discount: 100 EUR
http://eccb12.org

InCoB2012: 11th International Conference on Bioinformatics
Thailand - Bangkok
Hosted By: National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA) Ministry of Science and Technology (MOST), King Mongkut's University of Technology Thonburi (KMUTT) and Asia Pacific Bioinformatics Network
Oct 03, 2012 - Oct 05, 2012
ISCB Member Discount: 50 USD
http://incob2012.org/

Bio-IT World Europe Conference & Expo
Austria - Vienna
Hosted By: Cambridge Healthtech Institute
Oct 09, 2012 - Oct 11, 2012
ISCB Member Discount: 10%
www.bio-itworldexpoeurope.com

BioVis 2012: 2nd IEEE Symposium on Biological Data Visualization
United States - WA - Seattle
Hosted By: IEEE Visweek
Oct 14, 2012 - Oct 15, 2012
ISCB Member Discount: 20%
Restrictions: Discount varies by reg type
www.biovis.net

3rd Annual PhD Symposium in Computational Biology & Innovation
Ireland - Dublin
Hosted By: University College Dublin
Dec 05, 2012 - Dec 07, 2012
ISCB Member Discount: 10%
www.ucd.ie/phdsymposium/

Pacific Symposium on Biocomputing 2013
United States - HI - Kohala Coast
Hosted By: Pacific Symposium on Biocomputing (PSB)
Jan 03, 2013 - Jan 07, 2013
ISCB Member Discount: 50 USD
http://psb.stanford.edu/

RECOMB 2013: 17th Annual Conference on Research in Computational Molecular Biology
China - Beijing
Hosted By: Tsinghua University
Apr 07, 2013 - Apr 10, 2013
ISCB Member Discount: 10% or greater
http://bioinfo.au.tsinghua.edu.cn/recomb2013

OTHER CONFERENCES & EVENTS OF INTEREST

Resources for Computational Drug Discovery
United Kingdom - Cambridge - Hinxton
Hosted By: Joint EMBL-EBI/Wellcome Trust Course
Jul 02, 2012 - Jul 06, 2012
http://registration.hinxton.wellcome.ac.uk/display_info.asp?id=288

Pharmacogenomics
Italy - Sicily - Lipari Island
Hosted By: Lipari School on BioInformatics and Computational Biology
Jul 07, 2012 - Jul 14, 2012
http://lipari.cs.unict.it/LipariSchool/Bio/

NIMBioS Investigative Workshop: Modeling Dengue Fever Dynamics and Control
United States - TN - Knoxville
Hosted By: National Institute for Mathematical and Biological Synthesis
Jul 23, 2012 - Jul 24, 2012
www.nimbios.org/workshops/WS_dengue

Society of Mathematical Biology 2012 Annual Meeting & Conference
United States - TN - Knoxville
Hosted By: National Institute for Mathematical and Biological Synthesis and Univ. of Tennessee, Knoxville
Jul 25, 2012 - Jul 28, 2012
http://nimbios.org/SMB2012/

Galaxy Community Conference (GCC2012)
United States - IL - Chicago
Hosted By: Galaxy Project
Jul 25, 2012 - Jul 27, 2012
http://galaxyproject.org/GCC2012

Protist 2012
Norway - Oslo - Oslo
Hosted By: ISEP and ISOP
Jul 29, 2012 - Aug 03, 2012
www.protist2012.com

Joint CC3D/SBW User Training Workshop in Multiscale, MultiCell Tissue Modeling
United States - NC - Durham
Hosted By: The Hamner Institutes for Health Sciences
Jul 30, 2012 - Aug 03, 2012
www.compucell3d.org

The 26th Annual Symposium of The Protein Society
United States - CA - San Diego
Hosted By: The Protein Society
Aug 05, 2012 - Aug 08, 2012
www.proteinsociety.org/symposium

BIOKDD 2012 : The 11th International Workshop on Data Mining in Bioinformatics
China - Beijing
Hosted By: The 18th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining
Aug 12, 2012 - Aug 12, 2012
http://bio.informatics.iupui.edu/biokdd12/

(continued)

OTHER CONFERENCES & EVENTS OF INTEREST *(continued)*

Protein Interactions and Networks
United Kingdom - Cambridge - Hinxton
Hosted By: Wellcome Trust Advanced Courses
Aug 19, 2012 - Aug 25, 2012
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/index.htm

SSMBio 2012: International Summer School in Methods in Bioinformatics
Spain - Tarragona
Hosted By: Research Group on Mathematical Linguistics from Rovira i Virgili University
Aug 27, 2012 - Aug 31, 2012
http://grammars.grlmc.com/ssmbio2012

TACC 2012: Theory and Applications of Computational Chemistry
Italy - Pavia
Hosted By: University of Pavia, Italy
Sep 02, 2012 - Sep 07, 2012
www.tacc2012.org

First International Workshop on Hybrid Systems and Biology
United Kingdom - Newcastle upon Tyne
Hosted By: Co-located with CONCUR 2012
Sep 03, 2012 - Sep 03, 2012
http://hsb2012.units.it/

6th Workshop on Machine Learning in Systems Biology
Switzerland - Basel
Hosted By: Workshop at ECCB2012
Sep 08, 2012 - Sep 09, 2012
http://mlsb.cc

AIMM2012 - Annotation, Interpretation and Management of Mutations
Switzerland - Basel
Hosted By: European Conference on Computational Biology
Sep 09, 2012 - Sep 09, 2012
www.unbsj.ca/sase/csas/data/aimm2012/index.html

Joint Conference of the South African Bioinformatics and Genetics Societies
South Africa - Western Cape - Stellenbosch
Hosted By: University of Stellenbosch
Sep 10, 2012 - Sep 12, 2012
http://genetics.cmc-uct.co.za/

WABI 2012: Workshop on Algorithms for Bioinformatics
Slovenia - Lubljana
Hosted By: University of Lubljana, Slovenia
Sep 10, 2012 - Sep 12, 2012
http://algo12.fri.uni-lj.si/?file=wabi

3nd International Conference on Quantitative Biology and Bioinformatics in Modern Medicine
United Kingdom - UK - Belfast
Hosted By: Queen's University Belfast
Sep 20, 2012 - Sep 21, 2012
www.bio-complexity.com/QUB12/QB_ConfIndex.html

BIOCOMP BG 2012: International Conference on Bioinformatics and Computational Biology
Bulgaria - Varna
Hosted By: University of Plovdiv and GRC
Sep 20, 2012 - Sep 21, 2012
http://biocomp.bio.uni-plovdiv.bg/

EG VCBM: Eurographics Workshop on Visual Computing for Biology and Medicine
Sweden - Östergötland - Norrköping
Hosted By: Norrköping Visualization Center C
Sep 27, 2012 - Sep 28, 2012
www.vcbm.org

TPNC 2012: 1st International Conference on the Theory and Practice of Natural Computing
Spain - Tarragona
Hosted By: Research Group on Mathematical Linguistics - GRLMC from University Rovira i Virgili
Oct 01, 2012 - Oct 05, 2012
http://grammars.grlmc.com/tpnc2012/

BIBM12: IEEE International Conference on Bioinformatics and Biomedicine
United States - PA - Philadelphia
Hosted By: Drexel University
Oct 04, 2012 - Oct 07, 2012
www.ischool.drexel.edu/ieeebibm/bibm12/

CSBW: The 2012 Computational Structural Bioinformatics Workshop
United States - PA - Philadelphia
Hosted By: BIBM 2012
Oct 04, 2012 - Oct 04, 2012
www.cs.odu.edu/~lchen/CSBW.htm

ACM BDB 2012: International Conference on Bioinformatics, Computational Biology, and Biomedicine
United States - FL - Orlando
Hosted By: University of Florida
Oct 07, 2012 - Oct 10, 2012
www.cse.buffalo.edu/ACM-BCB2012/

UC Berkeley BioExec Institute - Creating Value
United States - CA - Berkeley
Hosted By: UC Berkeley Center for Executive Education
Oct 09, 2012 - Oct 10, 2012
http://executive.berkeley.edu/programs/bioexec-institute

TBC 2012: Translational Bioinformatics Conference
Korea, Rep - Jeju island
Hosted By: Translational Bioinformatics Conference
Oct 14, 2012 - Oct 17, 2012
www.snubi.org/TBC2012/

Systems Biology Europe
Spain - Madrid
Hosted By: Select Biosciences
Oct 16, 2012 - Oct 17, 2012
http://selectbiosciences.com/conferences/index.aspx?conf=SBE2012

RECOMB Satellite Workshop on Comparative Genomics
Brazil - Rio de Janeiro - Nietrói
Hosted By: Universidade Federal Fluminense, Niterói, Brazil
Oct 17, 2012 - Oct 19, 2012
www.uff.br/recombcg

Indian Lab Automation
India - Mumbai
Hosted By: Select Biosciences
Oct 30, 2012 - Oct 31, 2012
http://selectbiosciences.com/conferences/index.aspx?conf=ILA2012

Proteomics Bioinformatics
United Kingdom - Cambridge - Hinxton
Hosted By: Wellcome Trust Advanced Courses
Nov 05, 2012 - Nov 09, 2012
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Workshops/WTX054153.htm

UC Berkeley BioExec Institute - Managing Value
United States - CA - Berkeley
Hosted By: UC Berkeley Center for Executive Education
Nov 07, 2012 - Nov 08, 2012
http://executive.berkeley.edu/programs/bioexec-institute

PRIB 2012
Japan - Tokyo
Hosted By: IAPR
Nov 08, 2012 - Nov 10, 2012
http://prib2012.org/

NETTAB 2012 on "Integrated Bio-Search"
Italy - Como
Hosted By: Polytechnic of Milan
Nov 14, 2012 - Nov 16, 2012
www.nettab.org/2012/

UC Berkeley BioExec Institute - Growing Value
United States - CA - Berkeley
Hosted By: UC Berkeley Center for Executive Education
Dec 06, 2012 - Dec 07, 2012
http://executive.berkeley.edu/programs/bioexec-institute

13th Research Centers in Minority Institutions International Symposium on Health Disparities
Puerto Rico - San Juan
Hosted By: University of Puerto Rico, Universidad Central del Caribe, and Ponce School of Medicine
Dec 10, 2012 - Dec 13, 2012
www.rcmibiennial.org

ICDM 2012: Workshop on Biological Data Mining and its Applications in Healthcare
Belgium - Brussels
Hosted By: Xiao-Li Li, See-Kiong Ng, Jason T.L. Wang
Dec 10, 2012 - Dec 10, 2012
www1.i2r.a-star.edu.sg/~xlli/BioDM.html

Epigenomics Session at PSB 2013
United States - Hawaii - The Big Island
Hosted By: PSB
Jan 03, 2013 - Jan 07, 2013
http://noble.gs.washington.edu/proj/epigenomics2013

While ISCB provides for news, conference and event listings that may be of interest to members and bioinformaticians at large, ISCB is not responsible for the content provided by outside sources. Such listings are not meant as an endorsement by ISCB.

ISCB CONFERENCES

RECOMB Satellite Conference on Regulatory and Systems Genomics, with DREAM Challenges
United States - CA – San Francisco
Hosted By: Stanford University and Columbia University
Nov 12, 2012 – Nov 15, 2012
http://recomb-2012.c2b2.columbia.edu

Rocky 2012: 10th Annual Rocky Mountain Bioinformatics Conference
United States - CO - Snowmass
Dec 06, 2012 - Dec 08, 2012
ISCB Member Discount: 220 USD
www.iscb.org/rocky2012

ISCB-Asia/SCCG 2012
China - Shenzhen
Dec 17, 2012 - Dec 19, 2012
ISCB Member Discount: ~80 USD
www.iscb.org/iscb-asia2012

CSHALS 2013
United States - MA - Cambridge
Feb 27, 2013 - Mar 01, 2013
ISCB Member Discount: 220 USD
www.iscb.org/cshals2013

ISCB Africa ASBCB 2013
Tunisia - Tunis
Mar 13, 2013 - Mar 15, 2013
ISCB Member Discount: 80 USD International Participants
ASBCB Member Discount: 180 USD African Participants
www.iscb.org/iscbafrica2013

GLBIO 2013: Great Lakes Bioinformatics Conference
United States - PA - Pittsburgh
May 14, 2013 - May 16, 2013
ISCB Member Discount: 220 USD
www.iscb.org/glbio2013

ISMB/ECCB 2013
Germany - Berlin
Jul 19, 2013 - Jul 23, 2013
ISCB Member Discount: ~220 USD
www.iscb.org/ismbeccb2013

COVER IMAGE

The Queen Mary Luxury Cruise Liner is a historical landmark docked in Long Beach, California. On May 27, 1937, the Queen Mary departed from Southampton, England to embark on her maiden voyage. At that time, she was considered an innovative marvel, the pinnacle of luxury, and the model of Art Deco style. Some of the attractions included original art murals, paintings, sculptures. Over 50 different types of woods from all over the world were used to decorate the ship inside and out, giving the liner the nickname, *Ship of Woods*. British Royalty, Hollywood celebrities and dignitaries enjoyed five dining areas and lounges, two cocktail bars and swimming pools, a grand ballroom, a squash court, and even a small hospital.

When World War II started, the Queen Mary was transformed into a military troopship. Interestingly, Patrick Joseph Morrison, the late father of ISCB's Executive Officer BJ Morrison McKay, was among the soldiers transported to the war in Europe this way. But he never saw the ship in all her glory – the luxurious amenities were removed and she was painted grey, dubbing her the *Grey Ghost.*

During her rich history, the Queen Mary made 1001 transatlantic voyages. In 1967 she was relocated to Long Beach, California. The liner is now a full-service hotel, historical landmark, and entertainment venue.

Source: www.queenmary.com

How are We Doing?

Please email ISCB 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 in meeting this objective.

ISCB acknowledges the support from the San Diego Supercomputer Center, at the University of California, San Diego, which provides office space to the Society.