iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

NEWSLETTER

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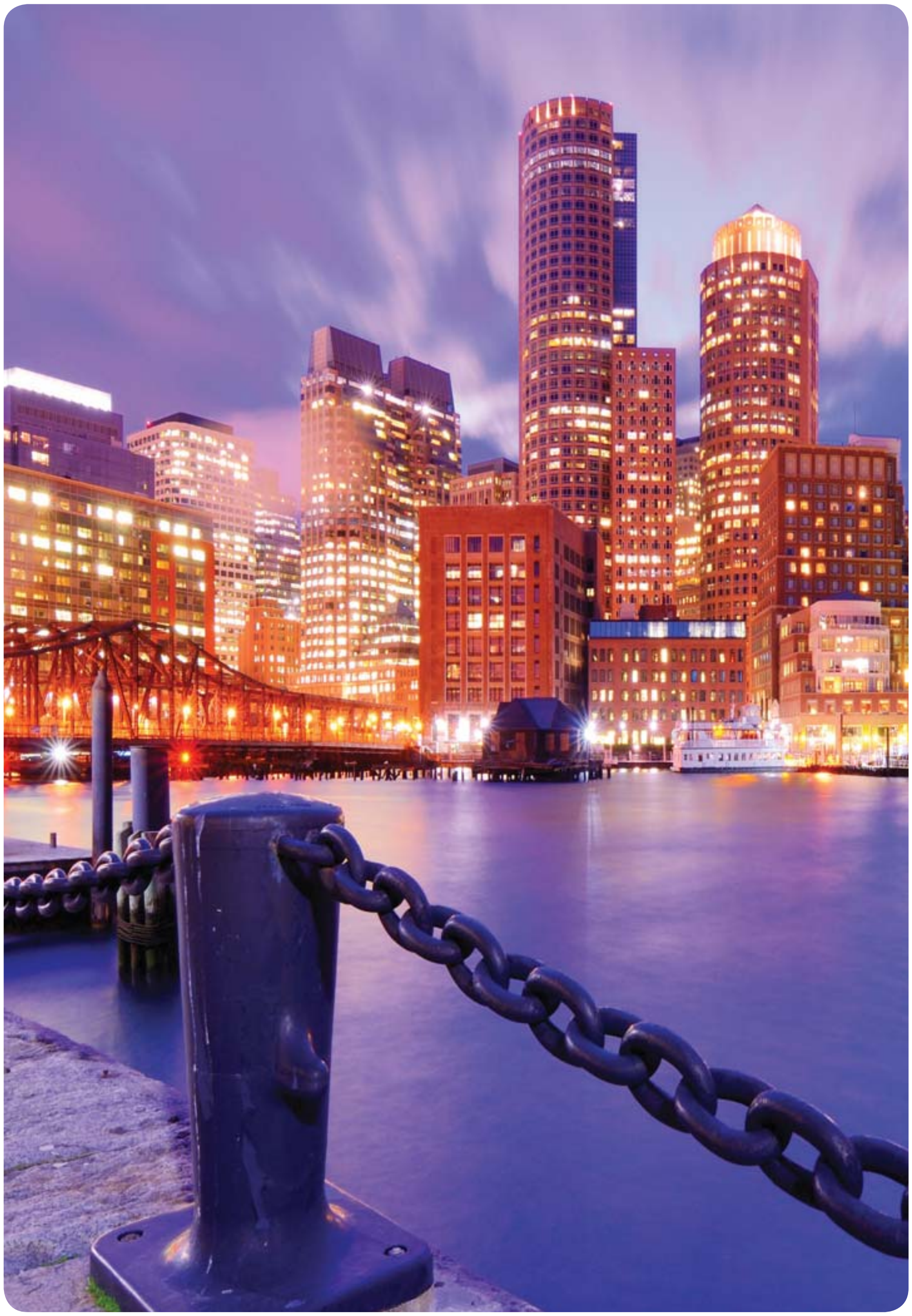
Features

Content



A Global Community Dedicated to Advancing Scientific Discovery Through Computation

www.iscb.org

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OFFICER AND STUDENT COUNCIL ELECTIONS - THE CHOICE IS YOURS

ISCB Board of Directors (left to right): Michal Linial (Vice President, ISCB), Olga Troyanskaya (Board Member); and Jill P. Mesirov (Board Member)

We are once again in the midst of our annual elections. This year the members will elect candidates for the ISCB Officer positions of Secretary and Vice-President, 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 2014 in Boston, by visiting the "voting booth" adjacent to the ISCB booth in the exhibition area. The online voting site opened on July 1, and can be accessed at www.iscb.org/elections until the close of ISMB 2014 on July 15.

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!

CALLING ALL MEMBERS!

When was the last time you updated your ISCB profile? ISCB encourages all of its members to keep an updated profile. We are rolling out a new Member Directory to enhance our connecting and networking offerings. This directory will allow members to look up other members by conference attendance, area of research interest, Communities of Special Interest (COSIs), and ISCB committees. Personal information will be protected so you are not spammed. The functionality of the directory depends on active engagement of the members completing their member profiles.

Log on My ISCB today and update your profile!

Email admin@iscb.org for assistance or visit us at the ISCB booth in the exhibit hall if you are attending ISMB 2014.

THANK YOU from ISCB

To all the members who participated in the survey – THANK YOU. Your feedback is enabling us to make key changes to better benefit you. We are humbled by your dedication to the Society.

Sincerely,
ISCB

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Congratulations to our Prize Winners:

Majid Masso
Anthony Mathelier
Marcelo Soria

GOBLET – GLOBAL ORGANIZATION FOR BIOINFORMATICS LEARNING, EDUCATION AND TRAINING

By Fran Lewitter

GOBLET, the Global Organization for Bioinformatics Learning, Education and Training, was conceived in 2012 to bring together a range of organizations involved in bioinformatics education and training activities. GOBLET was subsequently established as a Dutch Foundation, and held its first formal meet¬ing in Amsterdam in November 2012, hosted by The Netherlands Bioinformatics Centre (NBIC). ISCB is a founding member of GOBLET and an active participant of the consortium – e.g., together, we established the first education poster track at ISMB 2013; in 2014, we created the first Computational Biology Education (CoBE) Community of Special Interest; and we've also helped survey the gaps and perceived bioinformatics training needs amongst life scientists.

In addition to individual members, GOBLET members currently include about 25 institutions/organizations. An up-to-date list of member institutions and additional information is available at www.mygoblet.org. More details about GOBLET's formation and achievements in its first year can be found in *EMBnet.journal* 20 (dx.doi.org/10.14806/ej.20.0.751) and *EMBnet.journal*, 19 (http://dx.doi.org/10.14806/ej.19.1.606)

GOBLET's mission is to:

1. Provide a global, sustainable support and networking structure for bioinformatics educators/trainers and trainees (including a portal for sharing materials, tools, tips and techniques; guidelines and best practice documents; and facilities to help train the trainers)

2. Facilitate capacity development in bioinformatics in all countries

3. Develop standards and guidelines for bioinformatics education and training

4. Act as a hub for fund gathering
   Reach out to, amongst others, teachers at high schools, to bridge the gap to the next generation of bioinformaticians, and

5. Foster the international community of bioinformatics, biocomputing, biocuration and computational biology trainers

GOBLET's first elections were held in 2013 to appoint its officers and committee chairs. The executive committee (and their organizational affiliations) includes Terri Attwood, chair (EMBnet); Vicky Schneider, vice chair (TGAC);

continued on page 4

2014 ISCB ACCOMPLISHMENT BY A SENIOR SCIENTIST AWARD: GENE MYERS

*By Christiana N. Fogg[1], Diane E. Kovats[2]**

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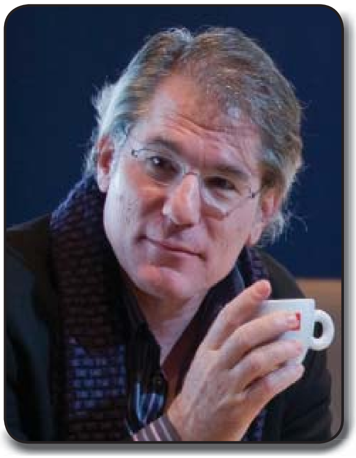
The International Society for Computational Biology (ISCB; www.iscb.org) annually recognizes a senior scientist for his or her outstanding achievements. The ISCB Accomplishment by a Senior Scientist Award honors a leader in the field of computational biology for his or her significant contributions to the community through research, service, and education. Dr. Eugene "Gene" Myers of the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden has been selected as the 2014 ISCB Accomplishment by a Senior Scientist Award winner.

Myers was selected by the ISCB's awards committee, which is chaired by Dr. Bonnie Berger of the Massachusetts Institute of Technology (MIT). Myers will receive his award and deliver a keynote address at ISCB's 22nd Annual Intelligent Systems for Molecular Biology (ISMB) meeting. This meeting is being held in Boston, Massachusetts, on July 11–15, 2014, at the John B. Hynes Memorial Convention Center (www.iscb.org/ismb2014).

Gene Myers: Coding and Decoding

Myers was captivated by computer programming as a young student. He remembered his fascination being stoked by a realization and recalls, "A computer is a programmable device, and once programmed, is a specific device for doing something that I conceived of. I found this magical." He completed a BS in mathematics at the California Institute of Technology, but his interest in biology came during his PhD studies at the University of Colorado in the late 1970s. Myers recounted that he initially considered molecular biology as "a source of interesting computational questions." He was studying computer science under the guidance of his dissertation advisor, Andrzej Ehrenfeucht, who had eclectic interests that included molecular biology. Myers, along with fellow graduate students and future bioinformaticians Gary Stormo and David Haussler, was drawn by Ehrenfeucht's curiosity about such basic questions as how to compare DNA sequences and how to build evolutionary trees.

Myers landed his first faculty position in the Department of Computer Science at the University of Arizona. Throughout his research career, he has been interested in sequence assembly. He recollected. "While I developed many seminal algorithms for sequence comparison and search in the '80s and early '90s, including BLAST (Basic Local Alignment Search Tool), the problem that has and continues to fascinate me to this day is sequence assembly."
He is well-known for being one of the authors of the 1990 manuscript that first described BLAST, a groundbreaking algorithm that is still used today for sequence comparison. This paper is also one of the most cited papers in scientific literature.


2014 ISCB Accomplishment by a Senior Scientist Award: Gene Myers

Myers's interest in sequence assembly led him to promote the idea that whole genome shotgun sequencing could be used on the large and unwieldy human genome. Craig Venter brought Myers to Celera Genomics in 1998 during their push to sequence the human genome. Myers recalled writing thousands of lines of code to build algorithms that could assemble the vast amounts of sequence data. He considers the success of this landmark sequencing project as a highlight of his career.

In 2002, Myers returned to academia in a position at the University of California, Berkeley's Center for Integrative Genomics. More recently, Myers headed a lab at the Howard Hughes Medical Institute (HHMI)'s Janelia Farm Research Campus. In 2012, he moved to Dresden, Germany to serve as a director at the Max Planck Institute of Molecular Cell Biology and Genetics and the K laus-Tschira chair of the Systems Biology Center. Myers describes that his "latest focus all started because [he] wish[es], like many, to 'decode' the genome." His work has evolved into building microscopic devices and image analysis tools that can be used to observe and model the inner workings of cells and biological systems. He sees this type of work as having the potential to revolutionize medicine. He said, "Really understanding (in molecular terms) what a cell can do and how what it does affects its role in a complex tissue or organ will greatly advance medicine and treatment as well as help us understand variation across species and how organisms develop."

Myers recounted the importance of key mentors in the success of his career. Myers met Webb Miller when he was a young faculty member at the University of Arizona in the early 1980s. The two struck up a fruitful collaboration that led to many early papers about sequence analysis. Myers explained, "Miller helped me greatly in the early part of my career in that he taught me, through example, that writing can be fun." Myers gained a different sort of insight while working for Venter at Celera. He described Venter as "a master of the sound bite, and while this may sound trivial, it is actually more important than one might think.

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Myers continued

Much of one's career success depends on the ability to present one's ideas in powerful, succinct, clear ways."

Myers believes that mentorship should be "about shaping the character of the individual and their understanding of their role within the research community." He starts with himself as he aims to "do [his] best to be a good role model, to instill values of integrity, objectivity, and openness." Myers has trained students from varied academic backgrounds throughout his career, and affirmed that, "there is no substitute for passion."

Myers's unique contributions to computational biology have been recognized by several awards, including election to the National Academy of Engineering (2003), the Association for Computing Machinery (ACM) Kannellakis Prize (2002), and the International Max Planck Research Prize (2004). Bonnie Berger (MIT), chair of the ISCB Nominating Committee, sees Myers as an exemplar of the Achievement by a Senior Scientist Award. Berger stated that, "Myers is one of the founders of the field, bringing his algorithmic expertise to the most fundamental problems in computational biology. From his role in creating the indispensable and widely used BLAST program for basic sequence search, to breaking the barrier of sequencing the human genome, to deciphering what is coded in DNA, he has launched our discipline. Myers has been a prominent member of the ISCB community, serving on the Board of Directors, as an ISCB fellow, and as chair and area chair for numerous ISMB meetings." Alfonso Valencia, leader of the Structural Computational Biology group at the Spanish National Cancer Research Center and president-elect of ISCB, also sees Myers as a stellar representative of the field. Valencia said of this year's award winner, "I am particularly happy about the election of Gene Myers, since he represents the strong roots of computational biology in algorithmic and method development. The intensity with which he lives science, the originality of his approaches, and the attention he dedicates to the technical details are characteristics of his work and a great example for our new generations of bioinformaticians and computational biologists."

Myers remains fervent and passionate about the work he does. He contends that his upbringing, which included traveling the globe with his family, as well as his innate passion for science and mathematics have helped make him "flexible, broad-minded, and curious." He also prefers to keep his research group small while keeping his research vision large. He advises future and active scientists, "Simultaneously be able to 'go deep' and yet continuously remain in an environment that keeps you in touch with the 'big picture.' And you always have to take on new challenges and new problems." In the end, he cannot speak strongly enough about the importance of passion and states, "My overarching advice is to do what you are passionate about. Ours is not a career for security or wealth. You have to love it, absolutely love it."

GOBLET continued

Teresa Attwood, GOBLET chair

Michelle Brazas, secretary (Bioinformatics.ca); and Fran Lewitter, treasurer (ISCB). The operational board also includes committee chairs for Learning, Education and Training; Outreach and PR; Standardization; Fundraising and chairs also hold meetings with their committees on a regular basis too. In addition, an Annual General Meeting (AGM) is held in the fall each year, which is open to all organizational and individual members.

The 2013 meeting was held in Norwich UK at The Genome Analysis Center (TGAC). The 2014 AGM is scheduled to be held in Toronto in November, hosted by Bioinformatics.ca, with additional funding from the Canadian Institutes for Health Research (CIHR).

Getting Involved

GOBLET is an energetic and young organization. Currently, around two-thirds of our member institutions are European. However, we are a global organization and are actively working to reach out to institutions around the world to join us. We welcome your ideas and involvement. Send email to info@mygoblet.org if you are interested in participating in GOBLET's activities. Please stop by to talk with us and see our poster at ISMB 2014 for more information.

GOBLET

Global Organisation for Bioinformatics Learning, Education & Training

Committee Structure & Activities

Responding to a recognised need to coordinate a spectrum of world-wide training activities, we aim to share, not duplicate effort; to share, not duplicate cost; to work together towards common solutions & a sustainable future.

Learning, Education & Training Committee

- ☐ Developing & sharing best practice in teaching & learning methods, & providing curriculum guidance
- ☐ Providing recognition, support structures & resources for trainers, including materials, methods & train-the-trainer programmes

Outreach & PR Committee

- ☐ Promoting GOBLET's mission, training resources, activities & events
- ☐ Maintaining social networking interactions & galvanising the community to participate in GOBLET initiatives

Standardisation Committee

- ☐ Providing accreditation mechanisms for learners & trainers, to better signpost the wide range of available training programmes
- ☐ Increasing the overall quality of training programmes

Fund-raising Committee

- ☐ Stimulating collaborative projects within GOBLET & the training community
- ☐ Raising funds to sustain GOBLET

Technical Committee

- ☐ Providing a support infrastructure for trainers & trainees
- ☐ Maintaining an open Training Portal for the community

Main Achievements

- ☐ Launched the GOBLET Training Portal
- ☐ Established a poster track for education at ISMB
- ☐ Presented ISMB education track posters
- ☐ Published two collaborative papers
- ☐ Won a Canadian grant to fund our next meeting in Toronto
- ☐ Formed an education COSI (CoBE) with ISCB

Committee Leadership

Learning Education & Training
Nicky Mulder, Chair
Celia van Gelder, Vice Chair

Outreach & PR
Erik Bongcam-Rudloff, Chair

Standardisation
Pascale Gaudet, Chair

Fund-raising
Patricia Palagi, Chair

Technical
Manuel Corpas, Chair

Training Portal
www.mygoblet.org/training-portal

GOBLET interim meeting, hosted by ISCB, Berlin, July 2013

BIOINFORMATICS CURRICULUM GUIDELINES AND CORE COMPETENCIES

By Lonnie Welch

The Curriculum Task Force of ISCB's Education Committee released a report in March 2014, detailing a set of guidelines for bioinformatics educators.

Rapid advances in the life sciences and in related information technologies necessitate the ongoing refinement of bioinformatics educational programs in order to maintain their relevance. As the discipline of bioinformatics and computational biology expands and matures, it is important to characterize the elements that contribute to the success of professionals in this field. These individuals work in a wide variety of settings, including bioinformatics core facilities, and medical research laboratories, software development organizations, pharmaceutical and instrument development companies, and institutions that provide education, service, and training. In response to this need, the Curriculum Task Force of the ISCB Education Committee seeks to define curricular guidelines for those who train and educate bioinformaticians.

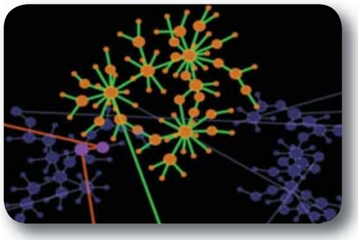
The bioinformatics literature provides valuable perspectives on bioinformatics education by defining skill sets needed by bioinformaticians, presenting approaches for providing informatics training to biologists, and discussing the roles of bioinformatics core facilities in training and education. The current report of the Curriculum Task Force expands the body of knowledge by presenting the results from a broad set of surveys (of core facility directors, of career opportunities, and of existing curricula). The article presents an initial set of core competencies that were derived from the surveys, and relates the competencies to three different categories of bioinformatics training.

The Curriculum Task Force is currently focusing on implementation and refinement of its curriculum guidelines. An open forum Birds of a Feather session will be held at ISMB 2014, on Tuesday July 15, 2014 at 12:45 p.m.

Read the full article:
Citation: Welch L, Lewitter F, Schwartz R, Brooksbank C, Radivojac P, et al. (2014) Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. *PLoS Comput Biol* 10(3): e1003496. doi:10.1371/journal.pcbi.1003496.

HOW TO BECOME COSI WITH A COMPUTATIONAL BIOLOGIST - JOIN US ON SUNDAY, JULY 13, AT ISMB TO LEARN MORE

By Christine Orengo



"That was a great meeting. Let's stay in touch." How often have you said this at the end of a meeting after connecting with new colleagues you wanted continue sharing ideas with? The internet has given us access to infinitely more data than we know how to manage and the potential for great insights if we know how to transform this data into knowledge. How can we better connect scientists within specialized research areas and facilitate meetings and discussions that only require the cost of a cup of coffee and a good internet connection?

In the best spirit of being a scientific society, the International Society for Computational Biology (ISCB) is exploring strategies to make this happen. In the 21st century, ISCB envisions connecting computational biologists in a virtual meeting place and is considering how to promote virtual networks and make the Society a year-round hub of electronic activity by setting up web communities that can share information, hold meetings, and discuss ideas "long distance" via the internet. These Communities of Special Interest (COSIs) will be built around major research themes within computational biology, or important activities such as networks of training, mentoring, or financial support. The COSIs will be founded initially with communities originating from Special Interest Groups (SIGs) or workshops who have been organizing events at ISMB.

A special session will take place at ISMB (recording will available online after the meeting) to launch the COSIs. Representatives from each COSI will describe their community and their current and future activities. This launch will also give the COSIs a chance to advertise social events or birds of a feather-type activities for people who didn't attend their corresponding SIG or workshop and will provide a venue for COSI members and meeting attendees to interact in person. ISCB will also make sure that all the talks that relate to COSI themes or activities are tagged as such in the conference program to make it easier for attendees to find talks that best fit their research interests or COSIs.

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COSI continued

This is just the beginning. One can imagine that special COSI social events during the main ISMB meeting will provide opportunities for people working on similar scientific problems or facing similar issues with training or bioinformatics support to meet and get to know each other better. It always helps to put a face to that name on the electronic forum you've been following or that person you've been exchanging emails with! We hope that you will support the COSIs, and let us know if there other emerging communities who might want to become a COSI in the future.

COSIs BEING LAUNCHED AT ISMB, BOSTON, JULY 2014	
3D-SIG	Structure-based drug discovery. Structure representation, classification and prediction Structure-based function prediction. Docking - protein-protein, protein-ligand and protein-nucleic-acid. Protein dynamics; Structural Evolution; Macromolecular assemblies; Structural genomics
Automated Function Prediction (AFP)	The mission of the Automated Function Prediction COSI is to bring togethercomputational biologists, experimental biologists and biocurators who are dealing with the important problem of gene and gene product function prediction, to share ideas and create collaborations.
sBioinfo-Core	Bioinfo-core is a worldwide body of people that manage or staff bioinformatics cores within organizations of all types. We provide a forum for bioinformatics core managers and staff to discuss issues pertaining to the operation of their core, evaluation of data analysis software tools, and management of relationships with the users of cores.
Bio-Ontologies	The latest and most innovative research in the application of ontologies and more generally the organisation, presentation and dissemination of knowledge in biomedicine and the life sciences.
CAMDA	CAMDA presents a crowd sourcing and open-ended data analysis challenge format which focuses on big heterogeneous data sets that are increasingly produced in several fields of the life sciences.
Computational Biology Education (COBE)	The ISCB Computational Biology Education (CoBE) COSI focuses on bioinformatics and computational biology education and training across the life sciences. A major goal of this COSI is to foster a mutually supportive, collaborative community in which bioscientists can share bioinformatics education and training resources and experiences, and facilitate the development of education programs, courses, curricula, etc., and teaching tools and methods.
Computational Mass Spectrometry (COMP-MS)	The ISCB CoSI CompMS is a joint initiative with the HUPO Computational Mass Spectrometry Initiative (HUPO CompMS). It promotes the efficient, high quality analysis of mass spectrometry data through dissemination and training in existing approaches and coordination of new, innovative approaches. The CompMS initiative aims to exploit synergies between different application domains, in particular proteomics and metabolomics.
Network Biology	As more research fields turn to network visualization and analysis for perspective, our Network Biology Community serves to introduce novel methods and tools, identify best practices and highlight the latest research in the growing and interconnected field of network biology.
Open Bioinformatics Forum (OBF)	The Open Bioinformatics Foundation or OBF is a non-profit, volunteer-run group dedicated to promoting the practice and philosophy of Open Source software development and Open Science within the biological research community.

2014 ISCB OVERTON PRIZE: DANA PE'ER

By Christiana N. Fogg1, Diane E. Kovats2*

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ISCB honors the achievements of an early- or mid-career scientist with the Overton Prize each year. The Overton Prize was established in memory of Dr. G. Christian Overton, a respected computational biologist and founding ISCB Board member who died unexpectedly in 2000. Winners of the Overton Prize are independent scientists in the early or middle phases of their careers that are recognized for their significant contributions to computational biology through research, teaching, and service.

ISCB is thrilled to recognize Dr. Dana Pe'er, Associate Professor in the Department of Biological Sciences and Systems Biology at Columbia University in New York, NY, as the 2014 winner of the Overton Prize. In recognition of this award, Dr. Pe'er will be a keynote speaker at this year's Intelligent Systems for Molecular Biology conference in Boston, Massachusetts and will present a talk titled "A Multidimensional Single Cell Approach to Understand Cellular Behavior" on Monday, July 14, 2014.

Dana Pe'er: From Mathematics to Mass Cytometry

Dana Pe'er encountered her first love in second grade. Her father was eager to instill a passion for learning in her, and one day he showed her the proof demonstrating why the same number of natural numbers and rational numbers exist whereas the number of irrational numbers is greater than the number of rational numbers. Pe'er recalled, "Grappling with different strengths of infinity and the elegance mathematical logic made me fall in love with math."

Pe'er received her bachelor's degree in mathematics, and her master's and Ph.D. degrees in computer science, all from the Hebrew University of Jerusalem. She did her Ph.D. research in the lab of Dr. Nir Friedman, where she had the realization that "statistical machine learning is a very powerful "math" to help elucidate biology, and the complexity of it all required computer science." She recalls gaining several insights during this period that have accompanied her throughout her career, including her affirmation that, "Good modeling of the biology is the most important ingredient toward a good computational method for biological discovery. Rather than applying the most sophisticated "nuclear powered" method to squeeze the most out of the data statistically, one can use biological insight to limit the space of possible models more than any statistical method ever can."

2014 ISCB Overton Prize:
Dana Pe'er

Making the right assumptions requires a good understanding of biology, knowledge Pe'er gained through her collaboration with Dr. Aviv Regev. They met as graduate students in Israel, where Regev greatly influenced how Pe'er thought of biological questions. Pe'er recalled, "She was my first real biology teacher and she taught me to think about biology more abstractly, rather than stick to more rigid and dogmatic thinking."

Pe'er did her postdoctoral work with Dr. George Church at Harvard University, where she began navigating the messy world of experimental biology. Church's mentorship gave Pe'er a new perspective of science, and she moved away from asking, "What type of computation can I do for this data?" and learned to ask instead, "What data do I need to answer a biological question I am passionate about?"

Pe'er describes the mentorship she received from Dr. Daphne Koller as being instrumental to her success as a trainee. Koller provided guidance and mentoring to Pe'er during her Ph.D. and postdoctoral training and instilled in her the importance of "good modeling assumptions." Although Pe'er was not an official student of Koller's, she recalls appreciatively the valuable career advice and insights Koller shared with her as she launched into her career as an independent researcher

In 2006, Pe'er started her own lab at Columbia University in the Department of Biological Sciences and Systems Biology. Her lab embodies the interdisciplinary nature of her research and is filled with trainees from a wide range of backgrounds. She genuinely appreciates working with her trainees and has enjoyed "Watching them grow,and seeing how much they matured as scientists. I really love mentorship and feel a form of motherhood towards my trainees."

Pe'er has developed several research projects that use large, complex data sets to examine how molecular networks respond to various external stimuli. One of her primary interests is using single cell technologies such as mass cytometry to better understand cellular heterogeneity. She is fascinated by this work and hopes "to reframe development not as a set of discrete cell types, but rather as a continuum, a dynamic process in which one can place each individual cell along a developmental trajectory that represents not only cell types, but their many

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Pe'er continued

cellular heterogeneity to cancer and the improvement of personalized cancer therapy.

Pe’er’s training in computer science and biology have given her a unique combination of skills and knowledge that have served her well as a computational biologist, but she sees her training experience becoming mandatory for future biology researchers. As she sees it, “Biology has become an information science. Enabled by an increasing number of technologies, the magnitude and complexity of the data is only increasing. In the future, computation will be an integral part of biology, like molecular biology is today.” Pe’er champions the power of doing science at the interface of biology and computation. “My “bilingual” training really lets me play at the interface,” she acknowledges. “It lets me communicate with both sides effectively and make connections. By understanding what powerful computation can do, I can design experiments and strive for technologies that might not be intuitive and obvious to a bench biologist that is less versed in computation. Designing the right data-rich experiment, matched with the right biology is truly empowering.”

Pe’er serves on the editorial board of the journal *Cell*, and she considers this role as a valuable opportunity to serve the scientific community. *Cell* has acknowledged computational biology as a critical rising field, and Pe’er sees her work on the advisory board as an important way to serve the computational biology community and help educate the journal about the field.

Outside of the lab, Pe’er has taken time to support and promote K12 science education by organizing a science expo. She was inspired to do this when she realized that her young daughter didn’t really know what she did. Pe’er recalled that her daughter “thought my job was ‘writing emails all day’. She did not realize that scientists are trying to figure out what we don’t know, rather than rehash what we do.” The expo was designed to transform a school into “a multi-story, hands-on, interactive science museum. Each volunteer scientist brings their lab and science to the kids, distilled in a way that is both engaging and clear to the kids.” She acknowledged that the expo presents a big but gratifying challenge to the volunteer scientists because they had to take “complex science and distill it in a way that can relate to a 5 year old. But, if you can explain your science to a 5 year old, you can explain it to anyone.”

Dr. Alfonso Valencia, chair of the ISCB Awards Committee, sees Pe’er’s selection as fitting recognition of her scientific contributions. He said, “I was very happy to see that Dana Pe'er was finally selected for the award. This is always a very difficult decision given the number of excellent young computational biologists in our community. Dana has published amazing papers with substantial impact in biology and cancer biology, together with other papers on method development that were very influential, some of them presented in ISMB.” Dr. Bonnie Berger, co-chair of the Awards Committee, also sees Pe’er as a rising luminary in the field of computational biology “for pioneering the use of Bayesian networks in cellular network inference.”

Pe’er is looking forward to where her research will take her, especially her ongoing work on single cell data. She is also enjoying and appreciating this moment of recognition. Pe’er was excited and uplifted when she was told she had been selected for the 2014 Overton Prize, and she recounted, “I got such an outpouring of congratulations from my colleagues, which was really the best.

DREAM CHALLENGES

The DREAM (Dialogue for Reverse Engineering Assessment and Methods) project was founded in 2006 to assess model predictions and pathway inference algorithms in systems biology. Today DREAM aims to foster collaboration amongst researchers, to evaluate computational biology methodologies, and to multiply the impact of data by making it available to a vast community. DREAM achieves its goals through the organization of Scientific Challenges and conferences.

The DREAM Challenges are open problems presented to the systems biology community of potential solvers. Participants submit their predictions, which are evaluated and scored, and eventually discussed in the annual DREAM conference. Eventually data, predictions, gold standards and source code are openly available. In the past 7 years, DREAM has run 28 successful Challenges, enabled the publication of over 60 DREAM Challenge-related papers, and aggregated a “crowd” of thousands of “DREAMERs.”

In 2013, Sage Bionetworks (www.sagebase.org) and DREAM partnered to co-lead a new generation of Challenges that leverage collaborative data hosting and analysis tools available on Synapse (www.synapse.org) such as real-time leaderboards and shared project spaces.

Announcing the DREAM9 Challenges

On June 2, 2014, we launched the DREAM9 "Challenge season" which consists of three new Challenges described below. These challenges will be discussed at the RECOMB/ISCB Systems and Regulatory Genomics/ DREAM Conference to be held in San Diego, CA November 10-14, 2014.

1. Alzheimer’s Disease Big Data DREAM Challenge #1
The goal of this Challenge is to identify accurate predictive Alzheimer’s disease biomarkers that can be used by the scientific, industry and regulatory

continued on page 19

PLOS COMPUTATIONAL BIOINFORMATICS OVERVIEW
JUNE 2014

By Clare Weaver, Publications Manager,
PLOS Computational Biology

In 2013–2014 *PLOS Computational Biology* saw a 2% increase in submissions since the previous year, with an average of 142 research articles submitted per month. As well as publishing high-quality research, *PLOS Computational Biology* enables members of the community to contribute to scientific communication through the creation of resources for current and future generations of computational biologists.

Between June 2013 and May 2014, *PLOS Computational Biology* has been delighted to host a series of *Message from ISCB* articles by the ISCB Student Council, entitled **'Stories from the Road'**(1), in which Student Council members present common themes emerging from ISCB Regional Student Council initiatives. The series will be drawn together into a formal PLOS collection in early July, and the final article will publish at the end of August.

The PLOS Computational Biology 'About My Lab' collection image.
Image Credit: PLOS.
www.ploscollections.org/aboutmylab

A new collection, **'About My Lab'**, was launched in November with the aim of sharing knowledge about lab organization and scientific management. Each Perspective article represents an interview with a Principal Investigator, who shares his or her experience of running a lab by discussing selected topics in an informal and personal style. The collection launched with two 'About My Lab' Perspectives, an Editorial by collection editor Theodore Alexandrov and Founding Editor-in-Chief Phil Bourne(2), and an article featuring interviews with young PIs conducted at ISMB 2013(3). Another 'About My Lab' Perspective was published in March, and new articles will be added to the collection over time.

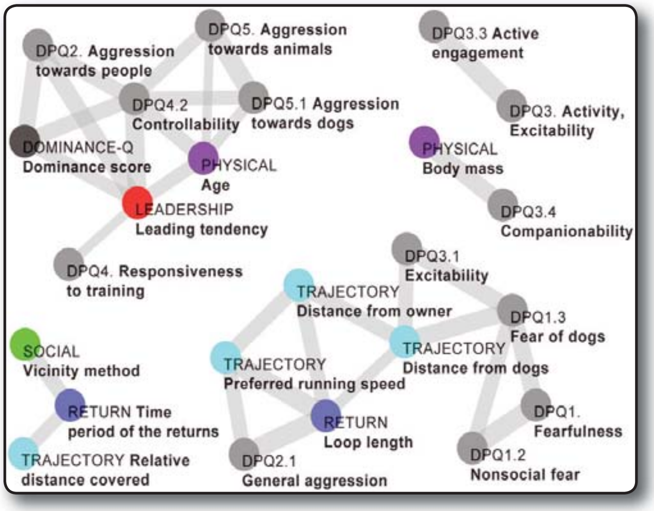
Our ever-popular **'Ten Simple Rules'** series of **Editorials** on professional development, led by Founding Editor-in-Chief Phil Bourne since 2005, reached the milestone of one million page views at the end of July. Dr Bourne describes this series as "one of the unexpected surprises and pleasures arising from the community journal *PLOS Computational Biology*" and, in a post on *PLOS Biologue*, looks back over the history of Ten Simple Rules: http://bit.ly/1kxHhav. The journal regularly publishes new Ten Simple Rules articles, but only in cases where there is something truly new to say.

In October the **first-ever *PLOS Computational Biology* Editor Summit** was held at George Washington University, Washington DC, with 26 editors in attendance.

The summit aimed to strengthen relations between editors from a diverse range of fields within computational biology and to identify journal strategy and priorities for the coming year. The main part of the meeting consisted of discussions on journal policy, processes and direction, and editors presenting their own research.

PLOS Computational Biology would like to thank the many members of the community who made contributions to the journal during the period 2013–2014. Over the past twelve months we have been pleased to welcome 15 new Associate Editors to the editorial board. Jason Papin, Olaf Sporns and Sebastian Bonhoeffer have been promoted to Deputy Editors-in-Chief. Joern Diedrichsen, Christophe Fraser, Jason Haugh, Erik van Nimwegen, Rachel Brem and Mark Alber have become Deputy Editors. We welcomed Francis Ouellette and Joanne Fox as Education Editors, as Fran Lewitter stepped down after seven years running the PLOS Computational Biology Education section.

PLOS Computational Biology is a 'Community Journal'; we value your ideas and comments, so please don't hesitate to come and visit us at Booth 409 at ISMB or via ploscompbiol@plos.org at any time.



Collective motion of dogs is influenced by underlying social network structures and by characteristics such as personality differences.
Image credit: Zsuzsa Ákos & Máté Nagy. doi:10.1371/journal.pcbi.1003446

Examples of Highly Downloaded Articles in 2013

- Bacteria-Human Somatic Cell Lateral Gene Transfer Is Enriched in Cancer Samples David R. Riley, Karsten B. Sieber, Kelly M. Robinson, James Robert White, Ashwinkumar Ganesan, Syrus Nourbakhsh, Julie C. Dunning Hotopp Research Article | published 20 Jun 2013 | *PLOS Computational Biology* 10.1371/journal.pcbi.1003107 Views: 30,775

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PLOS continued

- Mate Choice and the Origin of Menopause Richard A. Morton, Jonathan R. Stone, Rama S. Singh Research Article | published 13 Jun 2013 | *PLOS Computational Biology* 10.1371/journal.pcbi.1003092 Views: 25,939
- Do Ants Need to Estimate the Geometrical Properties of Trail Bifurcations to Find an Efficient Route? A Swarm Robotics Test Bed Simon Garnier, Maud Combe, Christian Jost, Guy Theraulaz Research Article | published 28 Mar 2013 | *PLOS Computational Biology* 10.1371/journal.pcbi.1002903 Views: 21,784

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2. Learning How to Run a Lab: Interviews with Principal Investigators . Theodore Alexandrov, Philip E Bourne. 11, s.l. : *PLoS Comput Biol*, 2013, Vol. 9. 10.1371/journal.pcbi.1003349.
3. The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013 . Jeroen de Ridder, Yana Bromberg, Magali Michaut, Venkata P Satagopam, Manuel Corpas, Geoff Macintyre, Theodore Alexandrov. 11, s.l. : *PLoS Comput Biol*, 2013, Vol. 9. 10.1371/journal.pcbi.1003350.

HELP FUTURE SCIENTISTS AND PROMOTE COMPUTATIONAL BIOLOGY & BIOINFORMATICS: THE 2014 ISCB STUDENT TRAVEL FELLOWSHP CAMPAIGN

By Stacy Slagor, ISCB Director of Corporate Relations and Development

Join ISCB in giving students access to the principal role models within the fields and help us influence the paths of scientific careers. By supporting travel for our future researchers—students and postdoctoral fellows—you support the future of computational biology and bioinformatics.

Each year ISCB receives over 300 travel fellowship requests. With currently available funds, we can only support approximately 70% of these requests by providing partial funding to each recipient. Government funding opportunities continue to decline, so ISCB reaches out to YOU to help this important initiative. Donating to the travel fellowship fund will help us to support even more students with higher travel awards.

David Kuo, a computational biology doctoral student at Memorial Sloan-Kettering Cancer Center, shares his experience as a travel fellowship awardee, “I was privileged to be awarded a Travel Fellowship for ISMB/EECB 2013 this past summer to attend the conference in Berlin. I was especially grateful for the potential that the fellowship committee sees in its young scientists and was humbled to be awarded the travel fellowship.”

“This would be my first major scientific conference and I was astounded by the sheer number of scientists presenting interesting work. It was a great opportunity for me to present my poster at an international conference attended by world-class scientists and build new networks from this experience. The quality of the keynotes was both inspirational and educational, particularly in seeing the career trajectory that I could potentially follow in the field. It is a conference that I will not soon forget and I look back upon it fondly. Without the support of the travel fellowship, I may not have been able to attend so I sincerely appreciate the efforts from the ISCB to provide support for young trainees.”

Student travel fellowships provide important opportunities for young scientists. Your contribution to ISCB at any level will help us not only to achieve our goals of assisting students but also exceed them. We continue to do all we can but there is still more to do—YOU can make a difference in the future of our science by supporting tomorrow’s researcher and ISCB.

To donate online: www.iscb.org/donation/donation.php

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MEET THE FELLOWS CLASS OF 2014

The ISCB Fellows Program recognizes members of the scientific community for their service and their noteworthy contributions to the fields of computational biology and bioinformatics.

Fellows are distinguished through a rigorous process that includes a call for nominations by the ISCB membership, selection by the Fellows Selection committee that is comprised of the previously named Fellows.

The 2014 ISCB Fellows are exemplary members of ISCB and the scientific community and embody the Society's mission to advance scientific understanding of living systems through computation. The research, teaching, and service records of each Fellow shows how their contributions are invaluable to the computational biology community.

AMOS BAIROCH

Amos Bairoch is a Professor and Director of Bioinformatics in the Human Protein Sciences department of the Faculty of Medicine at the University of Geneva, Switzerland, and he is also a Group Leader at the Swiss Institute of Bioinformatics in Geneva, Switzerland. Bairoch completed his doctorate at the University of Geneva, and his work has been dedicated to the field of protein sequence analysis. Bairoch was a key developer of several seminal protein analysis and prediction tools and databases including SWISS-prot, PROSITE, ENZYME, and Expasy, and is one of Switzerland's most notable bioinformatics researchers.

EWAN BIRNEY

Ewan Birney is an Associate Director at the European Molecular Biology Laboratory-European Bioinformatics Institute (EMBL-EBI). Birney completed his doctorate at the Wellcome Trust Sanger Institute, Cambridgeshire, United Kingdom, and his research interests include genomic variation, regulatory genomics, and next-generation sequencing data analysis. Birney has been a key player in several major genome projects and was involved in annotating the human, mouse, and chicken genomes, and was a leader of the Ensembl genome annotation project. Birney's outstanding contributions to genomics research have been recognized through several awards, including the 2005 ISCB Overton Prize.

NIR FRIEDMAN

Nir Friedman is a Professor in the School of Computer Science and Engineering and the Alexander Silberman Institute of Life Sciences at the Hebrew University of Jerusalem, Israel. Friedman earned his doctorate from Stanford University in Stanford, California, United States in the field of artificial intelligence, and he is well known for developing methods that apply Bayesian statistics to computational biology. Friedman's diverse research interests include molecular networks, epigenetics, cell regulation, and disease. Friedman's dual expertise in computation and biology has greatly influenced the scope of his research and strengthened his contributions to the computatational biology community.

ROBERT GENTLEMAN

Robert Gentleman is Senior Director of the Bioinformatics and Computational Biology Department at Genentech in San Francisco, California, United States. Gentleman completed his doctorate in statistics from the University of Washington, Seattle, Washington, United States and is well known for being an originator of the R programming language and Bioconductor, which are now some of the most widely used software programs in bioinformatics. Gentleman's research is focused on analyzing high throughput sequencing data to better understand biological mechanisms, including work on detecting low frequency mutations in tumors and gaining insight into RNA editing in various tissues.

ANDREJ SALI

Andrej Sali is a Professor of Computational Biology in the Department of Bioengineering and Therapeutic Sciences, Department of Pharmaceutical Chemistry, School of Pharmacy, University of California, San Francisco, and California Institute for Quantitative Biosciences. Sali completed his doctorate in molecular biophysics at the University of London, United Kingdom. His research is focused on developing and applying computational methods based on the laws of physics and rules of evolution to predict protein structures, determine the structures of macromolecules, and annotate protein functions based on their structures. Sali has \published over 300 papers, many of which are highly cited, and he has served the computational biology community as a member of several editorial boards, including *PLOS Computational Biology* and *Molecular and Cellular Proteomics.*

LATIN AMERICA BIOINFORMATICS MEETING - ISCB-LA

OCTOBER 28-30, 2014
BELO HORIZONTE, BRAZIL

By Guilherme Oliveira, Conference Chair

The ISCB-LA organizing committee is pleased to announce the ISCB-Latin America (ISCB-LA) Bioinformatics Meeting. The meeting will be hosted by the Brazilian Association for Bioinformatics and Computational Biology (AB3C) in collaboration with the Brazilian Bioinformatics Symposium (BSB) of the Brazilian Computer Science Society and the Ibero-American Society for Computational Biology (SolBio). The ISCB-LA meeting will be held October 28-30, 2014, at the Federal University of Minas Gerais in Belo Horizonte, Brazil.

The ISCB-LA is an official conference of ISCB that is held every two years. It is international, interdisciplinary forum for discussion of research findings, methods and for networking with researchers of the Latin America region and others worldwide.

The meeting program will include keynote speakers, original paper, flash talks, and poster presentations. On Monday, 27th Oct., an IT workshop will be held to discuss issues related to setting up local infrastructures. Four courses and one workshop for the industry will happen on the 31st Oct. Submissions to offer courses are open until July 17th. The conference will also mark the inaugural sympoisum of the ISCB Latin American Regional Student Group on Monday, 27th Oct.

Renowned keynote speakers addressing that attendees include, Bissan Al-Lazikani (The Institute of Cancer Research, London), Janet Kelso (Max Planck Institute for Evolutionary Anthropology), Kimmen Sjolander (Berkeley Phylogenomics Group) and Mauro Castro (Federal University of Rio Grande do Sul, Brazil).

The conference is now accepting Poster submissions on the following categories: Bioinformatics of Disease and Treatment, Computational aspects, Comparative Genomics, Education, Epigenetics, Functional Genomics, Genome Organization and Annotation, Genetic Variation Analysis, Metagenomics, Pathogen informatics, Population Genetics, Variation and Evolution, Protein Structure and Function Prediction and Analysis, Proteomics, Sequence Analysis and Systems Biology and Networks.

Submissions for original paper publication are open also open. Original research work will be published in *BMC Genomics* and there is also a track for a Lecture Notes Series. Selected submissions for the Lecture Notes may also follow a track for publication in *BMC Bioinformatics*.

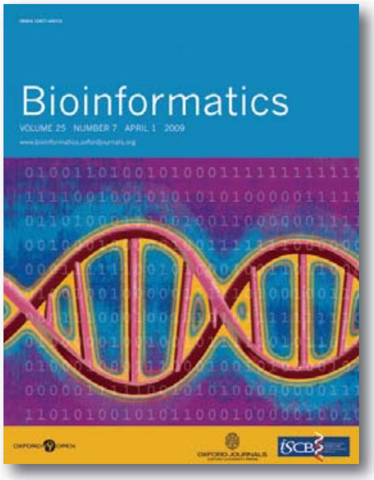
There will be ample space for oral presentations selected from these submissions.

ISCB-LA will happen together with the largest bioinformatics community in Latin America. The X-meeting / BSB are regular yearly events in Brazil. These events are now run together and have created strong links among its members in over 10 years of existence. We expect to have over 400 participants. You're your calendar and submit your poster or paper and join us in Brazil!

ATTENTION STUDENTS! A Student Council workshop will be held at the meeting venue on Oct. 27th. The workshop will involve ISCB Regional Student Groups from Brazil and Argentina. This will be a great opportunity to join these local RSGs, create strong links with fellow students and stimulate the formation of other RSGs in Latin America.

If you are interested in supporting the ISCB-LA meeting please look at sponsor tab in our web page or contact the conference chair, Guilherme Oliveira – oliveira@cpqrr.fiocruz.br.

BIOINFORMATICS



2013 was a significant year for *Bioinformatics*, as it marked 15 years of the journal in its current form. The contribution of the editorial team is of course vital to the success of the journal, and as such we have created a new category of Honorary Editors, comprising past editors Alex Bateman, Martin Bishop, Christos Ouzounis, Chris Sander and Gary Stormo. Their contributions to the journal have been exceptional. Martin has also finished his term as our longest-running Associate Editor, having handled well in excess of 5000 manuscripts during his time as an editor. In addition, we thank Mario Albrecht, whose term came to an end, and welcome Robert Murphy as Associate Editor focusing on biological imaging and information extraction.

Our submission rate continued to increase in 2013, to 2200 papers, of which around 30% were accepted. Of our published papers, 160 were published open access, with authors choosing between CC-BY-NC and CC-BY licences. *Bioinformatics* has an impact factor of 5.323, maintaining its position as one of the top journals in computational biology. At the time of writing the 2013 impact factors had yet to be published.

Our publication speed remains very fast – accepted articles are online within 5 days and are published in an issue within 7 weeks. Review time is also fast, with first decision within a month.

Bioinformatics is an official journal of ISCB, and we have collected together the ISCB articles published in the journal over the past year (www.oxfordjournals.org/our_journals/bioinformatics/iscb_articles.html).

A collection of papers have been published from a recent workshop organised by Bioinformatics Associate Editor David Posada. This 'virtual issue' will be populated with relevant articles as they are published (www.oxfordjournals.org/our_journals/bioinformatics/phylogenetics_virtual_issue.html).

As ever, we welcome comments or feedback on any aspect of the journal - please do not hesitate to get in touch with us (bioinformatics.editorialoffice@oup.com) or visit us at the OUP booth at ISMB 2014 in Boston.

With best wishes,
The *Bioinformatics* Editorial Team

MAKE PLANS TO JOIN US!

ISMB/ECCB 2015
July 11 - 14
Dublin, Ireland

ISMB 2016
July 16 - 19
Orlando, Florida, USA

ISMB/ECCB 2017
July 21 - 25, 2017
Prague, Czech Republic

ISMB 2018
July 7 - 10
Chicago, Illinois, USA

WOMEN IN SCIENCE - KEYNOTE TALKS SHINE SPOTLIGHT ON CUTTING EDGE RESEARCH

Each year, ISCB meetings feature keynote speakers who give talks on innovative research in computational biology and bioinformatics. These scientists are respected leaders in their fields and come from every corner of the globe. In 2014, ten women were among the keynote speakers who were selected based on their cutting edge work. Many of these women are deeply involved in service to ISCB and consider their membership in the Society as an important professional affiliation.

BISSAN AL-LAZIKANI, PhD

Bissan Al-Lazikani, PhD, leads the Computational Biology & Chemogenomics team in the Division of Cancer Therapeutics at the Institute of Cancer Research, London, United Kingdom.

Al-Lazikani received her Doctorate in computational structural biology from Cambridge University. During her postdoctoral training, she used structure analysis and modeling to understand SH2 domains. Al-Lazikani subsequently worked at a biotechnology company specializing in drug discovery, where she helped build a chemogenomics database. Presently, Al-Lazikani directs a group that develops and uses computational tools for cancer drug discovery.

Al-Lazikani has been a member of ISCB since 2013 and will be a keynote speaker at the October 2014 meeting of ISCB-Latin America in Rio de Janeiro, Brazil.

JANET KELSO, PhD

Janet Kelso, PhD, is the leader of the Minerva research group for bioinformatics in the Department of Evolutionary Genetics at the Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany. She received her Doctorate in bioinformatics from the University of the Western Cape in South Africa. Kelso's primary research focus is comparative primate genomics, and her team is currently participating in the Neanderthal, Bonobo, and Orangutan genome projects.

Kelso has been an ISCB member since 2004 and devoted her time and insight to the Society in many ways. She has been an ISCB Board member since 2005 and has served as ISMB Co-Chair '14, Secretary '06-'11,Vice President ' 11-'13, Conferences Chair '06-'12; Conferences Co-Chair '12, ISCB-Africa Co-Chair '11. Kelso will be giving a keynote talk at the 2014 ISCB-Latin America meeting.

KIMMEN SJÖLANDER, PhD

Kimmen Sjölander, PhD is a professor of bioengineering at the University of California, Berkeley and is the head of the Berkeley Phylogenomics Group. Sjölander earned a Doctorate in computer science from the University of California, Santa Cruz. Prior to setting up her lab at Berkeley, Sjölander worked in the biotechnology sector at Molecular Applications Group and Celera Genomics. Her research group at Berkeley works on computational structural biology and develops computational methods for diverse areas of analysis, including phylogenetic tree reconstruction, multiple sequence alignment, and protein structure prediction.

Sjölander has been an ISCB member since 2002 and will be a keynote speaker at the 2014 ISCB-Latin America meeting.

TANYA BERGER-WOLF, PhD

Tanya Berger-Wolf, PhD, is an associate professor in the Department of Computer Science at the University of Illinois in Chicago, United States. Wolf earned a Doctorate in computer science from the University ofIllinois, Urbana-Champaign. She has spent her career developing computational methods to address diverse questions in population biology that include movement of social animals, dynamic network analysis, and sibling relationship reconstruction.

Berger-Wolf has been an ISCB member since 2004 and was a keynote speaker at the May 2014 Great Lakes Bioinformatics Conference in Cincinnati, Ohio.

KRISTIN ARDLIE, PhD

Kristin Ardlie, PhD, is the Director of the Biological Samples Platform at the Broad Institute of Harvard and MIT, Cambridge, Massachusetts, United States. Ardlie earned her Doctorate at Princeton University in the United States. Prior to joining the Broad, Ardlie was a research scientist at the Whitehead Institute and was Vice President of Genetics at Genomics Collaborative, Inc. Ardlie's research has been focused on population genetics, and she is presently a co-principal investigator for the Genotype-Tissue Expression (GTEx) project, which is one of the largest human transcript sequencing projects to date.

Ardlie was a keynote speaker at the Next Generation Sequencing Conference (NGS) Conference held in June 2014 in Barcelona, Spain.

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CORNELIA VAN DUIJN, PhD
Cornelia Van Duijn, PhD, is a professor of genetic epidemiology at the Erasmus University Medical Center, Netherlands. She received a Doctorate in genetic epidemiology from Erasmus University and has pursued this area of research throughout her career. Van Duijn is a principle investigator of several large-scale population and family-based studies, and her research in genetic epidemiology has ease, Parkinson's disease, frontal lobe dementia, diabetes, and hypertension. Van Duijn gave a keynote talk at the NGS Conference held in June 2014 in Barcelona, Spain.

MICHAL LINIAL, PhD
Michal Linial, PhD, is the Director of The Sudarsky Center for Computational Biology, Department of Biological Chemistry, Institute of Life Sciences at the Hebrew University of Jerusalem, Israel. Linial earned her Doctorate in biochemistry from the Hebrew University. Linial's computational biology research interests include protein classification, functional genomics, and structural genomics. Linial also studies molecular and cellular aspects of neurobiology, with specific interests in exocytosis, the synapse, and neuron development.

Linial has been an ISCB member since 2002 and has served the Society in several ways. She has been a Board member since 2004, Vice President '09-'15, and Student Council Liaison '06-'08. Linial will be a keynote speaker at the 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), ISCB's flagship meeting, which is being held in July 2014 in Boston, Massachusetts, United States.

DANA PE'ER, PhD
Dana Pe'er, PhD, is an associate professor in the Department of Biological Sciences and Systems Biology at Columbia University, New York, United States. Pe'er received her Doctorate in computer science from the Hebrew University of Jerusalem, Israel. Pe'er has developed novel computational approaches to study a wide range of biological questions. Her primary research focus presently is developing and using computational tools to investigate multidimensional single cell data so as to better understand cellular heterogeneity and characteristics of tumor cells. Pe'er has been an ISCB member since 2014 and has served as co-chair of Late Breaking Research Committee for ISMB 2014. Pe'er is the winner of the 2014 ISCB Overton Prize, which honors the achievements of early- or mid-career computational biologists. In recognition of this award, Pe'er will be giving a keynote speech at the 2014 ISMB meeting in Boston, Massachusetts.

DEBORAH MCGUINNESS, PhD
Deborah McGuinness, PhD, is the Tetherless World Senior Constellation Chair and a professor of computer and cognitive science at Rensselaer Polytechnic Institute (RPI) in Troy, New York, United States. She is also the founding director of RPI's Web Science Research Center. McGuinness earned her Doctorate in computer science from Rutgers University. Her primary research areas include artificial intelligence, the semantic web, and descriptions logic.McGuinness has been a member of ISCB since 2010 and was a keynote speaker at the ISCB-sponsored Conference on Semantics in Healthcare and Life Sciences (CSHALS) in February 2014.

TERRY GAASTERLAND, PhD
Terry Gaasterland, PhD is a Professor of Computational Biology and Genomics at the University of California, San Diego and serves as Director of the Scripps Genome Center in the Scripps Institution of Oceanography in La Jolla, CA. Gaasterland received her Doctorate in Computer Science from the University of Maryland. Gaasterland's Laboratory of Computational Genomics develops and applies computational methods to understand how transcription and translation influence and modify the cell state through integrated analysis of genomic and proteomic data. Gaasterland is a founding member of the ISCB Executive Committee. She was a Co-Chair of ISMB 2012, has served on several other ISCB committees, and has represented ISCB as a FASEB advisor. Gaasterland will be an ISCB keynote speaker at the International Conference on Bioinformatics (InCoB) in Sydney, Australia on July 31st to August 2nd, 2014 and the ISCB-Latin America X-meeting with BSB and SoiBIo, in Belo Horizonte, in October 2014.

These women scientists lead successful research programs in diverse areas of computational biology and bioinformatics, and they exemplify the innovative and diverse nature of these fields. ISCB service is a vital component of the work done by several of these women, and these voluntary commitments have been essential to the growth and success of ISCB as a professional society.

NOBEL PRIZE IN CHEMISTRY – COMPUTATIONAL BIOLOGY AT CENTER STAGE

The 2013 Nobel Prize in Chemistry was awarded to Martin Karplus, Michael Levitt, and Arieh Warshel for the "development of multiscale models for complex chemical systems." This award has marked a major turning point for computational biology through recognition that computation transforms the way scientists study the structure and function of biochemical molecules.

The seminal work attributed to the development of multiscale modeling began in the 1970's when Warshel joined Karplus's lab at Harvard as a postdoctoral fellow. Warshel had just completed his doctorate in chemical physics at the Weizmann Institute of Science in Rehovot, Israel, where he worked under the guidance of Shneior Lifson to develop methods to calculate consistent force fields of molecules[1, 3]. Lifson, who passed away in 2001, is considered a founding father of computational structural biology and also mentored Levitt as a young student. Karplus had expertise in applying quantum mechanics to chemical reactions. Together they developed a computer program that used a combination of classical and quantum mechanical calculations to consistently determine the ground and excited state potentials of complex molecules[3]. This was the first time that classical and quantum mechanics were used together to model complex molecules, and a similar method was also used to calculate changes in the conformation of retinal isomers upon photoactivation[4,5]. This novel approach was based on partitioning electrons in planar molecules such that π-electrons were modeled using quantum chemical calculations and σ-electrons and nuclei modeled using classical mechanics.

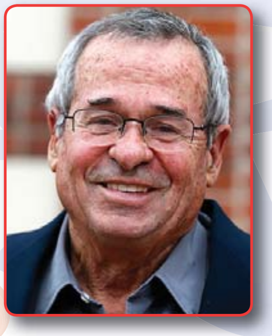
Warshel returned to Weizmann after his postdoctoral training and started working with Levitt, who had also come back to Weizmann after completing a research fellowship at Cambridge University. Their groundbreaking work involved developing a universal scheme to partition electrons in a molecule that are modeled using classical or quantum approaches. This hybrid quantum mechanics/molecular mechanics approach made it possible to model chemical reaction and complex molecules like proteins by combining the accuracy of quantum mechanics and the speed of classical molecular mechanics[6]. They used this hybrid approach to model how lysozyme cleaves a glycoside chain. Levitt and Warshel also developed computational methods to study the folding of bovine pancreatic trypsin inhibitor by grouping atoms that could be modeled classically in rigid "pseudoatoms," which greatly enhanced the speed by which folding could be modeled[7].

The work of Karplus, Levitt, and Warshel formed the foundation of molecular modeling and has been essential to moving forward research in both theoretical and experimental chemistry and biochemistry.

Levitt, a previous keynote speaker at the 3Dsig satellite meeting of ISMB, as well as Karplus and Warshel have been honored with lifetime membership in ISCB in recognition of this achievement.

Martin Karplus,
Université de Strasbourg,
Strasbourg, France, Harvard
University, Cambridge, MA,
USA

Michael Levitt,
Stanford University School of
Medicine, Stanford, CA, USA



Arieh Warshel,
University of Southern
California, Los Angeles, CA,
USA

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2014 FASEB UPDATES FOR ISCB

By Allison Lea and Jennifer Zeitzer

ISCB is a member of the Federation of American Societies for Experimental Biology (FASEB), a coalition of 27 scientific societies representing over 120,000 researchers from around the world. FASEB works to promote biological research and has become an organization that legislators, federal agencies, and the media turn to forinformation on policies related to biomedical science and engineering.

FASEB's Office of Public Affairs (OPA) staff and FASEB elected leaders meet regularly with National Institutes of Health (NIH) and National Science Foundation (NSF) officials to provide the prospective of the membership on a wide range of issues. On May 30, NIH Deputy Director, Kathy Hudson, PhD, spoke to FASEB's public affairs staff and society staff about upcoming and ongoing NIH initiatives, including Big Data to Knowledge (BD2K) and Brain Research through Advancing Innovative Neurotechnologies (BRAIN).

That same day, FASEB met with Phil Bourne, PhD, NIH's first Associate Director for Data Science. Dr. Bourne discussed the challenges NIH is facing with data sharing and the initiatives in the NIH pipeline to address them. For example, NIH plans to build The Commons – a public database that will be a part of a public-private partnership between government, academia, and industry to support data sharing and pre competitive collaboration to further scientific discovery. BD2K will support The Commons with data discovery index, software development, training centers, and grants.

On June 2, newly appointed NSF Director France Cordova, PhD, spoke at the FASEB Board meeting, where she shared NSF's priorities and initiatives, such as fundamental research for climate change, the BRAIN Initiative, promoting clean energy, collaborating with other federal agencies, and promoting minorities in science. She also recognized and praised FASEB for its support of the federal science agencies.

Federal Funding for Biomedical Research

This spring, FASEB released its factsheets demonstrating fiscal year (FY) 2013 NIH funding for all 50 states, DC, and Puerto Rico. In an effort to increase federal funding for biomedical research, Senator Tom Harkin (D-IA) sent a "Dear Colleague" letter to the members of the U.S. Senate highlighting the FASEB factsheets as an example of the critical support NIH provides to thousands of investigators around the country. Senator Harkin has been a long-time supporter of biomedical research and an advocate on Capitol Hill for increased funding for NIH.

The budget agreement Representative Paul Ryan (R-WI) and Senator Patty Murray (D-WA) reached in December has paved the way for Congress to get an early start on the FY 2015 spending bills. Having achieved consensus on the top-line spending limit ($1.014 trillion), the Appropriations Committees have made progress on the legislation that funds the federal agencies, including NIH and NSF.

The Senate Appropriations Committee passed the Commerce, Justice, and Science (CJS) bill by a unanimous 30-0 vote, providing $7.2 billion for NSF (the same as Obama's request and the FY 2014 level). Senator Richard Shelby (R-AL) noted that the Ryan-Murray deal left the appropriators with "extremely tough choices" to make.

NSF would fare slightly better under the CJS bill (HR 4660) approved by the House on a bipartisan vote of 321-87. The House raised NSF's budget to $7.41 billion, an increase of $237 million or 3.3 percent over the FY 2014 level.

On June 10, the Senate Labor, Health and Human Services (LHHS) Appropriations Subcommittee approved a bill that provides $30.45 billion for NIH, an increase of $605 million (1.8 percent) above the FY 2014 level. A press release summarizing the bill notes that the NIH funding level "is sufficient, when combined with the $1,000,000,000 increase appropriated in FY 2014, to fully replace the FY 2013 sequester cut to NIH." The Senate LHHS bill must still be approved by the full Appropriations Committee.
The House has not yet considered the NIH funding measure.

Regulatory Burden

In March, the National Science Board (NSB) released its report, Reducing Investigators' Administrative Workload for Federally Funded Research, which included the following overarching recommendations: (1) postpone certain administrative requirements until the grant proposal has been approved; (2) eliminate or modify ineffective regulations; (3) harmonize and streamline requirements; and (4) increase university efficiency and effectiveness. These proposals are similar to the recommendations FASEB made in May 2013 in response NSB's Request for Information on administrative burdens. FASEB's response was drawn from the feedback provided by FASEB's Science Policy Committee and a survey of over 1,300 scientists conducted by the Federation. FASEB will continue to work with the NSB and federal agencies as they seek ways to implement these recommendations.

FASEB
Federation of American Societies for Experimental Biology

MARC: Maximizing Access to Research Careers

continued on page 19

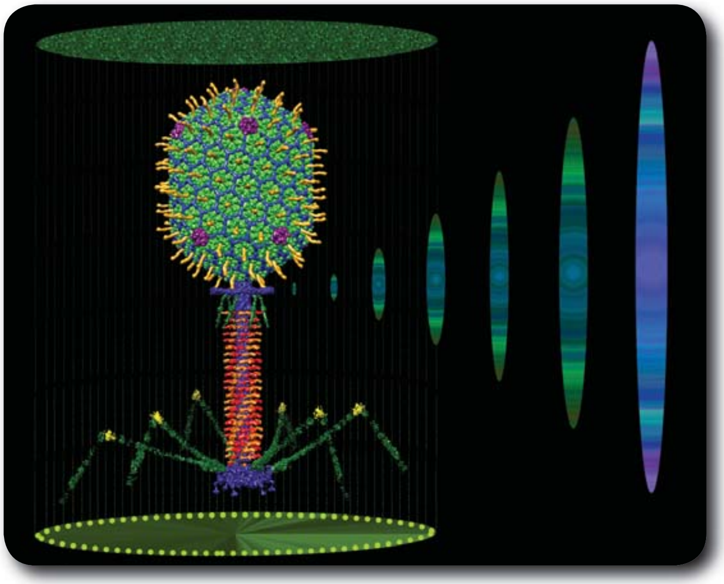
DREAM Challenges continued

communities to improve Alzheimer's diagnosis and treatment. Participants will work with genetics data, clinical data and imaging data to create predictive models of cognitive scores, predict discordance between cognitive ability and amyloid load and/or predict diagnostic groups.

2. The DREAM AML Outcome Prediction Challenge The goal of this Challenge is to develop the best predictive models of clinical outcome in AML. Participants are given the clinical correlates, genetics and cyto-genetics data and the expression level of 231 proteins probed by RPPA analysis of a cohort of AML patients. Challenge participants are asked to predict which AML patients will be primarily resistant to therapy and which patients will have complete remission as well as to predict remission duration and overall survival.

3. The Broad-DREAM Gene Essentiality Prediction Challenge The goal of this Challenge is to infer genes that are essential to cancer cell viability using gene expression and/or gene copy number features. This Challenge, which will leverage the data from the NCI funded project Achilles, is a natural progression of the NCI-DREAM7 Drug Sensitivity predictions challenge.

For more details about how to register to participate in these Challenges, a description of these and other ongoing Challenges, the incentives for participation (including publication opportunities and podium presentation at conference) and the collaborators and sponsors that enabled the Challenges please go to www.synapse.org/dream. Every participant can contribute to the solution of these important Translational Systems Biology challenges. Contacts: Thea Norman (thea.norman@sagebase.org) and Gustavo Stolovitzky (gustavo@us.ibm.com)



FASEB continued

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ANNOUNCING GIW/ISCB-ASIA 2014

By Paul Horton, Conference Co-chair

The International Society for Computational Biology (ISCB), the Japanese Society for Bioinformatics (JSBi) and the Association of Asian Societies for Bioinformatics (AASBi) are proud to announce GIW/ISCB-Asia 2014, the first joint conference between ISCB and GIW.

GIW has a strong history as a stage to communicate important scientific progress on computational biology in East Asia. As they say in that region, one look is worth more than a hundred reports. The photo below is from GIW 2013. Note the expression of astonishment on the faces of the 2014 conference co-chairs (Kiyoshi Asai and Paul Horton) as they intently focus on the lecture.

The positive influence of teaming up with ISCB-Asia for this year's GIW is evident in the exceptionally strong keynote speakers: Janet Kelso, Alfonso Valencia, Thomas Lengauer, Shinya Kuroda, Sang-Yup Lee and Masami Hirai, who will present the latest computational biology advances in areas ranging from archaic human genomes, cancer genomics, combination drug therapies, temporal coding of insulin action and metabolic engineering.

In addition to these exciting keynotes, the conference will continue the GIW tradition of a strong proceedings track, giving young researchers an opportunity to present "the devil in the details". Some selected presentations will subsequently be published in journals such as *Bioinformatics*, *IEEE/ACM Transactions on Computational Biology*,BMC Genomics, *BMC Systems Biology*, and *Journal of Bioinformatics and Computational Biology*. GIW/ISCB-Asia 2014 will be held on December 15-17 in Tokyo, the city where GIW started 25 years ago.

Tokyo is a convenient, safe and modern city with a moderate climate and despite its status as the world's largest metropolitan area, enjoys good air quality. The conference venue is on the newly developed, highly popular and yet surprisingly spacious "Odaiba" waterfront area.

In addition to recreational opportunities, Odaiba is a research hub, home of the Computational Biology Research Center (AIST), and other national and municipal research facilities.

Tokyo (or Edo) also enjoys a rich history as the center of Japanese civilization for the last 400 years and offers numerous museums and tours for the curious.

December is a sunny month with average temperature of 9°C and relatively long days (similar latitude to Malta). We are sure participants will greatly enjoy the conference, the venue, and the city as a whole.

Potential sponsors or exhibiters are encouraged to contact: Stacy Slagor, Director of Corporate Relations and Development, ISCB at stacy.slagor@iscb.org or the local administrator, Hiroko Sakai, at sakai-hiroko@aist.go.jp.

Important dates:

- **August 11** - Highlights Track Submission Closes
- **August 24** - Poster Submission Closes
- **Octobor 6** - Last Poster Submission Closes
- **November 10** - Early Bird Registration Closes

For more information please see the official website at www.jsbi.org/giw2014/

HIGHLIGHTS & CELEBRATIONS FROM THE 6TH ANNUAL RECOMB/ISCB CONFERENCE ON REGULATORY & SYSTEMS GENOMICS, WITH DREAM CHALLENGES

By Christopher M. Williams

In November 2013, close to 300 researchers gathered in Toronto, Canada for the 6th Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. In its second year as an official conference of the International Society for Computational Biology, the event featured 16 keynote lectures, 55 short talks, and nearly 100 poster presentations organized into two tracks that highlighted recent efforts to understand the organization, function, and regulation of complex molecular biological systems. In addition, the conference held the annual meeting of the Dialogue for Reverse Engineering Assessment and Methods (DREAM), which included short talks by the best performers in the DREAM8 Challenges.

DREAM

In advance of this conference, DREAM posed three to the systems and computational biology community that were designed to assess the relative usefulness of competing approaches for modeling complex biological systems, and to generate insights that could contribute to the solution of several practical biological problems. Over the course of the challenges, more than 600 teams registered and 369 submitted entries, doubling the participation of last year. The best performers in each of the challenges were announced at the conference, and representatives of the teams gave short talks explaining their approaches. These DREAM challenges were organized in close collaboration with Sage Bionetworks, and are the first round of challenges since DREAM and Sage Bionetworks announced their partnership in February 2013.

The HPN-DREAM Breast Cancer Network Inference Challenge, held in partnership with the Heritage Provider Network (HPN) and using previously unpublished data from a collection of breast cancer cell lines, invited participants to predict regulatory networks (subchallenge 1), generate dynamic models of phosphoprotein interactions (subchallenge 2), and devise novel approaches to visualizing these high-dimensional datasets as they change over time (subchallenge 3). The best performing teams in subchallenge 1 were Team DC_TDC (Artem Sokolov, Daniel Carlin, Evan Paull, Kiley Graim, Adrian Bivol, Chris Wong, Josh Stuart) from the Uniersity of California at Santa Cruz, and Team NMSUSongLab (Yang Zhang, Haizhou Wang, and Mingzhou Song), from New Mexico State University. Best performers in subchallenge 2 were Team GuanLab (Fan Zhu and Yuanfang Guan) from University of Michigan, Team StochasticChaos (Bahman Afsari, Ludmila Danilova, Alexander Favorov, Wai-shing Lee, Dane Taylor, and Elana Fertig) from Johns Hopkins University, and Team CGR (Ying Hu, Chunhua Yan, Chih-Hao Hsu, George Komatsoulis, Yu Liu, and Daoud Meerzaman) from the National Cancer Institute. The best performer of subchallenge 3 was Team ABCD (Wendy Hu, Alex Bisberg, Byron Long, Dave Noren, Amina Ann Qutub) from Rice University. All teams but one presented at the conference. For more information on this challenge, go to www.synapse.org/#!Synapse:syn1720047.

The NIEHS-NCATS-UNC DREAM Toxicogenetics Challenge, developed in collaboration with the National Institute of Environmental Health Sciences (NIEHS), the National Center for Advancing Translational Sciences (NCATS), and the University of North Carolina at Chapel Hill, asked researchers to participate in two subchallenges: 1) use genetics (SNPs), RNA-seq, and toxicity data to predict how individuals will respond to chemical toxicants, and 2) use intrinsic chemical properties to predict the toxicity in a population (median and interquartile distances) of new chemicals for which toxicologic studies have not been done. Team Yang_Lab (Tao Wang, Hao Tang, Xiaowei Zhan, Jichen Yang, Rui Zhong, Guanghua Xiao, and Yang Xie) from the University of Texas Southwestern) was the best performer in both subchallenges.

continued on page 22

Attendees from the Sixth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges held in Toronto, Canada

Left to right: Woychik Richard, National Institutes of Health; Elsa Bernard (Team Cassis, Mines ParisTech, France); Gustavo Stolovitzky, Conference Chair.

Interestingly, this team was also the best performer in one of the two NCI-DREAM challenges of DREAM7 in 2012. They, as well as Team Cassis (Elsa Bernard, Erwan Scornet, Yunlong Jiao, Veronique Stoven, Thomas Walter, and Jean-Philippe Vert) from the Institut Curie, who were the second best performers in subchallenge 1, presented their work at the DREAM track of the conference. For more information on this challenge, go to www.synapse.org/#!Synapse:syn1761567.

The third challenge, which developed from a presentation by Markus Covert (Stanford University) at the 2012 RECOMB-DREAM conference, called on participants to explore a computational whole-cell model of M. genitalium (WholeCellViz) and identify a set of parameters that had been altered in comparison with those in a model wild-type strain. The challenge was designed to address what Covert described as one of the biggest problems he and his colleagues have faced; namely, the problem of parameter estimation in light of the vastness and inherent stochasticity in the model. The best performers in this challenge were Team Crux (Clemens Kreutz, Andreas Raue, Bernhard Steiert and Jens Timmer) from the University of Freiburg, who also preformed best in a similar challenge in DREAM7, and Team Whole-Sale Modelers (Alex H Williams and Jeremy Zucker) from Brandeis University). Both teams presented their work during the conference. For more information about this challenge, go to www.synapse.org/#!Synapse:syn1876068

Trey Ideker, Keynote Speaker (University of California, San Diego)

DREAM also featured two keynote talks. In the first, Trey Ideker (University of California, San Diego) introduced a new web-based atabase called the Network Extracted Ontology (NeXO), which integrates data from large collections of gene and protein interactions to build a hierarchy of cellular components and processes. This approach inverts the traditional use of ontologies in genomics, enabling a shift away from using ontologies (such as Gene Ontology) as prior knowledge for evaluating new data sets and toward using new data sets to construct and evaluate ontologies. Tim Hughes (University of Toronto) described some of his lab's work with that of Quaid Morris to develop a database called the Catalog of Inferred Sequence Binding Preferences of RNA Binding Proteins. By identifying similarities between binding motifs across species, their approach makes it possible to predict motifs for 10,000 proteins. In particular, there seems to be a high degree of conservation in the 3' UTR, Hughes mentioned, suggesting that RBPs may play a major role in regulating the stability of transcripts.

Systems Biology

Beginning on the conference's second day, talks in the systems biology track covered topics related to the dissection of cell regulatory networks, studies of genetics and genomics, the characterization of signaling pathways and metabolic networks, the systems biology of development and disease, and recent efforts to clarify drug mechanisms of action. Keynote addresses in this track provided a compelling snapshot of some key challenges that the discipline currently seeks to address.

Peter Jackson (Stanford University) opened the track by describing how his lab uses network building tools to understand drivers of genetic disease. He focused on studies of the molecular mechanisms that are important in cilia, and showed how intersections between these networks and those involved in obesity and diabetes are providing insights into the underlying genetic and signaling networks that drive disease. Peter Sorger (Harvard Medical School) drew attention to the problems posed by the high variability of drug response in individual patients. He suggested that in the future, drug development will have to consider not just complexity in the regulatory networks that drugs target, but also the complexity of the perturbations that drugs cause. Bernhard Palsson (University of California, San Diego) discussed some recent applications of constraint-based modeling — an approach that considers biological limits on possible network solutions — for the analysis of metabolic networks. Palsson described some interesting findings that this approach has produced related to synthetic lethal drug targets, the characterization of enzymes within metabolic networks, and studies connecting genotype to phenotype.

Opening the second day of the systems biology track, Olivier Pourquie (University of Strasburg) showed how combining genomic approaches with developmental biology manipulations in Drosophila can provide insights into cross-talk between physiological systems. Levi Garraway (Dana Farber Cancer Institute) described work in his lab to identify a phenomenon called chromoplexy, in which multiple DNA translocations and deletions arise in a highly interdependent manner. He also discussed the difficulty of understanding drug resistance in cancer, suggesting the "disturbing possibility" that there may be a range of mechanisms through which resistance occurs. If this is the case, finding downstream targets where resistance pathways "coalesce" may offer a more effective strategy than targeting individual pathways, he argued. Brenda Andrews (University of Toronto) described a technology her lab has developed called the synthetic genetic array, which systematically creates double mutants in order to produce

continued on page 23

RECOMB continued

comprehensive map of gene-gene interactions. She described some findings in her lab that have come from using this approach, as well as recent efforts to integrate high-throughput microscopy into this technology to observe protein abundance and localization within the cell.

Regulatory Genomics

Held on the final two days of the conference, the regulatory genomics track explored advances in scientists' efforts to understand genome regulation at multiple levels. Speakers presented talks about evolution at the molecular level, cell differentiation, enhancers of gene expression, genomic variation, and transcription factor binding, and about several new technologies for extracting biological insights from omics data. Collectively, the talks highlighted recent advances in the effort to explain the highly complex and dynamic molecular systems at work in cells.

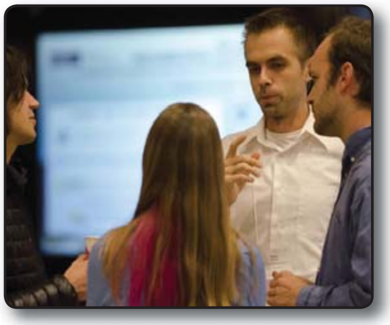

Fred Wright, Speaker, North Carolina State University

Aviv Regev (Broad Institute) discussed a protocol her lab has developed for using single-cell RNA sequencing to study variability in dendritic cells. Experiments identified a small subset of "early responder" dendritic cells that initiate interferon signaling, activating an antiviral response and dampening the inflammatory response across a cell population. Ziv Bar-Joseph (Carnegie Mellon University) also highlighted the dynamic nature of regulatory networks, and described methods his lab has developed forcombining genomic sequence, RNA-seq, and protein-protein interaction data with time-dependent data related to gene expression and epigenomic activity, in order to track changes in networks over time. Using an algorithm called mirDREM, his lab has reconstructed dynamic microRNA-regulated interaction networks to study lung development in mice, and ultimately hopes to use the approach to correlate underlying regulatory networks to disease phenotypes in patients. Galit Lahav (Harvard Medical School) presented recent work investigating the relationship between double-stranded DNA breaks and pulsing in expression of the transcription factor p53, a tumor suppressor that is mutated in 50% of all human cancers. In studies using gamma radiation and fluorescent reporters for quantifying DNA damage, her lab found that averaging the activation of p53 across a population of cells loses important features of the relationship between DNA breaks and p53 pulsation that can be seen more clearly in studies focusing on single cells. Describing studies of Drosophila development, Jason Lieb (Princeton University) explained that differences in the accessibility of enhancers of master regulator transcription factors on chromatin may account for the fact that different body parts can arise from the same genomic information.


Galit Lahav, Keynote Speaker, Harvard Medical School, Cambridge, United States

On the final day of the conference, Emmanouil Dermitzakis (University of Geneva) explained how combining RNA-seq with whole genome sequence data offers new opportunities for understanding the regulation of gene expression by noncoding DNA. Surveying research his lab has conducted as a part of the SysCol consortium, he suggested that there may be germline DNA variants that do not themselves cause colorectal cancer, but become drivers of cancer via cis-regulatory effects once a cell becomes cancerous. Jussi Taipale (University of Helsinki) described his lab's efforts to undertake genome-wide analyses of binding affinities between DNA and transcription factors, including studies comparing human and Drosophila. Recently, they have begun using software called the Enhancer Element Locator (EEL), which aligns the order of transcription factor binding motifs. The researchers have identified 600 high-quality binding for human, mouse, and fly genomes, and have gained valuable insights into the binding profiles of heterodimeric transcription factors. Brenton Graveley (University of Connecticut) gave an overview of his lab's efforts to characterize the dynamics and variability of alternative splicing events in Drosophila across time and in different tissues. In recent work focusing on the Drosophila Dscam gene, he has used a method called triple read sequencing to identify when and where individual isoforms of specific exons are expressed. His outcomes have uncovered the concept that alternative splicing is probabilistic, whereby the repertoire of RNA binding proteins expressed in subclasses of neurons determines the probability for each exon being expressed in that subclass of neurons.

For more information about this conference, go to www.iscb.org/recomb-regsysgen2013, where you can see a selection of talks and download the program guide, which includes abstracts for all of the talks and posters presented at the conference.



RECOMB/ISCB Regulatory and System Genomics Conference with DREAM 2014

The planning for the 2014 conference is well underway. Mark your calendars now and plan to join us in San Diego, California, USA, November 10-14. We are now accepting submissions of papers, abstracts, and responses to the DREAM Challenges. To learn more visit www.iscb.org/recomb-regsysgen2014-submissions/recomb-regsysgen2014-call.

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UPCOMING CONFERENCES AND EVENTS

ISCB CONFERENCES

ISCB Latin America Conference on Bioinformatics
Oct 28 - 30, 2014
Brazil - Belo Horizonte
www.iscb.org/iscb-latinamerica2014
The conference will feature an exceptional slate of keynote speakers and provide a forum for the dissemination of the latest developments in Computational Biology and Bioinformatics research conducted around the world and regionally.

RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2014
November 10 - 14, 2014
San Diego, California, USA
www.iscb.org/recomb-regsysgen2014
Now in its seventh year, the RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges is one of the premier annual meetings in the fields of regulatory genomics and systems biology.

12th Annual Rocky Mountain Bioinformatics Conference
United States - Colorado - Aspen/ Snowmass
December 11 - 13, 2014
www.iscb.org/rocky2014
12th Annual Rocky Mountain Bioinformatics Conference offers an opportunity to focus on regional development in the computational biosciences. Representing a broad spectrum of universities, industrial enterprises, government laboratories, and medical libraries from around the world, the meeting is a chance to get to know your colleagues near and far, seek collaborative opportunities, and find synergies that can drive our field forward.

GIW/ISCB-Asia International Conference on Genome Informatics
Dec. 15 - 17, 2014
Japan - Tokyo
www.jsbi.org/giw2014
The 25th anniversary of GIW – International Conference on Genome Informatics will feature a remarkable line up of keynote speakers over 3 days.

ISCB Africa ASBCB Conference on Bioinformatics
Tanzania - Dar es Salaam
March 09 -11, 2015
www.iscb.org/iscbafrica2015
This meeting constitutes the third joint meeting of ISCB and ASBCB, and the fourth conference of the ASBCB on Bioinformatics of African pathogens, hosts and vectors.

Great Lakes Bioinformatics Conference 2015 (GLBIO 2015)
May 18 - 20, 2015
United States - Indiana - West Lafayette
Purdue University
www.iscb.org/glbio2015
The 5th GLBIO provides an interdisciplinary forum for the discussion of research findings and methods. An important goal for the conference is to foster long term collaborative relationships and networking opportunities within the domain of computational approaches to biology.

ISMB/ECCB 2015
May 18 - 20, 2015
Ireland, Dublin
www.iscb.org/ismbeccb2015
As the world's premier conference on computational biology, ISMB/ECCB attracts top international scientists and key decision makers in the life sciences — experts in areas such as computer science, molecular biology and medicine,mathematics and statistics — from the world's largest and most prestigious research institutions.

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ISCB AFFILIATED CONFERENCES

9th Conference of the Hellenic Society for Computational Biology and Bioinformatics - HSCBB14
Oct 10 - 12, 2014
Greece - Attica - Athens
The Conference, which is the major annual event of HSCBB, aims at being a forum for researchers in the relevant fields from Greece, Cyprus and other countries to present their work and creatively interact for the establishment of scientific networks and collaborations.
Early Registration Deadline: 2014-09-19
ISCB Member Discount: 50 percent

NETTAB 2014 From high-throughput structural bioinformatics to integrative systems biology
Italy - Torino
Oct 15 - 17, 2014
The NETTAB 2014 Workshop will be a joint event with the Crystal (cl) Year meeting, in the International Year of Crystallography 2014, and it will be followed by the annual meeting of the Centre for Complex Systems in Molecular Biology and Medicine. The workshop may then represent a virtual bridge between these two events, showing how to manage and elaborate structural and high-throughput proteomics data so that it may be integrated with information from genomics and other life sciences disciplines with the aim of reaching a richer description and a deeper understanding of mechanisms and interactions in the involved system: the human being and its physiological and pathological states.
Early Registration Deadline: 2014-07-31
ISCB Member Discount: 10 percent

Benelux Bioinformatics Conference 2014
Dec 08 - 09, 2014
Luxembourg - Luxembourg-City
The Luxembourg Centre for System Biomedicine (LCSB) and the Centre de Recherché Public de la Santé (CRP-Santé) are organizing the 9th edition of the Benelux Bioinformatics Conference (BBC 2014). The event entitled "Bioinformatics: Integrating data, teams and disciplines" will take place in Novotel-Kirchberg in Luxembourg, on December 8th-9th 2014.
Event Registration: 2014-06-01 through 2014-11-15
ISCB Member Discount: 140 EUR

continued on page 29

Pacific Symposium on Biocomputing (PSB) 2015
Jan 04 - 08, 2015
United States - HI - Kohala Coast
The Pacific Symposium on Biocomputing (PSB) 2015 is an international, multidisciplinary conference for the presentation and discussion of current research in the theory and application of computational methods in problems of biological significance. Papers and presentations are rigorously peer reviewed and are published in an archival proceedings volume. PSB 2015 marks the 20th anniversary of PSB. PSB 2015 will be held January 4-8, 2015 at the Fairmont Orchid on the Big Island of Hawaii. Tutorials and workshops will be offered prior to the start of the conference.
Early Registration Deadline: 2014-10-31
ISCB Member Discount: 50 USD

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OTHER CONFERENCES OF INTERESTS

Galaxy Community Conference (GCC2014)
Jun 30 - Jul 02, 2014
United States - Maryland – Baltimore
Hosted By: Johns Hopkins University
http://galaxyproject.org/GCC2014

1st International Conference on Algorithms for Computational Biology, AlCoB 2014
Jul 01 - 03, 2014
Spain - Tarragona – Tarragona
Hosted By: Research Group on Mathematical Linguistics (GRLMC) from Rovira i Virgili University
http://grammars.grlmc.com/alcob2014/

Gordon Research Seminar on Intrisically Disordered Proteins
Jul 05 through Jul 06
United States - MA – Easton
Hosted By: Aurelia Ball and Charles Ravarani
www.grc.org/programsaspx?year=2014&program=grs_idp

Summer School in Computational Methods for RNA
Jul 06 - Jul 10, 2014
United States - MA - Chestnut Hill
Hosted By: Clotelab, Boston College
http://rna.bc.edu

Computational Methods for RNA 2014
Jul 06 - Jul 10, 2014
United States - MA - Chestnut Hill
Hosted By: Boston College, Clote Lab
http://rna.bc.edu

Joint 2014 MBI-CAMBAM-NIMBioS Summer Graduate Program
Jul 07 - 18, 2014
United States - OH – Columbus
Hosted By: Mathematical Biosciences Institute
www.mbi.osu.edu/eduprograms/graduate2014.html

Computational Genomics and Personalized Medicine
Jul 12 - 19, 2014
Italy - Isole Eolie – Lipari
Hosted By: Lipari School on Bioinformatics and Computational Biology
http://lipari.cs.unict.it/LipariSchool/Bio/

Protein Folding Conference 2014
Dominican Republic - Punta Cana
Hosted By: Zing Conferences
Jul 16 - 19, 2014
www.zingconferences.com/conferences/protein-folding/

DILS 2014 (10 Int Conf on Data Integration in the Life Sciences)
Jul 17 - 18, 2014
Portugal – Lisbon
Hosted By: Univ. of Lisbon
http://dils2014.inesc-id.pt/

The 28th Annual Symposium of The Protein Society
Jul 27 - 30, 2014
United States - CA - San Diego
Hosted By: The Protein Society
http://proteinsociety.org/symposium

Protein Interactions and Networks
Aug 04 - 12, 2014
United Kingdom - Cambridge – Hinxton
Hosted By: Wellcome Trust Advanced Courses
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/wtvm049891.htm

NIMBioS Tutorial: Evolutionary Quantitative Genetics
Aug 04 - 09, 2014
United States - Tennessee – Knoxville
Hosted By: National Institute for Mathematical and Biological Synthesis (NIMBioS)
www.nimbios.org/tutorials/TT_eqg

MBI Undergraduate Capstone Conference
Aug 11 - 15, 2014
United States - OH – Columbus
Hosted By: Mathematical Biosciences Institute
www.mbi.osu.edu/event?id=874

10th User Training Workshop Developing Multi-Scale, Virtual Tissue Simulations with CompuCell3D and Systems Biology Workbench
Aug 11 - 16, 2014
United States - NC - Research Triangle Park
Hosted By: The Hamner Institutes for Health Sciences and The Biocomplexity Institute at Indiana University
www.compucell3d.org/

Modeling Cellular Life: From single molecules to cellular function
Aug 19 - 22, 2014
Switzerland – Lausanne
Hosted By: CECAM
www.cecam.org/workshop-2-1070.html

2014 KDD Workshop: Big Data Analytic Technology For Bioinformatics and Health Informatics (KDDBHI)
Aug 24, 2014 United States - New York City
Hosted By: KDD
www.kddbhi.com

EMBO - EMBL Symposium: Epithelia: the building blocks of multicellularity
Aug 27 - 30, 2014
Germany – Heidelberg
Hosted By: EMBL Heidelberg
www.embo-embl-symposia.org/symposia/2014/EES14-04/index.html

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Other Conferences continued

Eighth International Workshop on Machine Learning in Systems Biology (MLSB 2014)
Sep 06 - 07, 2014
France – Strasbourg
Hosted By: ECCB 2014
www.mlsb.cc

SASB 2014 - 5th International Workshop on Static Analysis and Systems Biology
Sep 10, 2014
Germany – Munich
Hosted By: SAS
www.lri.fr/sasb2014/

The 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
United States - CA - Los Angeles
Hosted By: ACM SIGBio
Sep 20 - 23, 2014
www.cse.buffalo.edu/ACM-BCB2014/

ACM International Workshop on Big Data in Life Sciences (BigLS 2014)
Sep 20, 2014
United States - CA - Newport Beach
Hosted By: ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics
www.bigls.org/

German Conference on Bioinformatics
Germany – Bielefeld
Sep 28 - Oct 01, 2014
Hosted By: Bielefeld University
www.gcb2014.de

Immunogenomics 2014
United States - AL – Huntsville
Hosted By: HudsonAlpha Institute for Biotechnology–Science/AAAS
Sep 29 through Oct 01
http://haig.aaas.org/

5th International Conference on Biomedical Ontologies (ICBO 2014)
Oct 06 - 09, 2014
United States - TX – Houston
Hosted By: Health 2.0 Houston
http://icbo14.com

RECOMB CG 2014
United States - NY - Cold Spr Harbor
Hosted By: IBM Research
Oct 19 - 22, 2014
www.cs.nyu.edu/parida/RECOMB-CG2014/

TBC 2014, Translational Bioinformatics Conference
Oct 24 - 27, 2014
China – Qingdao
Hosted By: The Korean Society of Medical Informatics
www.snubi.org/TBC2014/

Workshop: Statistical Methods for Omics Data Integration and Analysis
Greece - CRETE – HERAKLION
Nov 10 - 12, 2014
Hosted By: Foundation for Research and Technology, Hellas
http://smodia2014.com/

EMBL-EBI-Wellcome Trust Workshop on Proteomics Bioinformatics
United Kingdom - Cambridge – Hinxton
Nov 10 - 14, 2014
Hosted By: Wellcome Trust Advanced Courses
www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Workshops/WTX054153.htm

Computational RNA Biology
United Kingdom - Cambridge – Hinxton
Nov 11 - 13, 2014
Hosted By: Wellcome Trust Scientific Conferences
http://registration.hinxton.wellcome.ac.uk/display_info.asp?id=437

EMBL/EBI - Wellcome Trust Workshop: Resources for Computational Drug Discovery
Nov 17 - 21, 2014
United Kingdom - Cambs – Hinxton
Hosted By: Wellcome Trust Scientific Conferences
http://registration.hinxton.wellcome.ac.uk/display_info.asp?id=434

Lyon SysBio 2014
France - 69622 - Lyon, Rhone-Alpes, France
Nov 19 - 21, 2014
Hosted By: Lyon SysBio 2014
http://lyonsysbio.sciencesconf.org

2nd Mathematical and Computational Medicine Conference 2014
Dec 01 - 04, 2014
Mexico - Mexico - Riviera Maya
Hosted By: Zing Conferences
www.zingconferences.com/conferences/mathematical-computational-medicine-conference-2014/

NIMBioS Investigative Workshop: Heart Rhythm Disorders
Dec 03 - 05, 2014
United States - TN - Tennessee – Knoxville
Hosted By: National Institute for Mathematical and Biological Synthesis (NIMBioS)
www.nimbios.org/workshops/WS_cardiac

2014 ICIBM
United States - TX - San Antonio
Dec 04 - 06, 2014
Hosted By: Vanderbilt, UTHSCSA and UTSA
http://compgenomics.utsa.edu/icibm2014/

BioDM: ICDM 2014 Workshop on Biological Data Mining and Its Applications in Healthcare
Dec 14, 2014
China – Shenzhen
Hosted By: ICDM 2014
www1.i2r.a-star.edu.sg/~xlli/BioDM2014/BioDM.html

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

OFFICIAL CONFERENCES OF ISCB

ISCB Latin America Conference on Bioinformatics

MARK YOUR CALENDARS for
October 28 - 30, 2014
Belo Horizonte, Brazil

www.iscb.org/iscb-latinamerica2014

RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges 2014

November 10 - 14, 2014 San Diego, CA

www.iscb.org/recomb-regsysgen2014

12th Annual
ROCKY MOUNTAIN BIOINFORMATICS
Conference

DEC 11 - 13, 2014
Viceroy Hotel
Aspen/Snowmass
Colorado

KEY DATES

AUG 08
Early Abstract Submission Opens

AUG 15
Registration and Housing Opens

OCT 10
Abstract Submission Deadline

NOV 08
Acceptance Notification

TBA
MARC Travel Fellowship Application Deadline

NOV 14
Early Registration Deadline

NOV 14
Academic Retreat Sign-Up Deadline

NOV 18
Housing Cut-off Deadline

DEC 11 - 13
Rocky 2014 Conference

www.iscb.org/rocky2014

2014
GIW ISCB-ASIA

December 15-17, 2014
Odaiba, Tokyo, Japan

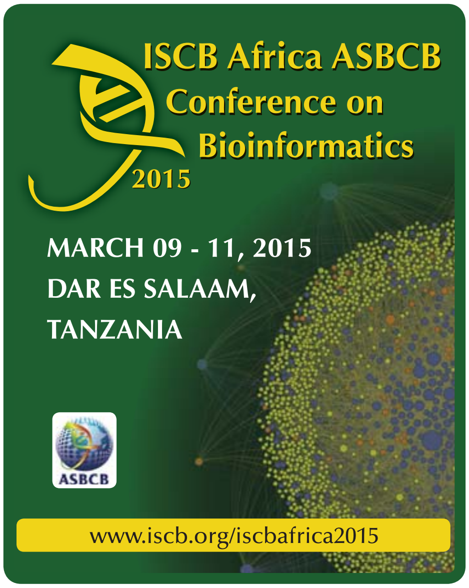
GIW
Celebrating
25 Years

www.jsbi.org/giw2014/

GLBIO 2015
GREAT LAKES BIOINFORMATICS CONFERENCE

May 18-20, 2015 Purdue University
West Lafayette, Indiana
www.iscb.org/glbio2015

DUBLIN
ISMB
ECCB
2015
JULY 10-14



ISCB Africa ASBCB
Conference on
Bioinformatics
2015

MARCH 09 - 11, 2015
DAR ES SALAAM,
TANZANIA

www.iscb.org/iscbafrica2015