ISCB NEWSLETTER

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ISCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

A LETTER TO OUR ISCB MEMBERS AND COLLEAGUES

The 1921 Nobel Prize for Physics was awarded to Albert Einstein for discovering the law of photoelectric effect. Over the course of his illustrious career, Einstein made such a name for himself that his surname is synonymous with “genius” in today’s vernacular. But he can also be credited as a whimsical philosopher, with statements such as, “People love chopping wood. In this activity one immediately sees results.” Obviously, a scientist is not motivated in the same way as a woodchopper, and the pursuit of science is not for everybody. In fact, if immediacy were our inspiration, no doubt our classrooms would be sparsely visited and our labs would be devoid of researchers.

But that is not the case at all. Over a period of time we steadily chip away at our research pursuits, enjoying the fruits of our labors a bit at a time, and regularly reaffirming our love of science. Securing sustainable funding and publishing high impact papers are constant challenges to achieving the goals we set for ourselves, but we generally do see the results of our efforts, even if not immediately so.

Running ISCB is no different in that regard. Some initiatives take hold like fast growing seeds, but more often than not they take time to develop, grow, and eventually bear fruit. In this newsletter, we are pleased to present you with a collection of some of ISCB’s most important and prominent initiatives, most of which were originated long ago, and have only in the last year produced the intended results.

We are particularly proud to publish the ISCB Policy Statement on Open Access to Scientific and Technical Research Literature (page 5), which is the result of a multi-year effort led by Richard Lathrop as head of ISCB’s Public Affairs & Policies Committee. We are also pleased to introduce our two annual award winners (pages 3-4), as well as our esteemed class of ISCB Fellows for 2011 (page 7). These awardees and Fellows have collectively produced an impressive body of work that has earned them high honors from their ISCB peers.

Throughout this newsletter you will find announcements of ISCB meetings taking place around the globe. Expanding our regional meetings portfolio has required a worldwide collaborative effort, and we are proud to be offering meetings on four continents in the span of less than one year. An announcement on the collaboration between ISCB and EMBnet (page 16) furthers our mutual commitment to providing education and training through these meetings, while an appeal to contribute to Wikipedia (page 10) as a means of communicating the significance of computational biology to the world-at-large is just the beginning of a newly adopted initiative, but one that clearly shows immediate results with each new edit.

To be commended are the members of the Student Council, who each year seem to build upon the previous year’s team in organizing exceptional events during ISMB and throughout the year that directly benefit the student community they serve (page 11).

In addition to what is reported in the limited pages of this newsletter, ISCB achieved a membership milestone at the end of 2010 by surpassing 3000 members for the first time. As Society revenues come primarily from a combination of membership dues and conference proceeds, our strong membership, financially successful meetings in 2010 and early 2011, and carefully controlled expenses are succeeding in stabilizing our financial standing. We believe ISCB’s long pursuit of financial security is finally within view as we continue to build up reserves to help weather any economic uncertainties that may lie ahead. We are not fully there yet, but we are much closer than just a few short years ago.

(continued)

As many of you are reading this at the ISMB/ECCB 2011 conference in Vienna, Austria, we offer sincere congratulations to our sister conference, ECCB, on its 10 Year Anniversary. ISCB's partnership with ECCB in jointly organizing this meeting every other year when ISMB is in Europe has been an enriching experience for all involved, and we are committed to strengthening our partnership through their 20th, 30th, 40th.... well, you get the picture.

Speaking of 20th anniversaries, we will be excited to celebrate 20 years of ISMB next year in Long Beach, California (near Los Angeles), July 15-17, 2012. At the first ISMB in 1993 we're sure the organizers knew they were starting something long lasting and impactful. Now that nearly 20 years have flown by, perhaps they feel a bit like they were chopping wood after all. Immediacy is, on balance, relative. It seems Einstein had something to say about relativity as well...

All the best,

Burkhard Rost
President

Terry Gaasterland
Vice President

Janet Kelso
Vice President

Thomas Lengauer
Vice President

Michal Linial
Vice President

Reinhard Schneider
Treasurer

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BLOGGERS WELCOME AT ISMB/ECCB

For each talk we have a feed entry under: http://friendfeed.com/ismbeccb2011

ISCB home page view
www.iscb.org

The Leading Professional Society for the New Era of Computational Biology

Conferences

ISMB ECCB 2011
Returning to the site of the very successful 2007 conference, ISMB ECCB 2011 is being held in Vienna, Austria, July 17 - July 19, 2011, with pre-conference meetings starting on the 15th. The conference features multiple parallel tracks of scientific talks and presentations, hundreds of posters, and internationally renowned keynote presenters including ISCB's annual Overton Prize and Sr. Scientist Award winners. Read more...

InCoB/ISCB-Asia Joint Conference 2011
ISCB is pleased to present the InCoB/ISCB-Asia Joint Conference 2011, organized in partnership with the Asia-Pacific Bioinformatics Network (APBioNet, www.apbionet.org/), in Kuala Lumpur, Malaysia, November 30 - December 2, 2011. The main objective of the conference is to provide a platform for experts and budding bioinformaticians to discuss and exchange ideas and thoughts on the development of bioinformatics in the Asia-Pacific region. Read more...

Rocky 2011
ISCB is organizing the 9th annual Rocky Mountain Bioinformatics Conference (Rocky 2011) in Snowmass/Aspen, Colorado from December 8 - 10, 2011. 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 Read more. . .

CSHALS 2012
The ISCB Conference on Semantics in Healthcare and Life Sciences (CSHALS 2012) returns for its fifth year as the premier annual event focused on the use of semantic technologies in the pharmaceutical industry, including hospitals/healthcare institutions and academic research labs. CSHALS will take place February 22-24,

Announcements

Subscribe here to the ISCB News Feed!

May 23: Rocky 2011 Save the Date & Academic Retreat

May 18: Last Call for Papers! InCoB/ISCB-Asia Joint Conference 2011

Apr 24: ISMB/ECCB 2011 – Register now and save!

Mar 28: Announcing InCoB/ISCB-Asia Joint Conference 2011 in Malaysia

Mar 04: Sign-on to ISCB's Open Access Policy Statement (for members-only)

....more....

ISCB Mailing List Policies

ISCB Journals

On January 1, 2009 *Bioinformatics* once again became an official journal of the ISCB. This was a "homecoming" of sorts, as Bioinformatics was the original Society journal from 1998-2004, and the ISMB Proceedings have been published in the journal continuously since 2001. Read more...

PLoS Computational Biology is an open-access, peer-reviewed journal published monthly by the Public Library of Science (PLoS) as an official journal of the ISCB. PLoS Computational Biology is run by an international Editorial Board, headed by the Editor-in-Chief, Philip E. Bourne (University of California, San Diego, USA). Read more...

ISMB / ECCB 2011 Live Blog

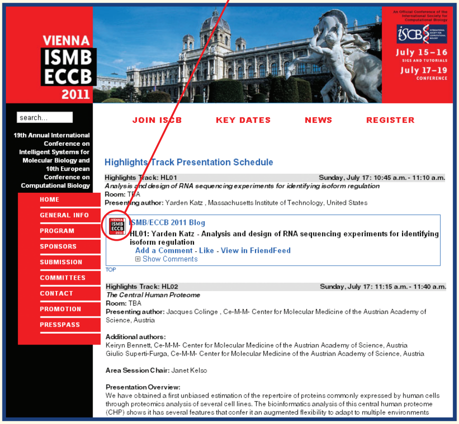
ISMB/ECCB
Keynote: Bonnie Berger - Computational biology in the 21st century: making sense out of massive data
June 10 - Comment
Exponential increase in genomic and biomedical data, which will soon outstrip advances in computing power to perform current methods of analysis - ISMB/ECCB

ISMB/ECCB
HL01: Yarden Katz - Analysis and design of RNA sequencing experiments for identifying isoform regulation
June 10 - Comment
Through alternative splicing, most human genes express multiple isoforms that often differ in function. - ISMB/ECCB
Results provide a probabilistic framework for... *more...* - ISMB/ECCB

ISMB/ECCB
Keynote: Olga Troyanskaya - Integrating computation and experiments for a molecular-level understanding of human disease
June 10 - Comment

ISMB/ECCB

ISMB/ECCB 2011 page view
www.iscb.org/ismbeccb2011-program



19th Annual International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology

Highlights Track Presentation Schedule

Highlights Track: HL01 — **Sunday, July 17: 10:45 a.m. - 11:10 a.m.**
Analysis and design of RNA sequencing experiments for identifying isoform regulation
Room: TBA
Presenting author: Yarden Katz , Massachusetts Institute of Technology, United States

ISMB/ECCB 2011 Blog
HL01: Yarden Katz - Analysis and design of RNA sequencing experiments for identifying isoform regulation
Add a Comment - Like - View in FriendFeed
⊞ Show Comments

Highlights Track: HL02 — **Sunday, July 17: 11:15 a.m. - 11:40 a.m.**
The Central Human Proteome
Room: TBA
Presenting author: Jacques Colinge , Ce-M-M- Center for Molecular Medicine of the Austrian Academy of Science, Austria

Additional authors:
Keiryn Bennett, Ce-M-M- Center for Molecular Medicine of the Austrian Academy of Science, Austria
Giulio Superti-Furga, Ce-M-M- Center for Molecular Medicine of the Austrian Academy of Science, Austria

Area Session Chair: Janet Kelso

Presentation Overview:
We have obtained a first unbiased estimation of the repertoire of proteins commonly expressed by human cells through proteomics analysis of several cell lines. The bioinformatics analysis of this central human proteome (CHP) shows it has several features that confer it an augmented flexibility to adapt to multiple environments

ACCOMPLISHMENT BY A SENIOR SCIENTIST AWARD

Michael Ashburner

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

If computational biology seems challenging in the second decade of the 21st century, spare a thought for those who pioneered the discipline in the 1980s. Michael Ashburner at the University of Cambridge was one of them. “His work is now seen as a landmark and an achievement in technology,” says Alfonso Valencia, chair of the ISCB awards committee.

Ashburner began his career with a degree in genetics from the University of Cambridge in 1964. He stayed on to do a PhD, studying *Drosophila* and, in particular, polytene chromosomes, which form when certain specialised cells undergo repeated rounds of DNA replication. Polytene chromosomes have a characteristic banded structure. In *Drosophila* there are some 5,000 bands and a subset of these undergo, during development, a reversible structural modification as the result of transcription; this is known as puffing and can be considered an analog of gene activity. In the late 1960s and early 1970s, Ashburner studied puffing patterns and inferred the existence of a cascade of genetic controls under the influence of the hormone ecdysone during larval development.

In the late 1970s, Ashburner turned his attention to the study of the Alcohol *dehydrogenase gene* and its environs. By the mid-1980s, he had the most detailed analysis in full genetic terms of any small chromosome region of any multi-cellular organism, and had the *Adh* gene sequences from several different species of *Drosophila*. “That drew me into bioinformatics because we needed a way of comparing sequences,” he says. “There was almost no software available to help.”

Two people came to his aid. The first was Walter Bodmer, director of the Imperial Cancer Research Fund, who gave Ashburner the use of a DEC computer with access to the early network. “We could access this machine by dial-up and do some analysis,” he says. The second was Doug Brutlag at Stanford University, who was developing MOLGEN, an early bioinformatics system, which he allowed Ashburner to access.

That presented a significant obstacle, however. Getting a computer in the United Kingdom to speak to one in Stanford was not straightforward. Today, everybody uses the Internet, defined by the TCP/IP protocol. But in the early ‘80 s, the UK and United States used different systems. The US was pioneering TCP/IP while the UK had a standard called the Coloured Book protocols. “The only place that had an interface between the two protocols was University College, London, and they were very helpful,” says Ashburner, “giving us 5 kb of disk space.”

The process of connecting to Stanford was far from simple. “The way you did it was to dial up your local packet switching exchange at the Post Office and connect to the Rutherford Appleton Laboratory. You then typed in some code which connected you to UCL where you could use TCP/IP,” he says. The signal was routed via Goonhilly satellite station in Cornwall to Carnegie Mellon University and from there to Stanford. “I had a dumb terminal, that is a box with no memory, so everything had to be captured by a printer in parallel.” Ashburner was far from deterred, however.

At about that time, the European Molecular Biology Laboratory (EMBL) in Heidelberg and GenBank in the US released the first nucleotide sequence libraries in quick succession. Using his network access, Ashburner and his colleagues, collaboratively with MOLGEN, set up one of the first bulletin boards, called BioNet, to keep people informed of changes to the library and to software. “This became well used and things evolved from there,” he says.

As the field of bioinformatics grew, the need for an institution to house the data and conduct research increased. So in 1992, the EMBL decided to set up an institute of bioinformatics that would house this library and carry out research. This organisation became known as the European Bioinformatics Institute, based in Hinxton, UK, with Ashburner and John Sulston having led the UK bid to host it. “I was persuaded to become the first program coordinator and took half-time leave from Cambridge to do that,” he says. He eventually took over as joint-director, a post he held until 2001. “At first, the finances were sticky and the politics were horrendous. But it has since gone from strength to strength,” he says.

At the same time, Ashburner continued his interest in *Drosophila* genetics. This is a field with a rich and long history of collecting and sharing mutations. The first catalogue of mutations was published in 1925 and it was still being revised in paper form in the late 1980s. But the field was beginning to expand quickly and the books were out of date as soon as they were published. “It became clear to me that we couldn't carry on publishing in paper form every 10 or 20 years,” he recalls.

So in 1989 he proposed that the community set up an electronic database to take over the role of the printed one. In 1992, the NIH funded the project that became known as FlyBase, one of the first genetic and now genomic databases.

Photo courtesy of European Molecular Biology Laboratory

FlyBase was a crucial factor in triggering Ashburner's interest in a structured, controlled vocabulary, a formal representation of knowledge about genes and gene products. He began to define terms for gene products by their biological processes, such as wing development, and then defined the data structure in which these terms were related to each other. “It occurred to me that if you were able to do this for several model species, you'd have a fantastic tool,” he says.

But this insight initially met with little interest. “My first presentation, at ISMB in Greece in 1997, went down like a lead balloon,” he recalls. Eventually, he and three like-minded colleagues settled the matter in a bar at the Montreal ISMB in 1998. Together, they decided to set up a cross-species ontology to be used by the Drosophila, yeast, and mouse databases. They called it the Gene Ontology, and it is now a major bioinformatics project that covers over 1,800 species. Their original paper on the idea in *Nature Genetics* is one of the most highly cited in the field. “His achievement is not just to have built this system but also to have organised the consortium behind it. It is now one of the most used resources in all of biology,” says Valencia.

He went on to collaborate with Gerry Rubin and Craig Venter in sequencing the *Drosophila* genome in 1999. “The process turned me into a nervous wreck,” he jokes. He published his account of this roller-coaster experience in a short but entertaining book called Won for All: How the Drosophila Genome was Sequenced (Cold Spring Harbor *Laboratory Press, 2006).*

“We're lucky to have such an inspirational figure in the community,” says Valencia. “This award has been well deserved for a number of years.”

This article is excerpted from the June 2011 issue of *PLoS Computational Biology*. To link to the full journal article please visit www.ploscompbiol.org/article/info:doi/10.1371/journal.pcbi.1002081

OVERTON PRIZE

Olga Troyanskaya

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

In the spring of 1997, Olga Troyanskaya was working on a degree in computer science and biology at the University of Richmond, Virginia, when she contacted Steven Salzberg, then at Johns Hopkins University, about a summer internship in his lab devoted to computational biology. "He took a chance on me—a random student from another school—and was tremendously inspirational," she says. She spent the following two summers working in Steven Salzberg's laboratory, first at Johns Hopkins and then at The Institute for Genomic Research.

And so began the career of one of the most promising young researchers in bioinformatics, and a deserving winner of this year's Overton Prize. "She is one of these forces of nature, full of energy," says Alfonso Valencia, chair of the ISCB awards committee.

Troyanskaya herself talks with infectious enthusiasm about her work. "I've always been fascinated by the problems of biology," she says. "I was just better at computer science and math than the wet lab research. And it seemed to me that there had to be a lot you could contribute with computer science that you couldn't do with experimental techniques alone."

From the University of Richmond, Troyanskaya moved to Stanford University to complete a PhD in biomedical informatics, under the supervision of Russ Altman, a bioinformatician, and David Botstein, a geneticist. "I wanted a setup that was close to real biological problems, and I got exactly that. I learned a great deal from both of them," she says.

In 2003, she moved to Princeton University as an assistant professor in the Department of Computer Science and the Lewis-Sigler Institute for Integrative Genomics. "I am fortunate that the computer science department appreciates the impact of computing in biology, and that I have many wonderful colleagues at both the department and in the Institute. I found several amazing collaborators, and this allowed me to begin a number of interesting projects."

One of the key problems she focuses on is making better use of the vast but unwieldy biological datasets in databases around the world. "So instead of focusing on one study, we can take the entirety of published data. That allows you to ask very specific questions in a data-driven way and to develop novel biological hypotheses," she says.

Photo courtesy of Princeton University, Office of Communications.

An important goal is to predict the function of genes or proteins. There have been many experimental approaches to determine what genes do and how they are controlled inside the cell. But this work tends to produce datasets that are large and noisy. Troyanskaya's approach is to develop new ways for extracting useful information from these datasets using techniques from computer science such as machine learning and data mining.

"Computation by itself is often not enough to discover new biology but it can direct experimental work," she says. And she has set up a wet lab to help test and validate the hypotheses that the computer science helps generate. In 2009, for example, she used this approach to identify 109 new proteins involved in mitochondrial biogenesis in yeast.

This combined approach is one of the things that sets Troyanskaya apart, says Valencia. "She is one of the first to have come from the computational side and then moved into the experimental area to combine both," he says.

Understanding the function of individual genes is only a small part of a much bigger story. Many genes and proteins play multiple roles within a cell as parts of various networks of biological processes. Mapping out these networks and understanding how they work and interact with each other is yet another strand of her research. "She has made important contributions to systems biology," says Valencia.

The process of evaluating and validating computational predictions is an area requiring a broad collaboration to develop standards and methods that can be used to achieve a consensus about the results. To this end, Troyanskaya is collaborating with the curators of model organism databases and members of the Gene Ontology Consortium.

Another problem that many researchers face is handling the data avalanches currently being generated. So Troyanskaya, in collaboration with Princeton colleagues Kai Li and Moses Charikar, is looking at ways to better search and visualise these huge datasets, something that is challenging because of high noise levels and the enormous volume of the data. "We are developing better ways to do this," she says.

The awards committee was also impressed by Troyanskaya's service for the community. She is involved in the Society's two official journals, *PLoS Computational Biology* and *Bioinformatics*. And she is involved in conferences: organizing, chairing tracks and program committees. "That is something that is very much appreciated," says Valencia. "We are lucky to have her."

And there is surely more to come. Troyanskaya points to numerous questions that are driving her research forward. She wants to know, for example, how we can predict which genes are involved in kidney disease, to understand their function and their clinical role on a molecular level. She works on these questions in close collaboration with experimental researchers, such as Matthias Kretzler and his group from the University of Michigan, Ann Arbor. And she is passionate about finding ways to ask questions in a data-driven way, not just in a knowledge-driven way that relies on what we already know about biology. "These are the questions that I'm really interested in," she says. "And we really haven't yet harnessed the full potential of our data collections."

This article is excerpted from the June 2011 issue of *PLoS Computational Biology*. To link to the full journal article please visit www.ploscompbiol.org/article/info:doi/10.1371/journal.pcbi.1002081

ISCB PUBLIC POLICY STATEMENT ON OPEN ACCESS TO SCIENTIFIC AND TECHNICAL RESEARCH LITERATURE

By Richard H. Lathrop, Chair,
ISCB Public Affairs Committee
Burkhard Rost, ISCB President and
the ISCB Membership,
Executive Committee, Board of Directors,
and Public Affairs & Policies Committee

ISCB Members are invited to add their names to the list of signatories at: www.iscb.org/iscb-policy-statements/literature_open_access/signup

Current signatories are listed at: www.iscb.org/iscb-policy-statements/literature_open_access/signatories

Preamble
The International Society for Computational Biology (ISCB) is dedicated to advancing human knowledge at the intersection of computation and life sciences. On behalf of the ISCB members, this public policy statement expresses strong support for open access, reuse, integration, and distillation of the publicly funded archival scientific and technical research literature, and for the infrastructure to achieve that goal.

Knowledge is the fruit of the research endeavor, and the archival scientific and technical research literature is its practical expression and means of communication. Shared knowledge multiplies in utility because every new scientific discovery is built upon previous scientific knowledge. Access to knowledge is access to the power to solve new problems and make informed decisions. Free, open, public, online access to the archival scientific and technical research literature will empower citizens and scientists to solve more problems and make better, more informed decisions. Attribution to the original authors will maintain consistency and accountability within the knowledge base. Computational reuse, integration, and distillation of that literature will produce new and as yet unforeseen knowledge.

We strongly encourage open software, data, and databases, issues that are not addressed here. A prior ISCB public policy statement on sharing software provides very clear support for open source/open access www.iscb.org/iscb-policy-statements/software_sharing). We support open database access, standards, and interoperability. We also recognize that databases are complex dynamic entities, with ongoing roles and needs that cannot be treated properly within this statement. In contrast, the publicly funded archival research literature, addressed here, is the static historical record of publicly funded research outcomes.

ISCB supports many of the principles set forth in other open-access policies and statements, including the "Budapest Open Access Initiative," the "Bethesda Declaration on Open Access Publishing," the *Bulletin of the World Health Organization* "Equitable Access to Scientific and Technical Information for Health," the *US National Academies of Sciences* report on "Sharing Publication-Related Data and Materials: Responsibilities of Authorship in the Life Sciences," the Organisation for Economic Co-Operation and Development "Principles and Guidelines for Access to Research Data from Public Funding," and the "Berlin Declaration on Open Access to Knowledge in the Sciences and Humanities." Details on the documents mentioned here and additional background information material may be found in the online version of this statement at www.iscb.org/iscb-policy-statements/literature_open_access.

The public policy statement put forward here builds upon these principles to elucidate in more detail the public policy position of ISCB and its members on this important issue in scientific dissemination.

Public Policy 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.

Supporting Statements
1. The possibilities latent in the digital information age make it essential to achieve open access, and computational reuse, integration, and distillation, of the publicly funded archival research literature.

a. Immediate access is preferable, and when access is at an interval following publication, that interval should not exceed one year.

b. At a minimum, every scientific journal should offer an open access option to every published research paper, as does every official or affiliated journal of the ISCB.

c. Copyright licenses explicitly should permit computational reuse, integration, and distillation, using standard existing language that eliminates the need for manual or legal review.

d. The format of the available article should be easy to parse by both human and machine (e.g., HTML). Ideally, a plain text version should be available as well (e.g., TXT), to facilitate computational reuse and integration (e.g., computational text mining for knowledge extraction).

e. Computational reuse, integration, and distillation should give attribution to the original authors.

2. Existing open access models show high impact, scientific benefit, feasibility, and acceptability.

a. The public benefit from open access to the world's online information via the publicly funded Internet provides a good model of expected impact.

b. The scientific fertilization from open access to genomic information via the publicly funded Human Genome Project provides a good model of expected scientific benefit.

c. Open access policies by the US National Institutes of Health, the Howard Hughes Medical Institute, and the Wellcome Trust provide good models of feasibility and acceptability.

d. The Creative Commons Attribution License and the Science Commons Open Access Data Mark provide good models of legal mechanisms for computational reuse, integration, and distillation.

3. Open literature access, reuse, integration, and distillation will enable a whole new generation of innovative computational tools and processes. The literature will be endowed with enriched commentary and usability. It will be connected seamlessly, by proper semantic links, to relevant Web sites, data, databases, and algorithms. Creating a web of knowledge around publications is an important consequence of semantic enrichment of the research literature. Such tools already are being built by publishers, researchers, entrepreneurs, and others. The further development of these tools should be supported aggressively. Removing all barriers to literature open access, reuse, integration, and distillation is critical to achieving such a knowledge-level transformation.

(continued)

4. Supplementary data and methods should be openly available online, in sufficient detail to replicate the reported research results and facilitate reuse. Such material should be deposited in appropriate public repositories, in compliance with accepted community standards, and in accord with the existing ISCB public policy statement on sharing software. It should allow for application of other computational methods to the data and application of other data to the computational methods.

5. Publishing high-quality peer-reviewed scientific literature incurs costs. We recognize that cost recovery is a serious issue that must be addressed carefully if open access is to be a mandated policy.

6. Open-access policy details—which version, where stored, how annotated and organized, what incentives, etc. —must be considered carefully. However, it has now become essential to put forward a broad policy mandate for public access to, and computational reuse, integration, and distillation of, the publicly funded archival scientific and technical research literature.

7. This statement is intentionally neutral about any specific funding policy. Many implementations all may achieve the same essential goal. Acceptable funding policies should:

   a. Remove barriers to open access and subsequent computational reuse, integration, and distillation.

   b. Encourage public, private, and philanthropic funding organizations to establish policies that mandate free, open, public, online access to, and computational reuse, integration, and distillation of, the research results funded from their public, private, or philanthropic support.

   c. Promote the body of publicly funded archival research literature as a public investment that bears interest, and not as an ongoing access cost to the public.

   d. Establish copyright licenses in standard terms that permit literature access, reuse, and integration.

   e. Specify a format that is easy to parse by both human and machine (e.g., HTML); and, ideally, also provide a plain text version (e.g.,TXT) to facilitate computational reuse and integration.

   f. Recognize the need to fund activities of peer review, copy editing, and publishing.

   g. Provide fairness to several groups, including the developing world and its health concerns, unfunded or under-funded researchers, and others.

   h. Provide fair interim support or compensation, if and where needed, to facilitate making transitions and adaptations to new models for publishing and sustaining essential revenue.

   i. Be consistent with government laws, patent requirements, other existing regulations, and research dissemination through viable commercial mechanisms.

8. The expected cost of complete open access to the publicly funded archival research literature is only a very small percentage of the entire publicly funded international research endeavor. Nevertheless, it is undesirable to divert funding from current research and thus risk underfunding basic science. New funding should be made available for open-access policy implementations.

Conclusion

Currently, scientific advancement is limited by article availability, access costs, copyright restrictions, document formats, bulk download limits, etc. All such barriers should be removed.

The publicly funded archival scientific and technical research literature represents a substantial investment by the public, governments, foundations, non-profit institutions, publishers, individuals, and others. We in the ISCB are committed to the continuous enhancement and leveraging of society's knowledge resources. One of our primary missions is the computational integration of individual pieces of knowledge from the research literature and databases, in ways that provide powerful new ideas and insights for next-stage research, for the benefit of the scientific community and society in general.

To achieve these public benefits, we strongly advocate free, open, public, online access to the publicly funded archival scientific and technical research literature, and the computational reuse, integration, and distillation of that literature into higher-order knowledge elements.

The example scenario illustrates an important public health benefit that could be achieved immediately: the opportunity to pursue useful knowledge-based innovations, by computational reuse, integration, and distillation of the publicly funded archival research literature, across many areas in biology and medicine.

Example Scenario

An automated malaria Web site might access location-specific information from thousands of publicly funded malaria research articles daily, and then integrate that information into a free online interactive world map. Such a map might be annotated with up-to-date information about disease occurrences, drug resistance profiles, current best control practices, etc., as distilled from the research literature extracted for and attached to each local region. A hypothetical user might be a public health official in the developing world responsible for controlling a sudden malaria outbreak in a remote area. Such a Web site should encounter no barriers while performing this free, useful, and potentially essential public service.

Example Discussion

A search for "malaria" in the US NIH/NLM PubMed literature database yielded more than 55,000 hits (July 2010; www.ncbi.nlm.nih.gov/pubmed/). The publicly funded portion of these 55,000 "malaria" hits should be freely available in bulk to this hypothetical malaria Web site, using technologies well suited to bulk tasks, for purposes of (i) the initial bulk literature download; (ii) regular updates; and (iii) intermittent bulk repeat downloads to reinitialize an improved knowledge base. The relevant copyright permissions should permit computationally recombining the publicly funded portion of these 55,000 texts into whatever final form is most useful and informative to the user.

This statement along with Appendices was published in full in the following journals: *Bioinformatics* (2011) 27(3):291-294. doi:10.1093/bioinformatics/btq687.
PLoS Computational Biology (2011) 7(2):e1002014. doi:10.1371/

ISCB PRESIDENT-ELECT ELECTIONS

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

To best tackle the variety of exciting challenges in the next few years of ISCB's growth and development, the three of us now jointly chair the Nominations Committee. We are pleased to contribute to ISCB in this important way, and our collective years of ISCB service, coupled with the varied perspectives and experiences we bring to the task, make for a fun and engaging collaborative process toward shaping the way ISCB manages its leadership nominations and elections.

The first big change we are orchestrating is holding the Officer elections much earlier this year so that members attending ISMB/ECCB in Vienna can participate in the process by casting their online ballots at the conference. A "voting booth" adjacent to the ISCB booth is planned in the exhibition area, where members can login to the elections site and select their candidate of choice. Of course, members can also login from their own computers anywhere and anytime, but the voting booth concept is intended to make the option to vote as inviting and easy as possible. The online voting site actually opened on July 5th, and closes as ISMB/ECCB 2011 comes to an end on July 19th. The voting site can be accessed here: www.iscb.org/elections.

We felt this was a great year to test an experimental voting procedure because it is the year of a President-Elect election. This means you are being asked to review the candidate statements posted at the voting site, and then cast your virtual ballot for this one Officer position by choosing between the two exceptionally qualified candidates:

David Rocke
University of California, Davis, USA
http://dmrocke.ucdavis.edu/

Burkhard Rost
Technical University Munich, Germany
www.rostlab.org

The successful candidate will begin a one-year President-elect term on January 21, 2012, which automatically transitions to being the next ISCB President for an additional two-year term, and is then followed by one additional year as an ISCB Board Member. All President-elect candidates must pledge to make every reasonable effort to attend the weekly Executive Committee teleconferences, the bi-monthly Board of Directors teleconferences, and the annual in-person Board meeting at ISMB through completion of the combined three year President-elect/President term, plus the additional year on the Board.

Such a level of commitment in time, in energy, and in dedication to leading ISCB into the future makes for arguably the most influential yet demanding elected position of the Society. We strongly encourage every ISCB member to participate in the election process, and hope those attending the conference who did not yet vote at home will take full advantage of the opportunity to do so in Vienna, while those not attending the conference make it a point to login and vote before the July 19th deadline.

The election results will be ratified by the ISCB Board of Directors, as required by our bylaws. This year we will do this through a special process in early 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 mid-August to see if your chosen candidate won the election.

We thank you in advance for your participation!

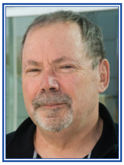
MEET THE ISCB FELLOWS CLASS OF 2011

The ISCB Fellows program honors members that have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. During the 2009 inaugural year of the program, ISCB committed to conferring Fellows status on all past and future winners of the ISCB Accomplishment by a Senior Scientist Award. To-date this includes David Haussler, David Lipman, Webb Miller, Chris Sander, David Sankoff, Temple Smith, Janet Thornton, and Mike Waterman. As the 2011 award winner, Michael Ashburner is now honored among them as well.

For this year's Fellows election, ISCB put out a call for nominations to our member community. The minimum criterion for nomination of highly accomplished and distinguished scientists was that the nominated member had maintained an active membership for at least three of the last six years. Leading up to the nomination period, Fellows Committee Chair Alfonso Valencia (who also chairs the Awards Committee) gained approval to reconfigure the voting group to include all current Fellows together with the ISCB Board of Directors, with a plan to phase into voting by only Fellows once a critical mass is reached in the coming years.

Many nominations were received for exceptional contributors to ISCB, and all represented researchers who have fulfilled important roles within our science. The outcome of the election is presented with great pride, and the ISCB Fellows Committee is pleased to announce these new Fellows, who now join their esteemed colleagues mentioned above in securing a place among our most highly honored members.

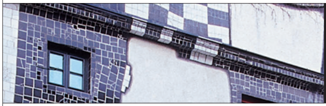
MICHAEL ASHBURNER
2011 Accomplishment
by a Senior Scientist Award
EMBL-EBI, UK



PHILIP E. BOURNE
University of California,
San Diego, USA

SØREN BRUNAK
Technical University
of Denmark

RICHARD DURBIN
Wellcome Trust Sanger
Institute, UK



FASEB UPDATES: CONTINUING TO SUPPORT ISCB THROUGH RESEARCH ADVOCACY AND OUTREACH

By the FASEB Office of Public Affairs Staff

Since 2003 ISCB has been a member society of the Federation of American Societies for Experimental Biology (FASEB; www.faseb.org), primarily for the high level advocacy that FASEB engages in with the U.S. government. This gives a voice to ISCB in issues related to science policy and funding that impacts scientists in the U.S. and around the globe. The following is an overview of the science policy initiatives FASEB has led on behalf of the biomedical research community during the last year.

FY 2011 – FY 2012 Budget Update

Although President Obama proposed a significant increase in funding for the U.S. National Institutes of Health (NIH) and other science agencies, Congress's attention was focused on cutting billions in federal spending. These cuts would have had global ramifications, as students and postdocs from all over the world conduct their training in the U.S. Without consistently strong U.S. government support for research, these opportunities for cross cultural collaboration and exchange could dry up.

FASEB mounted a concerted advocacy campaign to prevent these cuts, sending letters from President William Talman, MD, to key legislative committees, issuing e-action alerts that generated thousands of emails and phone calls to lawmakers, and organizing a Capitol Hill Day attended by ISCB member Dr. Judith Blake. Success was achieved in April when Congress passed the final fiscal year (FY) 2011 budget without any major cuts in funding for the U.S. science agencies. Policymakers have now turned their attention to the FY 2012 budget. Once again, President Obama is seeking increased funding for NIH while Congress is considering significant cuts. FASEB will continue to press lawmakers to sustain funding for biomedical science.

Research Information Technology and Infrastructure

With information technology playing an increasingly prominent role in research, FASEB has been working to educate policymakers on the opportunities associated with adoption of electronic health records (EHR) and the development of a national health information infrastructure. Under the leadership of ISCB member Dr. John Wooley, FASEB developed several policy statements arguing that EHR data will be important not just to clinicians, but also to scientists working to improve human health. This message has been taken to the White House Office of Science and Technology Policy, the President's Council of Advisors on Science and Technology, and the Centers for Medicare and Medicaid Services.

Science Training

In addition to advocating for science funding, FASEB has been working to shape research training policy. We endorsed many of the recommendations made in the National Research Council's *Research Training in the Biomedical, Behavioral, and Clinical Research Sciences* report, testified before an NIH task force charged with developing a model for a sustainable and diverse science workforce, and promoted policies incorporated into the National Institute of General Medical Sciences (NIGMS) strategic plan for training and career development. Specifically, FASEB has urged policy makers to facilitate training for a broad range of scientific careers, promote the creation of training plans by faculty mentors, and encourage trainees to develop individual career and professional development plans. FASEB continues to mobilize efforts to ensure that we maintain the quality of research training in the U.S.

Animals in Research and Education

FASEB is a strong proponent of the humane use of animals in research. We recently embarked on an international effort to help research institutions address the threat of animal rights extremism, and we are preparing comments on the *International Guiding Principles for Biomedical Research Involving Animals*. The principles provide a conceptual and ethical framework for countries using vertebrate animals in research. FASEB has also been leading an effort to defeat legislation pending in the U.S. Congress that would prohibit research on great apes, including chimpanzees. If adopted, the *Great Ape Protection and Cost Savings Act of 2011* could have a global impact as pharmaceutical companies based outside the U.S. frequently use U.S.-owned chimpanzees to test the safety of new compounds.

Service to ISCB Sudent and Minority Members

FASEB administers two multi-year NIGMS/NIH Minority Access to Research Careers (MARC) grants to help U.S. citizens and permanent resident underrepresented minority students with the costs of attending conferences, including any official meeting of ISCB. The **FASEB MARC** Program provided ISCB student and post doc members with full travel and registration costs to attend ISMB 2010 in Boston (7 supported), Rocky 2010 in Colorado (2 supported), ISCB Latin America 2010 in Uruguay (1 supported), and GLBIO 2011 in Ohio (1 supported). For ISMB/ECCB 2011 in Vienna FASEB has confirmed travel and registration support for 6 ISCB students and post docs. FASEB MARC also sponsored the Student Council booth space at ISMBs in 2008, 2009, and 2010, including the travel, registration, and fees for participation by an expert who provided CV critiques for trainees seeking career advice. For the past three years, FASEB has sponsored ISCB's booth and travel costs for participation in the Annual Biomedical Research Conference for Minority Students to broaden outreach to underrepresented minorities and foster interest in careers in computational biology and bioinformatics.

IMPROVING COMPUTATIONAL BIOLOGY CONTENT IN WIKIPEDIA. ISCB NEEDS YOU!

By Manuel Corpas and Alex Bateman,
The Wellcome Trust Sanger Institute

A prominent aim of the ISCB is to communicate the significance of computational biology to the wider scientific community, governmental organizations and the general public. It has come to our attention that Wikipedia represents a highly used resource for both public and scientists alike to learn more about science in general and computational biology. To illustrate the importance of Wikipedia a search in Google for ‘computational biology’ returns the Wikipedia entry as the top hit in the ranking. A search for ‘biological databases’, again, returns the corresponding Wikipedia entry top of the list. Together its popularity, scope and content make it one of the major global resources in knowledge provision. But most importantly, the success of Wikipedia is largely due to using volunteer input to provide rapid, accurate, free and accessible information to the general public. ISCB has recently supported the creation of a Wikipedia Task Force (WTF) with the following aims:

1. To disseminate knowledge in computational biology
2. To establish a community-wide public engagement effort
3. To create accessible articles about computational biology, to excite new people to join the field

The initiative is now accessible via the Computational Biology WikiProject at http://en.wikipedia.org/wiki/Wikipedia:WikiProject_Computational_Biology. This WikiProject is an online, Wikipedia-hosted portal to integrate computational biology relevant articles and people. There are many ways that you can help, from identifying articles that are within the scope of Computational Biology, to adding relevant information to articles in Wikipedia. If you would like to get some initial introduction on how to edit a Wikipedia entry the recent 10 Simple Rules article in *PLoS Computational Biology* provides some guidance (see www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1000941). Also there are a set of training pages available http://en.wikipedia.org/wiki/User:Rockpocket/Training. We believe Wikipedia provides a unique opportunity to educate and inform on a global scale, and urge ISCB members to engage with this initiative.

ISCB STUDENT COUNCIL OVERVIEW

HIGHLIGHTS

The 7th annual ISCB Student Council Symposium (http://symposium.iscbsc.org) is a global scientific forum for graduate students, post docs, and new researchers. Our goal is to provide an open, friendly and supportive environment for students to meet their peers, exchange ideas, and network. We encourage students to present their research through oral and poster presentations, offer travel fellowships to support symposium delegates, and host social events for students during ISMB.

Our 2011 Symposium program reflects the hard work and dedication of an amazing group of student volunteers who donated their time, expertise, and enthusiasm preparing for this event.

It showcases compelling research in a range of fields—from proteomics and genomics to the bioinformatics of health and disease—and features 12 student speakers and more than 50 student poster presentations. In addition, we are honored to have Curtis Huttenhower (Harvard School of Public Health), Ivet Bahar (University of Pittsburgh), and Chad Myers (University of Minnesota) as keynote speakers. With the help of our generous sponsors, we awarded 12 travel fellowships for symposium delegates (see http://symposium.iscbsc.org/content/travel-fellowships). Congratulations to all successful applicants!

The Student Council Symposium Committee and volunteer staff look forward to seeing you in Vienna! Please stop by our booth or visit our website at www.iscbsc.org to learn more and get involved! Prost!

By Lorena Pantano Rubino,
Student Council Symposium 2011 Chair
and Pedro Lopes, Student Council
Symposium 2011 Co-Chair

The ISCB Student Council is dedicated to promoting the development of the next generation of 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, and by attempting to influence policy processes affecting science and education. One of our key objectives is to provide support and financial assistance to computational biology students from developing countries.

Over the past year, our organization has continued to grow and evolve. Our volunteer student members have outdone themselves in putting together an outstanding program for the 7th Annual Student Council Symposium and organizing events for students throughout the ISMB conference. For example, our Art & Science Exhibition at ISMB 2011 will display images and videos generated as part of computational research projects and creative works that involve scientific concepts or employ scientific tools and methods. At the Student Council booth in the exhibition area, students can get career advice and review job boards. We are also hosting several fun social networking activities, such as “Scientific Speed-Dating, “Social HQ”, and “BLAST your Brain.” What does exactly does that mean? Come to our booth to find out!

At ISMB 2011, you’ll have an opportunity to see the ISCB Student Council in action. But our presence at this event is only one facet of our organization. We strive to reach out and support the computational biology student community throughout the whole year by:

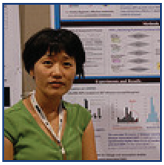
- Offering competitive mini-grants of up to USD 400 each to help fund innovative initiatives and events proposed by regional student groups (RSG). During the past year, 6 out of 14 proposals from RSGs in Central and Eastern Africa, France, Poland, Brazil, and India were approved for Student Council financial assistance. Our grant cycle for 2011-2012 will be starting soon.

- Establishing internships that provide students from developing nations an opportunity to work in a world-class computational biology laboratory. These internships enable students to gain international work experience and acquire new skills that they can share with research communities in their home country. Through this Student Council program, four students, representing India, Brazil, Kenya, and Nigeria, were given the opportunity to work for three months at the Rost Lab in Germany, under the direction of Professor Dr. Burkhard Rost.

- Organizing and supporting regional meetings, such as the 2010 European Student Council Symposium held in Ghent, Belgium, and the 2010 North Africa, Portugal and Spain Student Symposium on Bioinformatics held in Málaga, Spain. These regional meetings are an excellent forum for students to present preliminary research, learn about research activities and job opportunities close to home, and get recognition in their local research community.

You can read more about these and other ISCB Student Council initiatives at the ISCB Student Council 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 volunteer members. If you have a few minutes between sessions or if you’re feeling lost in the crowds at the Austria Center, stop by the ISCB Student Council booth. We will show you how we’re making a difference in the computational biology student community.

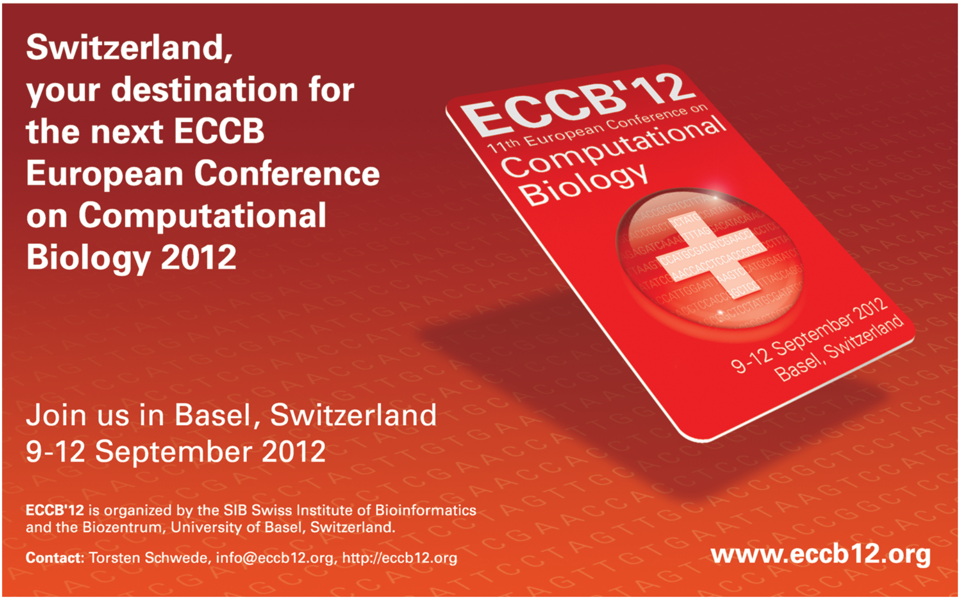
CALL FOR PROPOSALS TO ORGANIZE THE ISCB-ASIA 2012 MEETING



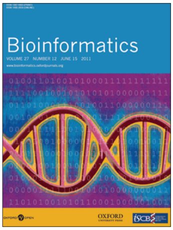
If you have experience organizing scientific meetings in Asia and would like to put a group together to co-organize the next ISCB-Asia, we would welcome your proposal. Please see the Call for Proposals at http://tinyurl.com/6xwo6us and start working on that proposal right away. Although the deadline may seem far away, September 1st will be here before we know it!

The motivation for this Call for Proposals was initiated several years ago when ISCB set out to expand services to our global membership by organizing or partnering in the organization of meetings in regions outside the European-North American rotation of ISMB. In a relatively short amount of time we have held African meetings in Bamako, Mali (www.iscb.org/iscbafrica2009), and in Cape Town, South Africa (www.iscb.org/iscbafrica2011), both in partnership with the African Society for Bioinformatics and Computational Biology (www.asbcb.org), an ISCB Affiliated Regional Group. In 2010 we organized a South American meeting in Montevideo, Uruguay (www.iscb.org/iscb-la2010), with Santiago, Chile scheduled for next year's event in that region of the world (www.iscb.org/iscb-latinamerica2012), and Brazil already designated for the 2014 meeting in this series (location and additional details still to be confirmed). Finally, our first Asian meeting, the InCoB/ISCB-Asia Joint Conference 2011 (www.incob2011.org), is fast approaching in Kuala Lumpur, Malaysia, November 30 - December 2, 2011.

With the aim of continuing these successful regional meetings, ISCB is now soliciting applications for the co-organization of our next meeting in the ISCB-Asia series, specifically for 2012. See the full CFP and let us hear from you by September!



BIOINFORMATICS JOURNAL



The impact factor release date is slightly later this year, and at the time of writing the 2010 impact factors have yet to be announced. However, some of the highly cited papers that will contribute towards *Bioinformatics'* impact factor include:

- DnaSP v5: a software for comprehensive analysis of DNA polymorphism data, Librado P, Rozas J *Bioinformatics* (2009) 25: 1451-1452
- Jalview Version 2-a multiple sequence alignment editor and analysis workbench, Waterhouse AM, Procter JB, Martin DMA, et al. *Bioinformatics* (2009) 25: 1189-1191
- Searching protein structure databases with DaliLite v.3. Holm, L; Kaariainen, S; Rosenstrom, P; and Schenkel, A. *Bioinformatics* (2008) 24: 2780-2781
- SOAP: short oligonucleotide alignment program. Li, RQ; Li, YR; Kristiansen, K; and Wang, J. *Bioinformatics* (2008) 24:713-714

The joint two top cited articles from 2010 are:

- Fast and accurate long-read alignment with Burrows-Wheeler transform, Li H, Durbin R, *Bioinformatics* (2010) 26:589-595
- edgeR: a Bioconductor package for differential expression analysis of digital gene expression data, Robinson MD, McCarthy DJ, Smyth GK, *Bioinformatics* (2010) 26:139-140

There have been some changes to the *Bioinformatics* editorial team – Mario Albrecht and Janet Kelso have both started terms as Associate Editors. We would like to thank Dmitrij Frishman and Joaquin Dopazo for their hard work as Associate Editors over their terms, and we are delighted that both have agreed to join the Editorial Board. We would also like to take this opportunity to thank over 3000 reviewers who enabled the peer review of around 2000 submissions in 2010.

Bioinformatics now has a mobile-optimized website (http://m.bioinformatics.oxfordjournals.org/) which has been developed to provide simpler, more intuitive browsing on mobile devices including iPhone and iPad, Android, Symbian and Windows Mobile smartphones, and Blackberry.

Bioinformatics has been at the forefront of OUP's improvements to the author experience – authors are now able to 'sign' their licences to publish online, and the journal is in a pilot scheme enabling authors to pay their open access fee online.

In 2010 over 30% of authors opted to publish their papers under our optional open access model, Oxford Open.

Once again *Bioinformatics* is sponsoring the high-throughput sequencing (HiTSeq) SIG at ISMB/ECCB this year and will award two prizes for the best papers during the event. Last year's award winners were:

- Leena Salmela 'Correction of sequencing errors in a mixed set of reads'
- Tianjiao Chu et al. 'Statistical Model for Whole Genome Sequencing and its Application to Minimally Invasive Diagnosis of Fetal Genetic Disease'

We will be distributing copies of the HiTSeq special issue at the SIG at ISMB/ECCB in Vienna.

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@oxfordjournals.org).

With best wishes,
Alex Bateman, Alfonso Valencia
and the *Bioinformatics* Editorial team

PLoS COMPUTATIONAL BIOLOGY OVERVIEW

By Rosemary Dickin, Publications Manager, PLoS Computational Biology

Since celebrating its fifth birthday last June *PLoS Computational Biology* has continued to nurture its community projects and accommodate ongoing growth in submissions. Each month, on average we now receive 120 new research articles and publish 32. Nearly half a million people visited the journal's website last year, an increase of over 30% from the previous 12 months. The steady growth we have seen in the journal's six years is a testament to the continuing high regard of and investment from the diverse groups we represent. While *PLoS Computational Biology's* primary objective remains to publish research of exceptional significance, we also relish our role as a community platform for discussion, advocacy and professional education.
The past year has seen many exciting new developments in these areas:

New for 2011 are **Editors' Outlook** articles, which aim to provide diverse commentary from our editors in the subjects they cover for the journal. We look forward to seeing the editors discuss the state of the art in their respective research areas, what they see as future developments, and what they are contributing to these areas themselves.
The first article, on "Bridging the Resolution Gap in Structural Modeling of 3D Genome Organization" by Marc Marti-Renom & Leonid Mirny will be published around the time of this year's ISMB meeting.

In the past year *PLoS Computational Biology* has also expanded its ongoing projects to document both the best of today's cutting-edge research and the field's rich history. **Conference Postcards**, which give a fresh summary of meeting highlights from young researchers, added articles from ISMB 2010 and PSB 2011, and we also hope to report on the best of this July's ISMB/ECCB. **The Roots of Bioinformatics**, a series of essays giving both historical and technical insights into the genesis of the field we know today, saw two new additions: "The Roots of Bioinformatics in Theoretical Biology" by Paulien Hogeweg and "The Roots of Bioinformatics in Protein Evolution" by Russell F. Doolittle.

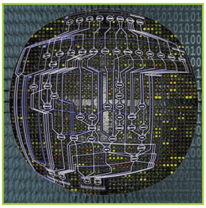
In addition, *PLoS Computational Biology's* new **Software Section** aims to provide a venue for outstanding open-source software that has already yielded important biological results. Article suggestions are coming in thick and fast, with the first articles set to appear later this year.

Like all PLoS journals, *PLoS Computational Biology* is committed to ensuring that research can be freely accessed and reused, to the benefit of both authors and readers. As such, we were delighted to support the ISCB by publishing the society's pivotal Public Policy Statement on **Open Access** to Scientific and Technical Research Literature (www.ploscompbiol.org/doi/pcbi.1002014) in February 2011 (the Statement is printed in full on pages 5 and 6 of this newsletter).

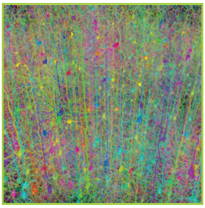
Of course, none of the above would be possible without the tireless support and generosity of the community we serve. *PLoS Computational Biology* would like to thank the reviewers, editors and authors who have made the journal what it is today.

EXAMPLES OF HIGHLY DOWNLOADED ARTICLES 2010-2011

- Gene Expression Network Reconstruction by Convex Feature Selection when Incorporating Genetic Perturbations *(Research Article)*
  Logsdon BA, Mezey J
  www.ploscompbiol.org/doi/pcbi.1001014
- Differentially Expressed RNA from Public Microarray Data Identifies Serum Protein Biomarkers for Cross-Organ Transplant Rejection and Other Conditions *(Research Article)*
  Chen R, Sigdel TK, Li L, Kambham N, Dudley JT, et al.
  www.ploscompbiol.org/doi/pcbi.1000940
- Infectious Disease Modeling of Social Contagion in Networks *(Research Article)*
  Hill AL, Rand DG, Nowak MA, Christakis NA
  www.ploscompbiol.org/doi/pcbi.1000968
- Ten Simple Rules for Editing Wikipedia *(Editorial)*
  Logan DW, Sandal M, Gardner PP, Manske M, Bateman A
  www.ploscompbiol.org/doi/pcbi.1000941
- The Roots of Bioinformatics *(Perspective)* Searls DB
  www.ploscompbiol.org/doi/pcbi.1000809



Network modeling to explore the dynamics of Th1 and Th2 cell regulation. *Image Credit:* Filippo Castiglione doi:10.1371/journal.pcbi.1001032



Forest of synthetic pyramidal dendrites grown using Cajal's laws of neuronal branching. *Image Credit:* Hermann Cuntz doi:10.1371/journal.pcbi.1000877

SPOTLIGHT ON PSB AND CSHALS CONFERENCES

PSB 2012

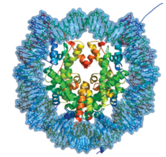
By Larry Hunter, PSB Co-Founder

The paper submission deadline for this year's Pacific Symposium on Biocomputing (PSB, http://psb.stanford.edu) is coming up July 11, 2011. PSB is perhaps best known because it takes place in Hawaii every January, but that's not the only reason it's popular. Mixing the immediacy of a computer science conference with the PubMed-indexed publications that biologists prefer, PSB papers have among the highest impact of any in bioinformatics, with an H-index from 2006-2009 of 47, which is in the same range as key journals like *PLoS Computational Biology* and *Briefings in Bioinformatics*. The relatively small size (typically about 250 registrants), and intimate resort location mean that PSB is an opportunity to get face time with many of the most well-known scientists in our field.

One of the reasons PSB is still going strong in its 17th year is the competitive organizational scheme. Each year, the participants submit proposals for specific topics that form the basis for the half dozen or so sessions that define each conference. You should think about submitting one yourself next February! This competition to be selected as a critical new area has kept PSB the perfect place to find out about the latest emerging and hot topics in computational biology. This year, the sessions are:

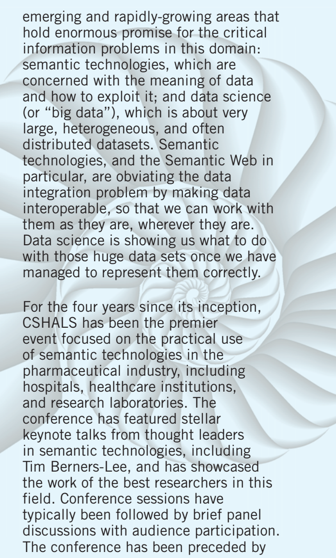
- Identification of Aberrant Pathway and Network Activity from High-Throughput Data
- Intrinsically Disordered Proteins: Analysis, Prediction and Simulation
- Microbiome studies: Analytical Tools and Techniques
- Modeling host-pathogen interactions: Computational biology and bioinformatics for infectious disease research
- Personalized Medicine: from genotypes and molecular phenotypes towards computed therapy
- Text and knowledge mining for pharmacogenomics: Genotype-phenotype-drug relationships

Since presentation slots are mostly based on peer-reviewed papers, PSB provides an outstanding opportunity for a young researcher to get podium time at a major conference. The design of the conference includes plenty of scheduled time for open discussions, so everyone gets to participate. An open poster session means everyone can present research as well.



Although one might expect that a conference in a first class resort in Hawaii would be expensive, PSB has long-standing relationships with the local hotels that make the conference surprisingly affordable. Registration includes many conference-provided meals, keeping one of the major costs down. The hotel cost is $204 per night this year, plus tax, which is less than an average hotel room in Washington DC in 2010. The conference offers discount codes for airfares and rental cars as well. The conference also provides travel scholarships for those most in need.

Submitting a paper to PSB before heading off to ISMB is a longstanding tradition in some bioinformatics labs. Even if you have never been to a PSB before, this is a great year to give it a try.



CSHALS: Semantic Technologies Meet Big Data

By Ted Slater, Merck & Co.,
and Joanne Luciano,
Rensselaer Polytechnic Institute

Researchers in healthcare and life sciences are reminded every day that theirs is fundamentally an information science. Success depends on the ability to use what is known about patients, their diseases, and their treatments to discover new knowledge in order to improve patient outcomes and advance human health. Despite this realization, the laments have been the same for years: too much data, and no way to interpret them. The traditional tools of bioinformatics, relying mostly on statistics and data integration ("putting everything in one place"), have proven to be insufficient to the task of telling us what it all means. Our best hope for true innovation in working with these data is to make them discoverable, interoperable, and meaningful, and provide the means by which to analyze and interpret them.

CSHALS (pronounced "sea shalls"), the Conference on Semantics in Healthcare and Life Sciences, focuses on two emerging and rapidly-growing areas that hold enormous promise for the critical information problems in this domain: semantic technologies, which are concerned with the meaning of data and how to exploit it; and data science (or "big data"), which is about very large, heterogeneous, and often distributed datasets. Semantic technologies, and the Semantic Web in particular, are obviating the data integration problem by making data interoperable, so that we can work with them as they are, wherever they are. Data science is showing us what to do with those huge data sets once we have managed to represent them correctly.

For the four years since its inception, CSHALS has been the premier event focused on the practical use of semantic technologies in the pharmaceutical industry, including hospitals, healthcare institutions, and research laboratories. The conference has featured stellar keynote talks from thought leaders in semantic technologies, including Tim Berners-Lee, and has showcased the work of the best researchers in this field. Conference sessions have typically been followed by brief panel discussions with audience participation. The conference has been preceded by tutorials to help attendees become familiar with semantic technologies, and in 2011 Rensselaer Polytechnic Institute (RPI) offered a popular hands-on introduction to the Semantic Web and Linked Data. In addition, commercial vendors with relevant offerings can provide brief "tech talks" to keep attendees informed.

Also in 2011, the scope of CSHALS began to include data science in addition to semantic technologies with a keynote presentation by Toby Segaran, author and software engineer at Google. In 2012, CSHALS will continue to expand with even more content from this exciting field. The CSHALS Organizing Committee believes that semantic technologies and data science provide the most compelling path forward for handling the vast amount of complex, heterogeneous data in healthcare and life sciences, and are committed to bringing the most inspiring thought leaders and the best practitioners in these areas together for the benefit of all CSHALS attendees.

Semantic technologies and big data are the future of information handling in healthcare and life sciences. Consider CSHALS 2012 in your February plans next year!

ANNOUNCING InCoB/ISCB-ASIA 2012 JOINT CONFERENCE AND ISCB-LATIN AMERICA 2012

Asia Pacific Bioinformatics Network's 10th InCoB 1st ISCB Asia Joint Conference 2011

NOVEMBER 30 - DECEMBER 2, 2011

APBioNet InCoB ISCBAsia

An official conference of the
International Society for Computational Biology

Key Dates

1 September
Poster submission deadline

Travel fellowship application deadline

15 October
Late-breaking abstract submission deadline

Early registration discount period ends

30 November – 2 December
Conference

ISCB-Latin America 2012 Main Conference Santiago - Chile Mar 19 - 21 2012

www.iscb.org/iscb-latinamerica2012/

INTERNATIONAL KEYNOTE SPEAKERS

Peer Bork
EMBL Director, Germany

Alessandro Sette
Center Head and Professor,
La Jolla Institute for Immunology and Allergy, USA

Manfred Sippl
Full Professor, University of Salzburg, Austria

Aleksey Zimin
Full Professor,
University of Maryland, USA

KEY DATES

Oral & Poster submission deadline
Oct 14, 2011

Travel Fellowship application deadline
Jan 13, 2012

Early registration discount deadline
Feb 10, 2012

Conference Tutorials
Mar 17 - 18, 2012

Conference
Mar 19 - 21, 2012

An official conference of the
International Society for Computational Biology

EMBNET COLLABORATION ON EDUCATION AND TRAINING

In April ISCB announced collaboration with the European Molecular Biology Network (EMBnet; www.embnet.org) to provide education and training in the use of bioinformatics tools to members of our communities. Having just sponsored and organized a successful workshop introducing the EMBnet eBioKit at the ISCB Africa ASBCB Conference on Bioinformatics 2011 (www.iscb.org/iscbafrica2011/), both EMBnet Executive Board member Erik Bongcam-Rudloff and ISCB President Burkhard Rost enthusiastically embraced the idea of a formal collaboration that provides a platform for EMBnet training courses at ISCB meetings whenever possible, particularly meetings in developing regions.

EMBnet has close working relationships with high-level members of our Society through their 28 national and eight specialists nodes. These strong ties complement ISCB's regional meetings expansion. "EMBnet is a very strong member of ISCB's Affiliated Regional Network, and formalizing our collaboration to incorporate their training into ISCB conferences makes perfect sense," commented Prof. Dr. Rost. "Our members will undoubtedly benefit from their expertise."

The next meeting that an EMBnet training workshop may be offered is the InCoB/ISCB-Asia 2011 joint conference in Kuala Lumpur, Malaysia, Nov 30-Dec 2. Following that, discussion is underway on incorporating an EMBnet training session into the next ISCB-Latin America conference, being held in Santiago, Chile, March 19-21, 2012.

Prof. Dr. Bongcam-Rudloff summed up the collaboration nicely: "This is a natural fit. Working together we will accomplish more, and everybody wins."

UPCOMING CONFERENCES AND EVENTS

ISMB/ECCB 2011 VIENNA AFFILIATED EVENTS

ISMB Satellite Meeting: 3D SIG – Structural Bioinformatics and Computational Biophysics
Jul 15, 2011 - Jul 16, 2011
http://bcb.med.usherbrooke.ca/3dsig11/Home.html

ISMB Satellite Meeting: CAMDA – Critical Assessment of Massive Data Analysis
Hosted By: Boku University Vienna
Jul 15, 2011 - Jul 16, 2011
www.camda.info/

ISMB SIG Meeting: AFP/CAFA – The Automated Function Prediction SIG featuring CAFA: Critical Assessment of Function Annotation
Jul 15, 2011 - Jul 16, 2011
www.biofunctionprediction.org/

ISMB SIG Meeting: Network Biology SIG – On the Analysis and Visualization of Networks in Biology
Jul 15, 2011 - Jul 15, 2011
http://nrnb.org/netbiowiki

ISMB SIG Meeting: SNP-SIG – Identification and Annotation of SNPs in the Context of Structure, Function, and Disease
Jul 15, 2011 - Jul 15, 2011
http://snps.uib.es/snp-sig/

ISMB SIG Meeting: AS-SIG – 8th Alternative Splicing - Special Interest Group
Jul 15, 2011 - Jul 16, 2011
www.alternative-splicing.org/as-sig-11

ISMB SIG Meeting: Bio-Ontologies
Jul 15, 2011 - Jul 16, 2011
www.bio-ontologies.org.uk

ISMB SIG Meeting: BOSC – 12th Annual Bioinformatics Open Source Conference
Jul 15, 2011 - Jul 16, 2011
www.open-bio.org/wiki/BOSC_2011

ISMB SIG Meeting: HiTSEQ 2011 – High Throughput Sequencing: Algorithms & Methodologies
Jul 15, 2011 - Jul 16, 2011
http://hitseq.org

ISMB SIG Meeting: BioRegSIG – 2nd Bioinformatics for Regulatory Genomics Special Interest Group
Jul 16, 2011 - Jul 16, 2011
http://light.ece.ohio.edu/bioreg/2011/

ISMB Satellite Meeting: RECOMB – BE – 3rd RECOMB Satellite Conference on Bioinformatics Education
Jul 20, 2011 - Jul 21, 2011
http://casb.ucsd.edu/bioed11/

ISMB Satellite Meeting: MLSB 2011 - 5th International Workshop on Machine Learning in Systems Biology
Jul 20, 2011 - Jul 21, 2011
http://mlsb11.informatik.tu-muenchen.de/

OFFICIAL ISCB CONFERENCES

InCoB/ISCB-Asia Joint Conference 2011
Malaysia - Kuala Lumpur
Nov 30, 2011 - Dec 02, 2011
ISCB Member Discount: up to 20%
www.incob2011.org/

Rocky 2011: Rocky Mountain Bioinformatics Conference
United States - CO - Snowmass Village/Aspen
Dec 08, 2011 - Dec 10, 2011
ISCB Member Discount: 200 USD
www.iscb.org/rocky2011

ISCB-Latin America 2012
Chile - Santiago
Mar 19 - 21, 2012
ISCB Member Discount: TBA
www.iscb.org/iscb-latinamerica2012/

CSHALS 2012: Conference on Semantics in Healthcare and Life Sciences
United States - MA – Cambridge
Feb 22 - 24, 2012
ISCB Member Discount: 200 USD
www.iscb.org/cshals2012/

GLBIO 2012
United States - MI - Ann Arbor
May 15, 2012 - May 17, 2012
ISCB Member Discount: TBA
www.iscb.org/glbio2012/

ISMB 2012 - Celebrating 20 Years
United States - CA - Long Beach
July 15 - July 17, 2012
ISCB Member Discount: 200 USD
www.iscb.org/ismb2012/

ISCB CO-SPONSORED & AFFILIATED EVENTS

Bio-IT Europe
Germany - Hanover
Hosted by: CHI and Biotechnica
Oct 11, 2011 - Oct 13, 2011
ISCB Member Discount: 10%
www.bio-itworldexpoeurope.com

Biological Data Visualization
United States - RI - Providence
Hosted By: IEEE Visweek
Oct 23, 2011 - Oct 24, 2011
ISCB Member Discount: approx. 20%
www.biovis.net

PSB 2012 - Pacific Symposium on Biocomputing
United States - HI - Kohala Coast
Jan 03, 2012 - Jan 07, 2012
ISCB Member Discount: 50 USD
http://psb.stanford.edu/

RECOMB 2012 – 16th Annual International Conference on Research in Computational Molecular Biology
Spain - Barcelona
Apr 21, 2012 - Apr 24, 2012
http://recomb2012.crg.cat/

Bio-It World Conference Expo
United States - MA - Boston
Hosted by: Cambridge Healthtech Institute
Apr 24, 2012 - Apr 26, 2012
ISCB Member Discount: 10%
www.bio-itworldexpo.com

ECCB12 - European Conference on Computational Biology 2012
Switzerland - Basel
Hosted By: SIB Swiss Institute of Bioinformatics & Biozentrum University of Basel
Sep 09, 2012 - Sep 12, 2012
http://eccb12.org/

OTHER CONFERENCES & EVENTS OF INTEREST

Proteomics Bioinformatics
United Kingdom - Cambridge - Hinxton
Hosted By: EBI/Wellcome Trust Advanced Courses
Jul 15, 2011 - Jul 19, 2011
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/AdvancedCourses/Workshops/WTX054153.htm

Beyond Next Generation Sequencing
Hungary - Budapest
Hosted By: Renyi Institute, Budapest, Hungary
Jul 20, 2011 - Jul 23, 2011
www.renyi.hu/conferences/bngs2011/

International Conference on Biomedical Ontology
United States - NY - Buffalo
Hosted By: University at Buffalo, National Center for Ontological Research (NCOR), National Center for Biomedical Ontology (NCBO), International Medical Informatics Association (IMIA) WG6
Jul 26, 2011 - Jul 30, 2011
http://icbo.buffalo.edu/

IEEE International Conference on Health Informatics, Imaging and Systems Biology
United States - CA - San Jose
Hosted By: IEEE Technical Committee on Bioinformatics, IEEE Computer Society
Jul 27, 2011 - Jul 29, 2011
www.ieee-hisb.org

ACM BCB 11: The 2011 ACM Conference on Bioinformatics, Computational Biology and Biomedicine
United States - IL - Chicago
Hosted By: ACM SIG Bioinformatics
Aug 01, 2011 - Aug 03, 2011
http://acmbcb.org/

Joint User-Training Workshop “Developing Multi-Scale, Multi-Cell Developmental and Biomedical Simulations with CompuCell3D and SBW”
United States - IN - Bloomington
Hosted By: Biocomplexity Institute at Indiana University
Aug 08, 2011 - Aug 19, 2011
www.compucell3d.org

UPCOMING CONFERENCES AND EVENTS

OTHER CONFERENCES & EVENTS OF INTEREST *(continued)*

5th Asian Young Researchers Conference on Computational and Omics Biology
Korea, Rep - Daejeon
Hosted By: ISCB Regional Student Group of Korea (RSG Korea)
Aug 10, 2011 - Aug 12, 2011
http://2011.ayrcob.org/

BIOKDD 2011: 10th International Workshop on Data Mining in Bioinformatics Bookmark and Share
United States - CA - San Diego
Hosted By: SIGKDD
Aug 21, 2011 - Aug 21, 2011
http://bio.informatics.iupui.edu/biokdd11/

Knowledge Discovery in Health Care and Medicine
Greece - Athens
Hosted By: ECML/PKDD 2011
Sep 05, 2011 - Sep 09, 2011
www.cs.gmu.edu/~hrangwal/kd-hcm/

WABI 2011
Germany - Saarbrücken
Hosted By: Max-Planck-Institute für Informatics, Saarbrücken
Sep 05, 2011 - Sep 07, 2011
http://pbil.univ-lyon1.fr/members/sagot/htdocs/wabi2011/wabi2011.html

Workshop on Parallel Computational Biology
Poland - Torun
Hosted By: 9th International Conference On Parallel Processing and Applied Mathematics
Sep 11, 2011 - Sep 14, 2011
http://pbc.ppam.pl/

Mathematical and Computational Approaches in High-Throughput Genomics
United States - CA - Los Angeles
Hosted By: Institute for Pure and Applied Mathematics (IPAM)
Sep 12, 2011 - Dec 16, 2011
http://ipam.ucla.edu/programs/gen2011/

Computational Systems Biology and Dose Response Modeling Workshop
United States - NC - Research Triangle Park
Hosted By: The Hamner Institutes for Health Sciences
Sep 12, 2011 - Sep 16, 2011
www.thehamner.org/about-the-hamner/education-training/dose-response-modeling

International Symposium on e-Health 2011
United Kingdom - Wales - Cardiff
Hosted By: Centre of Excellence in Mobile Applications and Services and Computational Biology Group, University of Glamorgan
Sep 15, 2011 - Sep 15, 2011
www.glacombio.net/iseh2011/

RoSyBA: Rostock Symposium on Systems Biology and Bioinformatics in Ageing
Germany - Rostock
Hosted By: IBIMA, Systems Biology Bioinformatics Rostock
Sep 15, 2011 - Sep 17, 2011
http://goethe.informatik.uni-rostock.de/ibima/rosyba2011/

CMSB 2011: 9th International Conference on Computational Methods in Systems Biology
France - Paris
Hosted By: INRIA
Sep 21, 2011 - Sep 23, 2011
http://contraintes.inria.fr/CMSB11

HiBi 2011: High Performance Computational Systems Biology
France - Paris
Hosted By: 9th International Conference on Computational Methods in Systems Biology
Sep 21, 2011 - Sep 23, 2011
www.hibi.it

Mathematical Oncology: New Challenges for Systems Biomedicine
Italy - Sicily - Erice
Hosted By: Ettore Majorana Foundation and Centre for Scientific Culture
Sep 26, 2011 - Sep 30, 2011
www.dm.unipi.it/~erice2011/

ISPB-2011: International Symposium on Plant Biotechnology towards Tolerance to Stresses and Enhancing Crop Yield
India - Jharkhand - Mesra, Ranchi
Hosted By: Department of Biotechnology, Birla Institute of Technology, Ranchi, Jharkhand, India
Sep 28, 2011 - Oct 01, 2011
http://ispb.bitmesra.ac.in/Default.aspx

RECOMB Comparative Genomics Galway 2011
Ireland - Galway
Hosted By: 9th Annual RECOMB Satellite Workshop on Comparative Genomics
Oct 08, 2011 - Oct 10, 2011
http://recombcg.org

Chemical, Synthetic and Systems Biology: New Directions of Biochemistry in the 21st Century
United States - Utah - Snowbird
Hosted By: American Society for Biochemistry and Molecular Biology
Oct 12, 2011 - Oct 16, 2011
www.asbmb.org/ASBMBMeetings/SpecialSymposia/symposia.aspx?mid=17

PRIB2011: Pattern Recognition in Bioinformatics
Netherlands - ZH - Delft
Hosted By: Pattern Recognition & Bioinformatics Group, Delft University of Technology, The Netherlands
Nov 02, 2011 - Nov 04, 2011
http://prib2011.org

Functional Genomics and Systems Biology
United Kingdom - Hinxton, Cambridge
Hosted By: Wellcome Trust
Nov 29, 2011 - Dec 01, 2011
http://registration.hinxton.wellcome.ac.uk/display_info.asp?id=231

The Seventh International Conference on Computer Engineering and Systems
Egypt - CAI - Cairo
Hosted By: IEEE and Ain Shams University, Egypt
Nov 29, 2011 - Dec 01, 2011
www.iceec.org

GIW-2011: The 22nd International Conference on Genome Informatics
Korea, Rep - Busan
Hosted By: AASBi and KSBSB
Dec 05, 2011 - Dec 07, 2011
http://giw2011.kobic.re.kr

SWAT4LS 2011: Semantic Web Applications and Tools for Life Sciences
United Kingdom - London
Hosted By: Rothamsted Research, MRC, LUMC, IST, Corporate Semantic Web, MRC
Dec 07, 2011 - Dec 09, 2011
www.swat4ls.org/2011

ICDM 2011: 2nd Workshop on Biological Data Mining and its Applications in Healthcare
Canada - Vancouver
Hosted By: 10th IEEE International Conference on Data Mining
Dec 10, 2011 - Dec 10, 2011
www1.i2r.a-star.edu.sg/~xlli/BioDM.html

Protein Interactions and Networks
United Kingdom - Cambridge - Hinxton
Hosted By: Wellcome Trust Advanced Courses
Dec 11, 2011 - Dec 17, 2011
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Workshops/WTVM049891.htm

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.

Cover Image:
Inspired by color blocks, irregular forms and thriving green plants: the eccletic **KunstHaus Wien** is a museum in Vienna, designed by the Austrian artist Friedensreich Hundertwasser (1928 - 2000). Hundertwasser transformed the Thornet furniture factory building into an international collection of modern art.

For more information, please visit www.kunsthauswien.com.

How are We Doing?
Please email ISCB at *admin@iscb.org* with any comments, questions, or concerns regarding this newsletter, the website (*www.iscb.org*), 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, for providing office space, fiscal management, and human resources management to the Society.