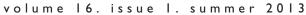
ISCB NEWSLETTER





About ISCB. The International Society for Computational Biology (ISCB) was the first and continues to be the only society representing computational biology and bioinformatics worldwide. ISCB serves a global community of 3,000 scientists dedicated to advancing the scientific understanding of living systems through computation by:

- convening the world's experts and future leaders in top conferences
- partnering with publications that promote discovery and expand access to computational biology and bioinformatics
- delivering valuable information about training, education, employment, and relevant news
- providing an influential voice on government and scientific policies that are important to our members



{contents}

A Letter to ISCB Members & Colleagues	1
Officer and Student Council Elections – The Choice is Yours	2
New Face at ISCB	3
Travel Fellowship Campaign	3
Fostering Relationships and Increasing Global Awareness	4
ISCB's Junior PI Initiative	5
Student Council Symposium Highlights	5
Bioinformatics & Nucleic Acids Research	6
PLOS Computational Biology Overview	7
Senior Scientist Award: David Eisenberg	8
Meet the 2013 Class of Fellows	9
Overton Prize: Goncalo Abecasis	10
Latest News from ISCB on the Society Pages	11
FASEB Activities	12
Bioinformatics Update	14
Career Corner	15
Announcing GLBIO 2014	15
Mark Your Calendar for ISMB 2014	17
FASEB Comments on the NIH Data Initiative	18
News from ISCB Student Council	20
Upcoming Conferences	21

A LETTER TO ISCB MEMBERS & COLLEAGUES

EXECUTIVE COMMITTEE

Burkhard Rost, President
Ferry Gaasterland, Vice President
Michal Linial, Vice President
Christine Orengo, Vice President
Reinhard Schneider, Treasurer
Scott Markel, Secretary

BOARD OF DIRECTORS

Teresa Attwood, Ph.D. Alex Bateman, Ph.D. Bonnie Berger, Ph.D. Judith A. Blake, Ph.D. Erik Bongcam-Rudloff, Ph.D. Alan Christoffels, Ph.D. Terry Gaasterland, Ph.D. Bruno Gaeta, Ph.D. Paul Horton, Ph.D. Janet Kelso, Ph.D. Richard H. Lathrop, Ph.D. Thomas Lengauer, Ph.D. Fran Lewitter, Ph.D. Michal Linial, Ph.D. Scott Markel, Ph.D. Jill P. Mesirov, Ph.D. Guilherme Oliveira, Ph.D. Christine Orengo, Ph.D. Burkhard Rost, Ph.D. Hershel Safer, Ph.D. Reinhard Schneider, Ph.D. Avinash Shanmugam, Ph.D. Donna Slonim, Ph.D. Tan Tin Wee, Ph.D. Anna Tramontano, Ph.D. Olga Troyanskaya, Ph.D. Alfonso Valencia, Ph.D. Lonnie R. Welch, Ph.D.

Society Staff

Diane E. Kovats, CMP, Executive Director Stacy Slagor Director of Corporate Relations and Development Nadine K. Costello, Administrative Assistant Suzi Smith, Administrative Support Steven Leard Markeywhys Corp

Newsletter Contributors

Tomás Di Domenico Bethany Drehman Christiana N. Fogg Margherita Francesco Anupama Jigisha Diane E. Kovats Allison Lea Scott Markel Umesh Nandal Cynthia Prudence Avinash Shanmugam Anna Tramontano Joe Tringali Olga Troyanskaya Clare Weaver Lonnie Welch

Copyright © 2013 International Society for Computational Biology. All rights reserved.

Dear ISCB Members and Colleagues,

2012 was a year of milestones for the International Society for Computational Biology (ISCB), the field of computational biology, and the Intelligent Systems for Molecular Biology (ISMB) conference. We celebrated the 20 year anniversary of our successful, world-premier conference; bringing together the brightest minds in the field and encouraging future researchers. ISCB also had its 15th anniversary as a professional society. During this time, we achieved our mission to build a strong, global community of researchers dedicated to computational biology and to communicate how important our field is in today's research.

It is with regret that we also said goodbye to our former executive officer, BJ Morrison McKay. BJ served as executive officer of ISCB for 10 years. Her skill and tact guided the organization through some challenging times and helped it flourish into the successful society it is today. I, for one, am grateful for all of her efforts and wish her the best in all her future endeavors.

The celebration has created a wonderful benchmark and we now look forward to the next 20 years and beyond. It is with pleasure and excitement that I take the reigns from BJ and, with the help of the amazing volunteer leadership and our members, lead ISCB into the next phase of its existence. While the road ahead may not be easy, our society continues to have a relevant voice in a fast-changing scientific landscape. We continue to see the economy slowly recover, aiding in our endeavors. However, historic lows in scientific funding and grant paylines also plague us. This reduced funding not only hurts scientific research but challenges our community by forcing the investigator to make some very tough decisions. One of these may be limiting the number of conferences you attend, or the number of students you can send. As this limits your opportunities to network, learn, and collaborate, as your society administration, we in the ISCB office are doing everything possible to make the conferences as affordable and valuable as we can for all participants.



Diane E. Kovats, CMP

ISCB recognizes the increasing challenges to our members and continues to look for ways to enhance your member benefits and provide support as you individually maneuver the potentially trying times ahead. This issue of the ISCB newsletter will highlight some of our programs and new initiatives such as the ISCB Society Pages. We will meet our incoming Class of Fellows, the recipients of the Senior Scientist Achievement Award and Overton Prize Award, and learn about their research. FASEB explains how they are working to give us as influential a voice on Capitol Hill as possible and highlights a new issue, how to deal with Big Data. Another article explores more deeply our Affiliated Groups program, which enables ISCB to partner with other computational biology societies from around the world. The newsletter also focuses on some of the upcoming sessions at ISMB/ECCB – the Student Council Symposium and Junior Principal Investigators Symposium. *PLOS Computational Biology* and *Bioinformatics* have provided their annual report to ISCB for your perusal. As a special feature to the newsletter, we have a professional development corner that addresses the use of CVs and resumes.

Throughout the remainder of the year and into 2014, I will be working with several member-appointed committees to take a deeper look at what ISCB has to offer and what else can be done for you - our members. We value your membership and dedication to the society and recognize that the more of us there are, the better we can collaborate and exchange information about science, funding, and the future. We will work together to build a stronger ISCB

continued on the next page

(continued)

but your opinions will be extremely important. I will be reaching out to you to get your feedback and assessment on the efficacy of ISCB activities and programs. Your participation in surveys and solicitations will help us achieve our goals, provide you with new programs, and evaluate our current programs.

I also want to remind you of your responsibilities as members. Please participate in the election that is now taking place. Take a few moments to review the candidate statements and submit your vote. No matter who you are, trainee, established investigator, mid-career scientist, etc.- if you are a member, we as a society want your vote. Each Spring, ISCB collects nominations for Board of Directors, Officer positions, and Student Council leadership positions. Participate by submitting your nominations for these leadership positions. These are the individuals who give their precious time to guide our Society to new levels. Think about the exceptional mentors, committed ISCB volunteers, and dedicated scientists that have transformed computational biology research and submit their names to our distinguished Fellows program. Each member has a voice and I strongly encourage you to use that voice.

I look forward to meeting many of you here at ISMB/ECCB and future conferences. I also welcome your feedback and suggestions. Please feel free to reach out to me at executive.office@iscb.org.

Enjoy this issue of the ISCB newsletter and ISMB/ECCB!

Sincerely,

Diane E Kants

Diane E. Kovats, CMP Executive Director

OFFICER AND STUDENT COUNCIL ELECTIONS - THE CHOICE IS YOURS

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

We are once again in the midst of our annual elections. This year the members will elect candidates for the ISCB Officer positions of President-Elect 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 2013 in Berlin, by visiting the "voting booth" adjacent to the ISCB booth in the exhibition area. The online voting site opened on July 9th, and can be accessed at www.iscb.org/elections until the close of ISMB/ECCB 2013 on July 23rd.

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!





SUPPORT THE SCIENTISTS OF THE FUTURE WHEN YOU CONTRIBUTE TO THE 2013 ISCB STUDENT TRAVEL FELLOWSHIP CAMPAIGN

NEW FACE AT ISCB



You may have noticed a new face on our website! ISCB welcomes Nadine K. Costello to our team where she will serve as an administrative assistant. Nadine is based in the Washington DC metro area along with executive director, Diane Kovats.

Nadine brings six years of work experience within the nonprofit scientific association sector. She is an alumnus of Mount Saint Mary's University where she studied political science.

After college, Nadine spent time abroad as a Teaching English as a Foreign Language (TEFL) teacher with the Via Lingua program. She started her associations career with the Cotton Council International, where she served as a budget coordinator assisting with federal funding programs and operational management of the society.

Nadine continued her career with the Society for Neuroscience, where she was responsible for program development, marketing, and program coordination.

"We are thrilled to have Nadine as part of the ISCB team," Diane Kovats said. "Nadine's experience will enable ISCB to enhance current programs and provide additional support, something we have been unable to do up until this point."

Nadine will be assist the executive office with administrative and operational support, particularly with our affiliated groups program and marketing and promotions. She can be contacted at assistant@iscb.org.

ISCB recognizes the need to support the future of the computational biology and bioinformatics by supporting travel for our future researchers—students and postdoctoral fellows. Student travel fellowships help propel young investigators toward important future discoveries. Join ISCB in giving students access to the principal role models within the field and help us influence the paths of scientific careers.

As government funding opportunities continue to decline, ISCB reaches out to YOU to help this important initiative. 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. Donating to the travel fellowship fund will enable us to support even more students with higher travel awards.

Manuel Corpas, ISCB member and a founder of the ISCB Student Council, tells of his experience, "In 2008, I received a travel fellowship from ISCB which made it possible for me to attend ISMB Toronto. The contacts I made with senior researchers and fellow students have had a tremendous impact in my scientific career to this day."

"Exposure to the best science in computational biology influenced my own research, and the networking opportunities strengthened my commitment to the field," says Manuel. "I am immensely grateful to ISCB for providing such great opportunities to junior scientists just when they need it most." Currently, Manuel is the leader of the Plant and Animal Genomes Project at the The Genome Analysis Centre, in Norwich, UK. His work focuses on the



Manuel Corpas, ISCB member and a founder of the ISCB Student Council

discovery of new knowledge in plant and animal genomes that can be quickly translated into the fields of bioenergy, crop productivity, and animal health.

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.



FOSTERING RELATIONSHIPS AND INCREASING GLOBAL AWARENESS



The ISCB Affiliates program is designed to forge links between ISCB and regional non-profit groups involved in the advancement of bioinformatics. These include professional societies, centers, institutes and networks that involve researchers from various institutions and/or organizations within a defined geographic region. The Affiliates Committee plays an integral role in the process as we continue to further the mission by fostering relationships with these groups. Every 3 years the Affiliates Committee elects a representative who sits on the ISCB Board of Directors to communicate and represent the interests of affiliated societies (currently Lonnie Welch).

ISCB welcomed four new affiliated groups in 2012 and early 2013: Bioclues.org (Indian Bioinformatics regional network), the Great Lakes Bioinformatics Consortium, the Hellenic Society for Computational Biology and Bioinformatics, and SolBio (Iberoamerican Society for Bioinformatics).

As of May 30, 2013, 23 confirmed affiliated groups spanning the globe. ISCB and the Affiliates Committee continue to develop ways to engage these groups to enhance the networking for all of our members around the world.

MAP 1. AFFILIATE GROUPS IN UNITED STATES AND CANADA



KEY FOR MAP 1. AFFILIATE GROUPS IN UNITED STATES AND CANADA

- 1. BAMBCT Boston Area Molecular Biology Computer Types
- 2. GLBC Great Lakes Bioinformatics Consortium
- 3. Ohio BioInformatics Consortium
- 4. MCBIOS Midsouth Computational Biology and Bioinformatics Society
- 5. Vancouver Bioinformatics User Group

continued on page 16



4



ISCB'S JUNIOR PI INITIATIVE – JUNIOR PI MEETING, SATURDAY, JULY 20, ISMB/ECCB 2013

In the career ladder of any scientist, transitioning from Post-doc to (junior) PI presents many new challenges. Key among these are moving from single to many project responsibilities, supervising students, writing grants, etc. The scientist is thus having to confront multiple higher level expectations where experience may be lacking.

This meeting brings together scientists who recently started or expect to start their own research group. It will serve the purpose of launching a community of junior PIs within the broader field of Computational Biology, providing the ideal platform for networking opportunities and the sharing of valuable experiences. In the context of ISCB, the Junior PI initiative is a much-needed solution to fill the to help those who transition between the ISCB Student Council and future positions the ISCB Board of Directors or as members of other committees.

The meeting will give delegates a chance to network with scientists in similar situations/positions, in a setting that stimulates in-depth scientific discussion and fosters new collaborations.

The program includes a series of four "frontiers in science talks" with speakers presenting the state of the art science in their research field. The talks will have a more 'review-like' character and the focus should therefore not be on the speaker's own work, but rather on an overview of current technologies, scientific questions and future challenges of his/her field. Of course, the speaker's own work could (and probably should) be part of that. Another series of round tables will follow to allow every participant to speak in small groups. Round tables are purposely created to encourage discussion of a particular topic of interest. At the end of these, the main points will be presented to all and further discussed.

Organizers:

- Jeroen de Ridder Delft University of Technology The Netherlands
- Venkata P. Satagopam University of Luxembourg Luxembourg
- Manuel Corpas
 The Genome Analysis Centre, UK
- Magali Michaut Netherlands Cancer Institute The Netherlands
- Yana Bromberg Rutgers University, USA
- Nils Gehlenborg Harvard Medical School, USA
- Geoff Macintyre, University of Melbourne, Australia

STUDENT COUNCIL SYMPOSIUM HIGHLIGHTS

By Tomás Di Domenico, Chair, Student Council Symposium Steering Committee, University of Padua

The ISCB Student Council Symposium (http://symposium.iscbsc.org) is a forum for students, post docs, and young researchers in the fields of computational biology and bioinformatics. Organized by student volunteers from all over the world, this Symposium is designed to enable students attending ISMB/ECCB to network with their peers, and to participate in a global exchange of ideas and scientific knowledge.



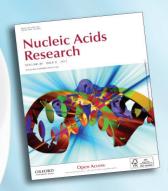
This year, the Student Council Symposium will showcase ten student speakers and more than fifty student poster presentations on a broad range of scientific subjects – from protein structure prediction and analysis to the bioinformatics of disease and treatment. In addition, this year's keynote addresses will be delivered by Dr. Alex Bateman from the European Bioinformatics Institute, Prof. Satoru Miyano from the University of Tokyo, and Dr. Gonçalo Abecasis from the University of Michigan (winner of the ISCB Overton Prize 2013). We are honored to be able to offer ourdelegates such an outstanding lineup of speakers, and we are certain that their lectures will be thought-provoking and inspiring to all.

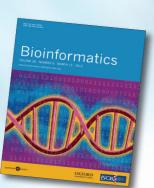
Thanks to the generous contributions of our sponsors and to the work of volunteer peer reviewers, we have been able to award five travel fellowships for symposium delegates. Congratulations to the fellowship recipients!

On behalf of the organizing committee and volunteer staff, we look forward to seeing you at the session here in Berlin! If you're not able to attend our Symposium on July 19th, please stop by the ISCB Student Council booth during ISMB/ECCB, or visit our website at www.iscbsc.org to learn more about how you can get involved.

Bioinformatics and Nucleic Acids Research

are proud to sponsor this year's ISCB Student Council best poster and best presentation prizes.





Stop by OUP's booth for free journal copies and promotional materials from Bioinformatics and Nucleic Acids Research, as well as Database, Briefings in Bioinformatics, Briefings in Functional Genomics, Human Molecular Genetics, and Molecular Biology and Evolution.

OXFORD UNIVERSITY PRESS



PLOS COMPUTATIONAL BIOLOGY OVERVIEW

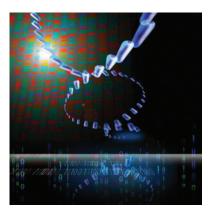
By Clare Weaver Publications Manager PLOS Computational Biology

In 2012-13 PLOS Computational Biology published 15% more research articles than the previous year, with an average publication volume of 42 per month. While publishing the highest quality research remains the main focus of the journal, PLOS Computational Biology also aims to serve the community by providing shared resources that engage and educate our readership and offering scientists a way of making less traditional contributions.

One such resource is our newest collection of Education articles. Translational Bioinformatics. an online textbook that is intended for use as a reference or tutorial for a graduate level introductory course on the science of translational bioinformatics. Edited by Maricel Kann and Fran Lewitter, the collection of 14 chapters from leading experts in the field was published in December 2012, along with an introduction by Russ Altman (1). An ebook version (a first for PLOS) was released in January 2013, and 3 new chapters were added in April. Translational Bioinformatics has been well received by the community and the editors are considering proposals for additional chapters.

In November 2012 we pulled our existing **Software articles** together into a collection, and in recent months *PLOS Computational Biology* has published four new **Topic Pages**. (Topic Pages were a new initiative for 2012 aimed at increasing coverage of computational biology in Wikipedia.) Some interesting articles from the ISCB have also featured in the journal over the past year, including Todd Gibson's history of the ISMB as told through interviews with some of the personalities involved in the formation and early years of the meeting (2).

PLOS Computational Biology underwent a leadership change in July 2012, welcoming Ruth Nussinov as our new Editor-in-Chief. Phil Bourne, Editor-in-Chief since the journal's launch, took on the new title of Founding Editor-in-Chief and



The *PLOS Computational Biology* Translational Bioinformatics collection image. Image Credit: PLOS. www.ploscollections.org/translational-bioinformatics

remains involved in special projects and the journal's non-research section. In October 2012 we announced an expansion of the journal's scope, in response to discussions among the editorial board and the community, to include papers describing outstanding methods of exceptional importance that have been shown to, or have the promise to, provide new biological insights. **Methods articles** are a distinct category of research articles, and are handled by our Methods Deputy Editor Thomas Lengauer.

PLOS Computational Biology is grateful for the contributions made by many members of the community during 2012-13. To accommodate the high numbers of submissions to the journal and the broad range of topics they cover we have introduced 16 new Associate Editors to the Editorial Board in the last 12 months, and Paul Gardner has joined us as a Software Editor. In addition, Rob de Boer, Arne Elofsson, Bill Noble and Jason Papin all took on more senior roles at the journal as Deputy Editors.

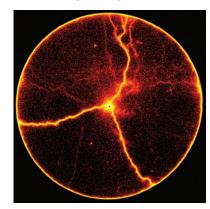
PLOS Computational Biology is a 'Community Journal': we value your ideas and comments, so please don't hesitate to come and visit us at Booth 13 at ISMB or contact us via ploscompbiol@plos.org at any time.

Examples of Highly Viewed Articles in 2012 (total no. of views/downloads as of June 1, 2013)

- Google Goes Cancer: Improving Outcome Prediction for Cancer Patients by Network-Based Rankingof Marker Genes.
 Winter C, Kristiansen G, Kersting S, Roy J, Aust D, et al. (2012) PLOS Comput Biol 8(5): e1002511. doi:10.1371/journal. pcbi.1002511 19,291 views
- The Regulation of Ant Colony Foraging Activity without Spatial Information.
 Prabhakar B, Dektar KN, Gordon DM (2012) PLOS Comput Biol 8(8): e1002670. doi:10.1371/journal. pcbi.1002670 16,363 views
- Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. Abubucker S, Segata N, Goll J, Schubert AM, Izard J, et al. (2012) PLOS Comput Biol 8(6): e1002358. doi:10.1371/ journal.pcbi.1002358
 13,117 views

References

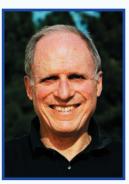
- 1. Introduction to Translational Bioinformatics Collection. Altman, R. PLoS Comput Biol, 2012, Vol. 8(12): e1002796. doi:10.1371/journal. pcbi.1002796.
- 2. The Roots of Bioinformatics in ISMB. Gibson, Todd A. PLOS Comput Biol, 2012, Vol. 8(8): e1002679. doi:10.1371/journal.pcbi.1002679.



Visualization of an ant trail pattern. Image Credit: Andrea Perna, Department of Mathematics, Uppsala University doi:10.1371/ journal.pcbi.1002592

2013 ISCB SR. SCIENTIST AWARD: DAVID EISENBERG

By Christiana N. Fogg, Freelance Science Writer, Kensington, MD



Each year, ISCB honors an esteemed member of the computational biology community with the Accomplishment by a Senior Scientist Award. This award recognizes an individual's significant contributions to computational biology through research, service, and education. The winner of 2013 ISCB Accomplishment by a Senior Scientist Award is Dr. David Eisenberg, Professor of Chemistry and Biochemistry and Biological Chemistry at the University of California, Los Angeles.

David Eisenberg's love of medicine and science was cultivated first during his childhood by his father, a gentle and beloved pediatrician. Eisenberg recalled, "Every night after dinner he would make house calls. I saw how appreciated—even loved—he was in our village."

Eisenberg's father also stoked his scientific curiosity by encouraging him to try some experiments in their basement, including attempts to petrify an egg and to grow worms in chocolate. Eisenberg reminisced, "None of these [experiments] worked, but they were fun.

Eisenberg strongly considered following in his father's footsteps and pursuing a career in medicine. With that goal in mind, he focused his undergraduate studies on biochemical sciences at Harvard University. As a sophomore, he was assigned to Dr. John T. Edsall as a tutor.

Edsall was a pioneering researcher in the field of biophysical chemistry, and under his guidance, Eisenberg had his first encounter with laboratory research. "In my junior year, he assigned me to read scientific papers, most of which baffled me, and at the end of that year, I started a research project in his lab, which became the subject of my senior thesis." Eisenberg recounted. "After graduation, Dr. Edsall turned my thesis into a short paper which was published in Science."

In spite of Eisenberg's eye-opening undergraduate research experiences, he applied and was accepted to medical school. Edsall was also trained as a medical doctor, but Eisenberg remembered how "Dr. Edsall convinced me that if my goal was to improve the health of mankind, I might have a greater impact working in biochemistry, than as a practicing physician."

Eisenberg took Edsall's advice to heart and "finessed making an immediate choice by going to Oxford to study theoretical chemistry under Dr. Charles Coulson, one of the founders of quantum chemistry." Edsall's guidance had also given him a strong foundation in math and physics, which served him well as a graduate student at Oxford as he recalled being "(just) able to work with Coulson on the energetics of hydrogen bonding."

Eisenberg's postdoctoral studies took him to Princeton in 1964 to work with Dr. Walter Kauzmann, well known for his discovery of the hydrophobic interaction. Eisenberg recollected his ambitious postdoctoral plan "to compute the energy of the hydrophobic interaction in myoglobin, the first protein with a known 3D structure. This plan now seems hopelessly naïve: computers were not yet up to such a calculation, potential functions and theory had not advanced to the point that this was a practical problem, and the early protein crystallographers were not eager to release their atomic coordinates.'

In light of these challenges, Eisenberg's work with Kauzmann culminated in "a monograph on ice and water, which, incidentally, is still in print 44 years later."

His failed postdoctoral research plan also opened his eyes. He knew if he wanted to pursue protein energetics, which required knowing protein coordinates, he had to learn X-ray crystallography. Eisenberg's next postdoc took him "to Caltech to study X-ray crystallography with Richard Dickerson, who had been part of the team who had determined the structure of myoglobin."

His X-ray crystallography training was pivotal to establishing his own lab at UCLA that focused on studying diverse protein structures. Melittin, a component of bee venom, was one of the first structures he determined with his then graduate student Tom Terwilliger. Eisenberg vividly recalled that, "At last I was able to get down to energetic calculations on a protein, and came up with the idea of the hydrophobic moment. This and related ideas gave me for the first time the feeling that I could make discoveries."

Eisenberg also remembers the excitement of solving the structure of diphtheria toxin dimer, which he worked on with John Collier, Senyon Choe, and Melanie Bennett (Brewer). He recalled the excitement that stemmed from Bennett (Brewer)'s observation that "two monomers of the dimer swapped their third domains, and we called this phenomenon "3D domain swapping." We explored the implications of 3D domain swapping, again calling on my background in energetics. Diphtheria toxin was the first structural example of 3D domain swapping; now there are hundreds."

Eisenberg's work on protein structures awakened his interest in how protein sequences relates to 3D structures. While on sabbatical at the Laboratory of Molecular Biology in Cambridge, he worked with Andrew McLachlan and Mike Gribskov to develop methods to examine protein sequences and use profile analysis to predict the presence of potential structural motifs. These studies led to his work on 3D profiles with Jim Bowie and Roland Luethy, which Eisenberg has now seen "applied to many protein problems."

Burkhard Rost, president of the ISCB, considers Eisenberg's work on hydrophobicity profiling as groundbreaking as it "describes an important feature of the constituents

continued on page 11

MEET THE ISCB FELLOWS CLASS OF 2013

By Christiana N. Fogg, Freelance Science Writer, Kensington, MD

The ISCB Fellows Program was established in 2009 to recognize members that have made significant contributions to the fields of computational biology and bioinformatics and service to the Society.

Fellows are identified through a rigorous process involving a call for nominations from the ISCB membership, and selection by the Fellows Selection Committee, which includes the ISCB Board of Directors and previously selected Fellows. Additionally, recipients of the ISCB Accomplishment by a Senior Scientist Award are also granted Fellows status.

The 2013 ISCB Fellows epitomize the mission of ISCB to advance scientific understanding of living systems through computation. Each Fellow has made outstanding contributions to computational biology through research, teaching, and service to the scientific community.



PIERRE BALDI

Pierre Baldi is a Chancellor's Professor in the Department of Computer Science and Director of the Institute for Genomics and Bioinformatics at the University of California in Irvine. Baldi is a leader in the fields of artificial intelligence and machine learning and has used these approaches for comparative genomics, computerbased drug design, and modeling of metabolic, neural, and signaling networks.



DAVID EISENBERG

David Eisenberg is a Professor in the Departments of Chemistry and Biochemistry, and Biological Chemistry at the University of California, Los Angeles, and he is also a Howard Hughes Medical Institute Investigator. Eisenberg is the winner of the 2013 ISCB Accomplishment by a Senior Scientist Award.



MINORU KANEHISA

Minoru Kanehisa is a Professor in the Institute for Chemical Research at Kyoto University in Japan. Kanehisa is one of Japan's most recognized and respected bioinformatics experts. He is the co-founder of the GenBank database and the National Cancer Institute of the National Institutes of Health.



SATORU MIYANO

Satoru Miyano is a Professor at the Human Genome Center, Institute of Medical Science at The University of Tokyo. Miyano is a leader in the computational biology community, is a former member of the ISCB Board of Directors, and has been a key organizer of numerous international bioinformatics and computational biology meetings.



SAIC-Frederick, Inc.

RUTH NUSSINOV

Ruth Nussinov is a Principal Investigator at the National Cancer Institute of the National Institutes of Health and a Professor in the Department of Human Genetics of School of Medicine at Tel Aviv University, Israel. She is the Editorin-Chief of *PLOS Computational Biology* and has served on the editorial boards of several other biomedical journals.



STEVEN SALZBERG

Steven Salzberg is a Professor in the Departments of Medicine, Biostatistics, and Computer Science, and Director of the Center for Computational Biology McKusick-Nathans Institute of Genetics Medicine, Johns Hopkins University School of Medicine. He is well known for developing scalable algorithms for genomic analysis.

2013 ISCB OVERTON PRIZE: GONCALO ABECASIS

By Christiana N. Fogg, Freelance Science Writer, Kensington, MD

ISCB recognizes the achievements of an early or mid-career scientist annually with the Overton Prize. The Overton Prize honors the memory of G. Christian Overton, a prominent bioinformatics researcher and founding ISCB Board member who died suddenly in 2000. Winners of the Overton Prize are up-and-coming independent scientists honored for their significant contributions to computational biology through research, teaching, and service. ISCB is thrilled to recognize Dr. Goncalo Abecasis, Felix E. Moore Collegiate Professor of Biostatistics at the University of Michigan, as the 2013 winner of the Overton Prize.

Goncalo Abecasis was drawn to biology ever since he was a child. "From a young age, I have always been fascinated with understanding how life works," said Abecasis. He fondly recalls spending Sundays at a bookstore with his parents and gradually collecting a small library of wildlife books.

But it was his experiences in a high school computer programming club that opened his eyes to an entirely different field. "Although I didn't know it at the time, a key skill that later contributed to my success in genetics was my interest in computer programming," recalled Abecasis. "The club was meant to keep us busy and out of trouble, but they did encourage us to try programming and point us in the direction of very useful techniques, like object oriented programming and the like."

Human genetics appealed to Abecasis as he pursued his undergraduate studies at the University of Leeds, and he landed a position in the lab of Dr. Mary Anne Shaw studying "how genetic variation in the interleukin-1 gene cluster, a set of immune genes where variation was easy to measure with then available techniques, was related to infection by Leishmania and other tropical parasites." This experience proved

invaluable for helping Abecasis to receive funding for his Ph.D. training in the lab of Dr. William Cookson at the University of Oxford.

Cookson's lab was studying genes that contribute to asthma susceptibility at the Wellcome Trust Center for Human Genetics at Oxford. In the late 1990's and early 2000's, Abecasis described this Center as "a mecca for human geneticists at the time, with great support from the Wellcome Trust, and lots of smart people trying new ways to run genetic studies and looking to make rapid progress in many different traits." Abecasis also recalled that, "as we pushed the limits of the sequencing and genotyping technologies of the time, we were soon generating datasets that were beyond the reach of existing analysis tools and methods."

Abecasis saw that, "It was easy to realize that new analysis methods and computer software were needed -- and being in Oxford, working at the Wellcome Trust Center was just the right place to be." With Cookson's support, and under the comentorship of statistical geneticist Dr. Lon Cardon, Abecasis developed software to tackle the analysis of large genetic datasets. Abecasis remembered dealing with many software bugs along the way, but then, as now, he repeated the mantra to himself that "all software is buggy, and this is no exception!"

Abecasis was pursuing his Ph.D. at the same time as the race to sequence the first human genome was wrapping up. As the field of genomics was emerging, he realized that several of the methods he had developed could be used to look at how "individual genomes differed from this initial sequence and to understand how these differences contribute to the great diversity we see among people today." The application of these methods to genome data also shifted his research focus away from "laboratory methods, technology and data generation," and toward "issues related to study design and analysis."



Abecasis's unique knowledge and training in human genetics, biostatistics, and computational analysis landed him a faculty position in the Biostatistics Department at the University of Michigan. Abecasis recounted the support and mentorship of Dr. Michael Boehnke in the department. "Mike somehow convinced the Biostatistics Department at the University of Michigan to take a flutter on me, when I had just finished my Ph.D. and had much less formal training in statistics than most of my colleagues. He has always been generous with his time, and I probably can't count the times that I have interrupted him in his office, bounced some ideas off him, and came out energized and thinking about something new to try."

Along with Boehnke, Abecasis acknowledged how fortunate he has been in the mentorship he received throughout his training, including the volunteers who taught him to code in his high school club. "As I knew them, I remember my mentors as demanding, generous with their time, unrelentingly positive and encouraging, and totally transparent. It is obviously a standard I'd like to meet, although I doubt I am there yet."

Their example also motivates Abecasis to be a good mentor. "It is great to set a student free on an interesting open problem and have them solve it. You can do so much more with a few good trainees than you could ever accomplish on your own."

continued on page 13



SR. SCIENTIST AWARD (continued from page 8)

LATEST NEWS FROM ISCB ON THE SOCIETY PAGES

By Olga Troyanskaya, PLOS Society Pages Editor and Lonnie Welch, Bioinformatics Society Pages Editor



Throughout 2013, ISCB will be rolling out a new and improved line-up on the ISCB Society Pages, which are part of PLOS Computational Biology and Bioinformatics. Articles in the column describe the specific programs of ISCB, highlight significant accomplishments of the communities and individuals, and provide opportunities for those who oversee the society's activities to communicate their vision and plans. The Society Pages provide a valuable means for members of the computational biology and bioinformatics community to learn how to get involved in numerous ongoing activities that cover the full spectrum of research, education and professional service.

The pages will also enable ISCB to more frequently cover the society's activities within the pages. The plan includes the following elements:

- enhanced breadth and depth,
- systematic coverage of all major ISCB activities, and
- expansion into both of ISCB's official journals via a coordinated plan, which ensures that
 - critical topics are given broad exposure, and
 - synergistic articles are featured at times.

As we continue to develop and fine-tune the plan, we welcome feedback and guest authorship for articles the highlight conferences, highlights of breakthroughs in the field, or other areas of interest. Contact executive.office@iscb.org to offer your suggestions.

which] we found we could extract information on protein interactions from sequenced genomes." These cutting edge studies resulted in several publications that showed how protein function and protein-protein interactions could be predicted from genome sequences.

Eisenberg has focused his research over the last decade on studying amyloid-forming proteins. Several neurodegenerative diseases are associated with amyloid-forming proteins, including Alzheimer's. Parkinson's and amyotrophic lateral sclerosis (Lou Gehrig's) disease. "Just before the turn of the century, I realized that amyloid diseases represent the greatest unmet medical problem facing the world." Eisenberg recounted. "And at the same time, I realized that structural and computational biology, which have illuminated other areas of biomedicine so well, have not been widely applied to the fundamental problems of amyloid disease. In particular, there had been almost no single crystal x-ray studies of amyloid-forming proteins.'

Eisenberg also acknowledges that, "Having several friends afflicted with amyloid disorders is a great inspiration. I would love to be able to help them, and others. If we can, it would validate Dr. Edsall advice that sometimes biochemists can do as much or more to help mankind than physicians."

Eisenberg's group has studied the structural basis of how normal proteins convert to amyloid fibrils. They have gained great insight into this conversion process by determining the atomic structures of the spines of many different types of amyloid fibrils. The use of computational biology with this structural data has helped support the definition of the "amyloid state" of proteins. "Bioinformatics and computational biology are great partners with structural biology. Using the tools together can be

surprisingly powerful," said Eisenberg.

Eisenberg remains humble about his accomplishments. When asked about being the recipient of the ISCB Senior Scientist Accomplishment Award, he felt "honored, but perhaps over-honored. There are many others who are equally or more deserving of this recognition." But he also recognizes that this award helps highlight the importance of studying amyloid diseases, especially using the tools of computational biology.

Eisenberg speaks warmly of the mentors that have guided and shaped his scientific training. "I was enormously fortunate to find myself in the research groups of four great mentors: John Edsall, Charles Coulson, Walter Kauzmann, and Richard Dickerson, not to mention my father. All were creative scientists, and also humanists. Watching them I saw their pleasure in scientific discovery, and also saw their insistence on fairness to all those involved in the process of science."

Their examples have not only served him well as a scientist, but also as a mentor. Eisenberg delights in working with trainees because he loves "their eagerness to learn and to succeed, and their willingness to think freshly about hard problems."

Eisenberg's scientific curiosity remains insatiable, and when asked for advice to motivate young scientists, his sage answer was "work on fundamental problems, maintain your curiosity, and above all, persevere."

This article is excerpted from the June 28, 2013, issue of *PLOS Computational Biology*.

To link to the full journal article please visit: www.ploscompbiol.org/article/info%3Adoi%2F10.1371%2Fjournal.pcbi.1003116

FASEB ACTIVITIES

By Allison Lea

Since 1912, the Federation of American Societies for Experimental Biology (FASEB) has worked continuously to promote biological research and has become an organization that legislators, federal agencies, and the media turn to for information on policies related to biomedical science and engineering. This year, the number of combined membership of FASEB's 26 societies surpassed 115,000 researchers and scientists. For ISCB, 2013 marks its ten-year anniversary as a FASEB society.

FASEB's dedication to increased federal funding for research, led the Federation to be one of the first groups to call attention to the threat of sequestration. FASEB's Office of Public Affairs (OPA) released factsheets, along with an analysis (updated in May 2013), demonstrating how sequestration cuts to the National Institutes of Health (NIH) budget would affect each state. The factsheets were set to each state governor to highlight the importance of supporting local research institutions that depend on federal funding.

In addition, FASEB's e-Action alert, sent out in December, generated nearly 20,000 e-mails sent to members of Congress, urging them to prevent sequestration, and OPA's legislative affairs staff organized two Capitol Hill Days, where 40 FASEB society members met with 70 members of Congress to impress the importance of biomedical and biological research for our nation's future. Although sequestration could not be averted, FASEB continues to strongly advocate, on behalf of its members and scientists nationwide, for continued federal funding for science and engineering.

The Federation has also been engaged in several other activities relevant to biological and biomedical research over the past several months. For example:

This spring, FASEB submitted a proposal to NIH for a National Research Mentoring Network planning grant that aims to (1) identify and analyze best practices



MARC: Maximizing Access to Research Careers

in mentoring; (2) develop new models for enhanced mentoring and create resources to expand mentees accessibility to potential mentors; and (3) design a system for managing and sharing mentoring resources and establish a plan for evaluating outcomes.

OPA staff created an online survey to collect opinions of scientists in response to the National Science Board's Request for Information (RFI) on Regulatory Burden. The survey, which yielded over 1,300 participants, was turned into a comprehensive report to supplement FASEB's response to the RFI.

FASEB submitted a response to NIH on its Big Data to Knowledge (BD2K) training plans and sent comments to NIH on its Data and Informatics Implementation Plan.

In May of this year, FASEB announced its second annual BioArt competition, for federally-funded scientists to submit captivating, high-resolution images and videos representing cutting edge, 21st Century biomedical research. The selected winners (ten images and two videos) will be announced on August 1.

FASEB had an "op/ed" letter published in Nature to express its concern of the recent criticisms in a Nature editorial regarding communications spending by the National Cancer Institute's Office of Communications and Education that prompted a Congressional inquiry into "PR" expenditures across NIH. In the letter (which has been accepted for publication), FASEB emphasized that this inquiry detracts attention from the larger issue of sequestration, and while further cuts to NIH's communications and education will do little to improve its economic situation, it could potentially make biomedical discoveries less accessible to those who need them.

GET TO KNOW YOUR ISCB FASEB REPRESENTATIVES

Judith Blake, PhD, FASEB Board Representative - Dr. Blake is an Associate Professor of Bioinformatics and Computational Biology at the Jackson Laboratory. She has been a member of the FASEB Board of Directors since 2003.

David M. Rocke, PhD, FASEB Board Advisor - Dr. Rocke is Distinguished Professor in the Division of Biostatistics, Department of Public Health Sciences and the Department of Biomedical Engineering at the University of California, Davis, where he has been on the faculty since 1980.

Harel Weinstein, DSc, FASEB Science Policy Committee Representative - Dr. Weinstein is the Maxwell Upson Professor of Physiology and Biophysics and Chairman of the Department of Physiology and Biophysics, and the Founder and Director of the Institute for Computational Biomedicine at Weill Cornell Medical College of Cornell University.

Scott Markel, PhD, FASEB
Publications and Communications
Committee - Dr. Markel is the
Principal Bioinformatics Architect
at Accelrys and is a part of
the Research & Developement
group. He is also the secretary of
ISCB and the Chair of the ISCB
Publications and Communications
Committee.

Fran Lewitter, PhD, FASEB Science Research Conferences Advisory Committee - Dr. Lewitter is the Director of Bioinformatics and Research Computing at Whitehead Institute. She also is the ISCB Education Committee Chair and leads the ISCB GOBLET collaboration.

Taner Sen, PhD, FASEB Excellence in Science Award Committee

- Dr. Sen is a Computational Biologist for the USDA-ARS and a Collaborator Assistant Professor, Department of Genetics, Development and Cell Biologist at Iowa State University. He is also a member of the ISCB Public Affairs Committee.



2013 ISCB OVERTON PRIZE (continued from page 10)

Abecasis's research, and the field of human population genetics in general, have been transformed by the advent of high-throughput genetics. "We now have very clear answers about the degree and structure of genetic variation in the world today, but have also gained a lot of detail on human population history -- including very ancient events, like admixture with Neanderthals," said Abecasis.

Abecasis's lab is now focused primarily on identifying genetic variants relevant to human disease. They look at linkage disequilibrium within human genomes in order to describe, "how groups of variants are shared among individuals." One of the observations that Abecasis's group and others made several years ago that he recalled as being surprising was "that much of the genetic variation in any individual could be recovered very accurately by comparing each individual to a reference set of individuals and, more recently, we have used the process to make it relatively inexpensive to sequence large numbers of individuals. At our last count, >30,000 human genomes had been sequenced using our "low-coverage" linkage disequilibrium based approach."

One of the highlights of Abecasis's career was being invited to the White House in 2010. "I was thrilled. I remember I had very short notice (perhaps a couple of days) and had to rush and find something to wear,

recalled Abecasis. Although it is cheesy, it is really amazing to live in a country that functions so much like a meritocracy. I didn't have to write a check, join a committee, vote - anything. I had a good idea about how to sequence a lot of genomes more rapidly, proposed it, and not only did I get funded to try it out (it worked, by the way), but my work was selected as one of the highlights for Vice President Biden's speech on the important of technology development and biomedical research."

Abecasis described the importance of collaborations to his research and is a strong proponent of sharing data and software tools. "So many great discoveries and advances come from bringing in insights, ideas and approaches from a different field," said Abecasis.

But Abecasis also agreed that data sharing is not without challenges. "There are legitimate concerns about protecting the identity and privacy of research subjects and, once in a while, people do use data you share pre-publication to gain an advantage," said Abecasis. "Still, there is no doubt we are moving in the right direction -- expectations for data sharing and collaboration are so much more open than when I started."

Abecasis has felt fortunate to work with so many great collaborators. One of his most interesting collaborations has been his work with Drs. David Schlessinger, Francesco Cucca, and Serena Sanna and many others on the

"SardiNIA project." "When I first met David, and he described the idea of conducting a thorough genetic study in an isolated valley in Sardinia, I never thought it would happen," remembered Abecasis. "It seemed so ambitious. But David and our Sardinian colleagues have boundless energy and real dedication, and the study probably accounts for most of my highly cited papers!"

"The work of Goncalo underscores the importance of the theoretical developments and their implementation in computational method for the progress in current biomedical research, bringing genomic information closer to the study of the complex genetic basis of common diseases," said Alfonso Valencia, chair of the ISCB's Awards committee.

Abecasis feels truly honored and humbled to be the 2013 recipient of the Overton Prize. Abecasis also hopes that, "If this award encourages members of the ISCB to bring some of their considerable expertise to bear on the big open problems in genetics, that would be an amazing outcome."

This article is excerpted from the June 28, 2013, issue of *Bioinformatics*.

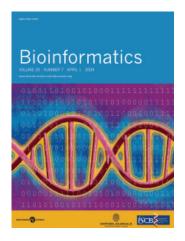
A transcript of the full interview with Dr. Abecasis can be found at http://genome.sph.umich.edu/wiki/Goncalo_Abecasis:_Interview_with_Christiana_Fogg.



Student attendees enjoying ISMB

BIOINFORMATICS UPDATE

Following a successful eight year term, Alex Bateman stepped down from his role of co-Executive Editor of *Bioinformatics* at the end of 2012. We thank Alex for all his efforts on behalf of the journal, and were very pleased to welcome Janet Kelso to the role of co-Executive Editor of *Bioinformatics*, working alongside Alfonso Valencia from 2013.



We are also pleased to welcome Gunnar Rätsch, Ziv Bar-Joseph, John Hancock and Igor Jurisica as new Associate Editors. We thank Trey Ideker for his hard work as an Associate Editor for the journal over many years, and are delighted that he has joined the Editorial Board.

Once again we received around 2000 submissions in 2012 – around 30% were accepted, with an average time from submission to first decision of 30 days. Once a manuscript is accepted for publication, it is usually published online ahead of print within 5 days and in an issue within 8 weeks.

In June 2012 we received the news that *Bioinformatics'* Impact Factor had risen to 5.468, making it the top ranked journal in the Mathematical & Computational Biology JCR category. At the time of writing, the 2012

impact factors have not been announced but based on our own citation analysis we are hoping to see *Bioinformatics*' maintain its position.

A new form of Creative Commons licence was introduced during 2012 for new *Bioinformatics* content published under an open access model. In short, we have moved from a CC-BY-NC licence to a CC-BY licence. The CC-BY licence allows unrestricted use, distribution, and reproduction in part or whole provided that the original work is properly cited (under the previous CC-BY-NC licence users were required to seek permission for commercial reuse).

During 2012 we also introduced a new article category - Bioimage informatics. In an editorial to introduce the new category, Peng et al. write 'Tremendous volumes of multi-dimensional bioimaging data are now being generated in almost every branch of biology. How to interpret such image datasets in a quantitative, objective, automatic and efficient way has become a major challenge in current computational biology. Bioimage informatics methods have begun to turn image data into useful biological knowledge....' The full editorial can be read at http://bioinformatics.oxfordjournals. org/content/28/8/1057.full

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/ECCB 2013.

With best wishes,

The Bioinformatics Editorial team

JOIN ISCB!

A global community for scientific leaders making life sciences discoveries through computation



ISCB members enjoy:

- Access to a global community
- A leading platform to present research
- Latest knowledge and news from journals and conferences
- Worldwide conference discounts
- Travel fellowships
- Professional development tools

Membership fees starting at \$49 for students and \$119 for professionals.

Lower rates available for those in low-to-middle income countries.



Visit www.ISCB.org to learn more!





THE RÉSUMÉ AND CV IN YOUR JOB SEARCH

By Joe Tringali, Tringali & Associates

The Résumé and the Curriculum Vitae (CV) are two distinct documents, each with their own unique characteristics and each meant to capture the attention of a specific audience. The terms are often used interchangeably, but upon closer examination, one can see nuances that make each a better choice for different employment application types and different readers. What follows are a few thoughts on the résumé, the CV and which might be the better document to use for each type of position applied to.

Both the CV and résumé include the candidate's name, contact information, education, work experience and relevant work-related skills. In general, the résumé is shorter in length than the CV, usually running about 1- 2 pages and geared to the first reviewer who typically is not trained as a scientist. There are always exceptions to this rule, of course. The résumé is used primarily when applying to industrial positions and its purpose is to capture the non-scientist's attention so that he/ she moves your application forward in the hiring process. Typically, whenever you apply to a posting through any sort of job board or employer website, the application is forwarded to the Human Resources staff or corporate recruiter who is screening each application for keys words as they pertain to the job for which you have applied. The key words may be training-related (i.e. Ph.D.) or skills-related (i.e., Java, C/C++). They may also give an indication of how much related research experience you may be bringing to the table, including your graduate research work or post

graduate experience. This said, as a candidate your goal is to make sure the first reader is able to find those key words/phrases easily and quickly on the first page your résumé so that he/she will move your application to the next level of review by the hiring scientific department within the organization.

One way to accomplish this is to include a skills section, listing any and all appropriate technical tools at your disposal that have either been asked for in the job posting, or that you feel may be relevant to the role, given the nature of the role. This list can be modified with each application so that it reflects your skills that the reader is hoping to see (but never at the expense of falsifying your qualifications, of course).

Alternatively, the CV is typically a lengthier document (usually 2-4 pages) and includes a summary of academic background as well as teaching and research experience, publications, presentations, awards, honors, affiliations and any other related details. This document is used primarily when applying for academic, teaching, and scientific/ research positions in an institute, or when applying for fellowships and/ or grants. In these settings, the first reviewer of your application is most often a trained scientist, serving as a faculty member, Department Chair, Principal Investigator, or search committee member. This screener will be reviewing your CV well beyond the key word search method, eliminating the need to include such a section on page one, although you may want to include it later in the document. The screening scientist is more interested in the graduate program you are completing, the



nature/quality of your publications, and your research interests and how they may dovetail with the activities in his/her lab.

Simply put, if you as a candidate suspect that the first reviewer will be a Scientist, your application may be best served by submitting a full CV rather than a résumé. If, however, you are applying to industrial positions and are asked to send your "résumé" to a generic email address such as careers@abcbiosciences, you may assume that the first reader is not a scientist and that a résumé is probably the better document to use.

The motivated candidate will have a version of both the CV and the résumé at their disposal and will feel good about the content and format of each document. Remember that neither the CV nor the résumé alone will get you the job offer...their only purpose is to draw interest to you as a candidate for subsequent discussions.

Good luck in your current or upcoming job search!



GREAT LAKES BIOINFORMATICS CONFERENCE

May 16 - 18, 2014 Cincinnati, OH Cincinnati Children's Hospital Medical Center

www.iscb.org/glbio2014



An Official Conference of the International Society for Computational Biology



(continued from page 4)

MAP 2. GLOBAL ISCB AFFILIATE GROUPS



KEY FOR MAP 2. GLOBAL ISCB AFFILIATE GROUPS

- 1. ASBCB African Society for Bioinformatics and Computational Biology (Africa)
- EMBNet European Molecular Biology Network (Europe)
- 3. NBIC Netherlands Bioinformatics Center
- 4. German Informatics Society
- SocBIN Society for Bioinformatics in the Nordic Countries (Denmark, Finland, Iceland, Norway, Sweden, Estonia, Latvia, Lithuania, and Poland
- 6. FOBIA Czech Free and open Bioinformatic Association
- 7. PBIS Polish Bioinformatics Society
- 8. BITS Bioinformatics Italian Society
- Israeli Society for Bioinformatics and Computational Biology

- 10. Hellenic Society for Computational Biology and Bioinformatics (Greece and Cyprus)
- A2B2C Associacion Argentina de Bioinformatica y Biologia Computacional
- 12. Brazilian Association for Bioinformatics and Computational Biology
- 13. SolBio Sociedad Iberoamericana de Bioinformatica (Argentina, Bolivia, Brazil, Chile, Colombia, Costa Rica, Cuba, Dominican Republic, Ecuador, El Salvador, Guatemala, Honduras, Mexico, Nicaragua, Panama, Paraguay, Peru, Portugal, Spain, Uruguay, Venezuela)
- 14. APBioNet Asia Pacific Bioinformatics Network
- 15. Bioclues India
- 16. JSBI Japanese Society for Bioinformatics
- 17. KSBSB Korean Society for Bioinformatics
- 18. AMBIS -Association for Medical and Bioinformatics Singapore

An Official Conference of the International Society for Computational Biology



SMB 2014 boston, usa

JULY 11-15

22nd Annual

International Conference

on Intelligent Systems for

Molecular Biology





www.iscb.org/ismb2014

FASEB COMMENTS ON THE NIH DATA INITIATIVE



By Bethany Drehman

On December 7, 2012, the National Institutes of Health (NIH) unveiled an implementation plan in response to its Advisory Committee to the Director (ACD) Data and Informatics Working Group Report. The plan is comprised of two initiatives: the Big Data to Knowledge (BD2K) and Infrastructure Plus, which together were estimated to cost a combined \$125 million per year for the next five to seven years; however, due to sequestration, this projection may be revised.

Infrastructure Plus is primarily an in-house program focused on intramural and administrative data handling and computing capabilities. BD2K, the larger component of the implementation plan, aims to transform the use of data particularly "big data" – within the biomedical sciences and includes the following main components:

- Supporting database/resource creation, resource accessibility, and community-based development of data standards for each field of research
- Developing and distributing analytical software
- Increasing the number of

- computational biomedical trainees and improving qualitative and computational training among all NIH supported trainees and researchers
- Establishing centers of excellence for biomedical big data, with the majority being investigator -initiated centers

In fiscal year 2013, BD2K activities will primarily focus on accessing needs and current data practices to inform activities in future years. As a part of this plan, NIH released a request for information (RFI) in February to obtain insight from the biomedical research community about qualitative training needs and provide background for developing a workshop on the topic.

The Federation of American Societies for Experimental Biology (FASEB) provided comments to the ACD Working Group on the implementation plan in March of this year. In its response, FASEB thanked NIH for addressing this critical and rapidly expanding field, and listed the following points that might limit the value of this initiative if not addressed:

Reiterated the need for NIH leadership to facilitate data

sharing through informed consent practices and intellectual property law

- Emphasized the value of funding mid-level information technology that is available and easily assessable to other federally funded investigators regardless of the funding agency
- Recommended that relevant education and training be developed by the scientific community and that NIH avoid instituting a prescriptive approach to qualitative training
- Expressed concern regarding the historical efficacy of the National Centers for Biomedical Computing
- Expressed concern of how the initiative would be funded in this current fiscal climate

FASEB also provided comments previously to the ACD working group during the development of the Data and Informatics report in 2012. In collaboration with FASEB constituent societies, FASEB will continue to monitor and develop policy recommendations for "Big Data," data sharing, and computation bioscience issues.

ISCB appreciates the generous contribution from the following donors, as well as those who wish to remain anonymous:

Thomas Abeel Sudin Bhattacharya Janos Binder

Danail Bonchev Philip Bourne Barbara Bryant

Tolga Can

Deborah Chasman Chandra Sekhar Reddy Chilamakuri

Karen Dowell Bruno Gaeta Joerg Geiger Paul Godden

Ricardo Gonzalez Mendez

Priscila Grynberg Molly Hammell Laura Hardulak Emna Harigua Joshua Ho Paul Horton

Jieun Jeong Jeffrey Jones Ezequiel Juritz Sarinder Kaur Kashmir Singh Pekka Kohonen Anthony Kusalik

Daniel Kurth Andrew Kuzneski Carlos Lagos Armin Lahm

Mark Leiserson Madeleine Lemieuz, Ph.D. Shan Li

Hanah Margalit Scott and Danette Markel Jill Mesirov Kirk Moldoff

Tuong Nguyen Rod K. Nibbe, PhD. Diana Magalhães de Oliveira

Mary Jo Ondrechen Christine Orengo R. Taylor Raborn Jovan Rebolledo-Mendez

Hershel Safer Clare Sansom

Reinhard Schneider Steven Sewe Stacy Slagor

Marcelo Soria Prashanth Suravajhala Jyothi Thimmapuram

Elinor Velasquez Barbara Verduzco John Walshaw

Andrew Warren Jennifer Weller

Min Xu Liudmila Yafremava



OFFICIAL ISCB CONFERENCES



ISCB-Asia/TBC Seoul, Korea October 2 - 4, 2013



RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges Toronto, Canada November 8 - 12, 2013



Annual Rocky Mountain Bioinformatics
Conference
Aspen/Snowmass, CO, USA
December 12 - 14, 2013



Conference on Semantics in Healthcare and Life Sciences Boston, MA, USA February 26 - 28, 2014



Great Lakes Bioinformatics Conference Cincinnati, OH, USA May 16 - 18, 2014



Intelligent Systems for Molecular Biology Boston, MA, USA July 11 - 15, 2014



ISCB-Latin America Rio de Janeiro, Brazil October 2014



Next Generation Sequencing Conference Barcelona, Spain May 2014

www.iscb.org/iscb-conferences

NEWS FROM THE ISCB STUDENT COUNCIL

By Umesh Nandal (SC Vice Chair), Margherita Francesco (SC Secretary), Avinash Shanmugam (SC representative to the ISCB Board of Directors), Cynthia Prudence (SC Finance Chair) and Anupama Jigisha (SC Chair)

Nine years have passed since ISCB Student Council was established with the goal to promote the next generation of computational biologists. These nine years have seen the organization and its extended regional student group network expand across 20 countries, reaching over 2000 students. The Student Council (SC) supports the student community by organizing and promoting scientific symposia and providing networking opportunities, educational resources and career development activities. Read on to learn about our initiatives and how we operate! You can also find more information on www.iscbsc.org.

STUDENT COUNCIL INITIATIVES

The largest yearly event organized by the SC is the Student Council Symposium, held in conjunction with ISMB. In the past years, the symposium has regularly attracted over 100 delegates, with high quality submissions and a number of high-profile keynotes. The 2013 edition will be no exception, with presentations by Dr. Alex Bateman, Dr. Satoru Miyano, and Dr. Gonçalo Abecasis. Find out more information about the Student Council Symposium program for this year and the additional activities offered by the SC at ISMB 2013 at http://symposium.iscbsc.org/.

Since 2009, the SC has been running the Internship Program, an initiative that aims at offering to students from developing nations an opportunity to gain experience in an established lab. Since its foundation, the program has filled 7 internship positions. We received great feedback, both from the students and the group leaders involved: a snapshot of the program structure with PI and student testimonies will be presented in a poster at ISMB. If you are a PI and you are interested in the initiative do not hesitate to contact us: we are always looking for new positions! You can also write to us at internships@iscbsc.org.

Among the most active and successful initiatives promoted



"....what is definitely sure is that this internship has changed me a lot. It has encouraged me to more eagerly look for opportunities and pursue my research interests."

- Kaur Alasoo, Intern at Schneider lab at EMBL (2010) selected from the SC Internship Program

in the context of the SC there are the Regional Student Groups (RSGs), the 'regional' associations of young researchers in the fields of bioinformatics and computational biology working in close collaboration with the SC. There are almost 20 RSGs spread across the world now and we are looking forward to the return of RSG Northern Africa and to welcoming *RSG Switzerland* to the RSG family. Looking for an RSG in your country? Please visit: www.iscbsc.org/content/regional-student-groups. You might have the chance to establish one!

The RSGs are providing valuable initiatives to support and promote students in bioinformatics and computational biology. Their experiences are worth sharing and perhaps will inspire many more students to join these groups. An article series documenting the various RSG initiatives, experiences and concerns was proposed by the SC and approved by the ISCB publications committee to be published in the PLOS Computational Biology ISCB Society pages. Two articles have already been submitted and 10 more will be, over the coming months.

The RSG funding program was conceived and begun by the ISCB-SC in 2010 with the aim of providing funding support for small events and programs proposed by our Regional Student Groups from around the world. These events, which are typically targeted towards the local

bioinformatics student community of the RSG, help the SC to directly deliver value to these communities and also helps motivate the RSGs in organize more events and be more active. This year, 4 RSGs have submitted their proposals and we are looking forward to supporting their activities.

This year will also see the Arts and Science exhibition at ISMB, organized by Dr. Milana Frenkel-Morgenstern and supported by the SC. Come and see some beautiful microscope images and photographs of protein models, phylogenetic trees, graphs among many other submissions to witness the true amalgamation of Art and Science.

"As a volunteer organization, the Student Council attracts a fantastic group of students and young scientists from around the world. Meeting, interacting and working with these people through RSGs and the SC has been a rewarding experience both in terms of skills learnt and the motivating and positive environment it provides."

- Avinash Shanmugam, Former RSG India, active SC volunteer (at several positions) and a PhD student at the University of Michigan Program

You can read more about the ISCB Student Council at the SC website (www.iscbsc.org) or look us up on Facebook, LinkedIn, and Twitter. Of course, the best way to find out about the Student Council is to talk to our members! At ISMB 2013 if you have a few minutes between sessions or if you are feeling lost in the crowds, stop by the ISCB Student Council booth (we are at booth 1). We'll show you how we're making a difference in the computational biology student community.

UPCOMING CONFERENCES AND EVENTS

ISCB CONFERENCES

ISCB-ASIA/TBC

October 2 - 4, 2013 JW Marriott Hotel, Seoul, Korea www.iscb.org/iscb-asia2013

Translational Bioinformatics Conference (TBC) will aim to highlight the multi-disciplinary nature research field and provide an opportunity to bring together and exchange ideas between translational bioinformatics researchers.

TBC puts its initial emphasis on promoting translational bioinformatics research activities initiated in Asia-Pacific region

RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenge

November 8 - 12, 2013
Toronto, Ontario, Canada
www.iscb.org/recomb-regsysgen2013
The conference will present the latest findings
about regulatory and systems genomics, foster
discussion about current research directions,
and establish new collaborations that will
advance the development of a systems-level
understanding of gene regulation. It will feature
keynote presentations, oral presentations, and

ROCKY 2013

December 12 - 14, 2013 Aspen/Snowmass, Colorado www.iscb.org/rocky2013 www.iscb.org/rocky2013

11th 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.

CSHALS 2014

February 26 - 28 2014

place to be in 2014!

Boston, MA www.iscb.org//cshals2014 CSHALS is the premier annual event focused on the use of semantic technologies in the pharmaceutical industry, including hospitals/ healthcare institutions and academic research labs. With an expanded scope that includes the emerging field of data science, CSHALS is the

GLBIO 2014

May 16 – 18, 2014 Cincinnati, OH www.iscb.org/glbio2014/ Hosted by: Cincinnati Children's Hospital Medical Center

The 4th 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.

ISCB-Latin America

October 2014

Rio de Janeiro, Brazil

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.

ISCB AFFILIATED CONFERENCES

poster presentations.

InCoB2013 - 12th International Conference on Bioinformatics

September 20 - 22, 2013
Jiangsu, Taicang, China
Hosted by: Taicang Center for Translational
Bioinformatics (TCTB), Center for Systems
Biology (CSB), Soochow University, AsiaPacific Bioinformatics Network (APBioNet)
ISCB Member Discount: 10 percent
http://ictbi.imed-cn.org/incob2013/

IEEE BioVis 2013

October 13 - 14, 2013 Atlanta, GA, United States Hosted by: Vis 2013 http://biovis.net

NETTAB 2013 on Semantic, Social, and Mobile Applications for Bioinformatics and Biomedical Laboratories

October 16 - 18, 2013 Lido of Venice, Italy Hosted by: Next Generation Bioinformatics (NGB) ISCB Member Discount: 30 EUR www.nettab.org/2013/

BRAZILIAN SYMPOSIUM ON BIOINFORMATICS 2013

November 3 - 7, 2013
Recife, PE, Brazil
Hosted by: Federal University of Pernambuco,
Brazil
ISCB Member Discount: 10 percent
http://bsb2013.cin.ufpe.br/

Clinical Genomics & Informatics Europe

December 4-6, 2013 Lisbon, Portugal www.ClinicalGenomicsInformatics.com

4th Annual PhD Symposium in Computational Biology & Innovation December 5 - 6, 2013

Dublin, Ireland Hosted by: University College Dublin ISCB Member Discount: 15 percent http://bioinfo-casl.ucd.ie/phdsymposium/

Pacific Symposium on Biocomputing (PSB) 2014

January 3 - 7, 2014 Kohala Coast, HI, United States Hosted by: Pacific Symposium on Biocomputing ISCB Member Discount: 50 USD http://psb.stanford.edu/

OTHER CONFERENCES OF INTEREST



Moscow Conference on Computational Molecular Biology (MCCMB'13)

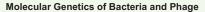
July 25 - 28, 2013
Moscow, Russia
Hosted by: Lomonosov Moscow
State University
http://mccmb.belozersky.msu.ru/2013/
index.html

1st International Conference on Statistical Language and Speech Processing, SLSP 2013

July 29 - 31, 2013
Tarragona, Spain
Hosted by: Research Group on
Mathematical Linguistics (GRLMC)
from Rovira i Virgili University,
http://grammars.grlmc.com/slsp2013/

continued on the next page

(continued)



August 6 - 10, 2013 Madison, WI, United States Hosted by: University of Wisconsin www.union.wisc.edu/phages/

Protein Interactions and Networks

August 8 - 16, 2013

Hinxton, Cambridge, United Kingdom Hosted by: Wellcome Trust Advanced Courses www.wellcome.ac.uk/hinxton

12th International Workshop on Data Mining in Bioinformatics

August 11, 2013
Chicago, IL, United States
Hosted by: 19th ACM SIGKDD International
Conference on Knowledge Discovery
and Data Mining
http://home.biokdd.org/biokdd13/

Undergraduate Research Program: Capstone Conference

August 12 - 16, 2013 Columbus, OH, United States Hosted by: Mathematical Biosciences Institute www.mbi.osu.edu/eduprograms/ upcapstone2013.html

MAGE: Models and Algorithms for Genome Evolution

August 23 - 26, 2013
Bromont, QC, Canada
Hosted by: University of Montreal, University
of Ottawa, IBM Research, Fields Institute,
Canadian Institute for Advanced Research,
Pacific Institute for the Mathematical Sciences
www-etud.iro.umontreal.ca/~lafonman/
MAGE2013/

13th annual Workshop on Algorithms in Bioinformatics (WABI 2013)

September 2 - 4, 2013 Sophia Antipolis, France Hosted by: INRIA and Campus SophiaTech http://algo2013.inria.fr/wabi.shtml

Workshop on Parallel Computational Biology (PBC 2013)

September 8 - 11, 2013 Warsaw, Poland Hosted by: International Conference on Parallel Processing and Applied Mathematics http://pbc.ppam.pl/

Theoretical Approaches to BioInformation Systems - TABIS 2013

September 17 - 22, 2013
Belgrade, Serbia
Hosted by: Institute of Physics - Belgrade
www.tabis2013.ipb.ac.rs

Quantitative Biology and Bioinformatics in Modern Medicine

September 19 - 20, 2013
Belfast, NI, United Kingdom
Hosted by: Queen's University Belfast
www.bio-complexity.com/QUB13/QB_
ConfIndex.html

2013 ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM-BCB)

September 22 - 25, 2013 Washington, DC, United States Hosted by: ACM Sigbioinfo www.cse.buffalo.edu/ACM-BCB2013

Mayo Clinic Individualizing Medicine Conference

September 30 - October 02, 2013 Rochester, MN, United States Hosted by: Dr. Richard Weinshilboum http://individualizingmedicineconference.mayo.edu/

EMBO | EMBL Symposium: Seeing is Believing - Imaging the Processes of Life

October 3 - 6, 2013 Heidelberg, Germany Hosted by: EMBO - EMBL www.embo-embl-symposia.org/symposia/2013/ EES13-03/index.html

IEEE BioVis 2013

October 13 - 14, 2013 Atlanta, GA, United States Hosted by: Vis 2013 http://biovis.net

RECOMB Satellite Workshop on Comparative Genomics

October 17 - 19, 2013 Lyon, France Hosted by: Université Claude-Bernard Lyon, France http://rcg2013.sciencesconf.org

NIMBioS Investigative Workshop: Multidisciplinary Approaches to Analyzing Animal Vocal Communication Sequences

October 21 - 23, 2013 Knoxville, TN, United States Hosted by: National Institute for Mathematical and Biological Synthesis (NIMBioS) www.nimbios.org/workshops/WS_vocal

Proteomics Bioinformatics

November 11 - 15, 2013 Hinxton, Cambridge, United Kingdom Hosted by: Wellcome Trust Advanced Courses www.wellcome.ac.uk/Education-resources/ Courses-and-conferences/Advanced-Coursesand-Scientific-Conferences/Workshops/ WTX054153.htm

AAAI Fall Symposium in Discovery Informatics

November 15 - 17, 2013 Arlington, VA, United States Hosted by: AAAI www.discoveryinformaticsinitiative.org/dis2013

ICDM-2013 Workshop on Biological Data Mining and its Applications in Healthcare

December 8, 2013
Dallas, TX, United States
Hosted by: Xiao-Li Li, See-Kiong Ng,
Jason T.L. Wang
www1.i2r.a-star.edu.sg/~xlli/BioDM2013/
BioDM.html

24th International Conference on Genome Informatics (GIW2013)

December 16 - 18, 2013
Singapore
Hosted by: National University of Singapore
www.comp.nus.edu.sg/~g

Cancer Panomics: Computational Methods and Infrastructure for Integrative Analysis of Cancer High-throughput "Omics" Data

January 3 - 7, 2014
Big Island, HI, United States
Hosted by: A session of the Pacific Symposium
on Biocomputing
ISCB Member Discount: 50 USD
http://psb.stanford.edu/cfp-cp.html



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

UPCOMING ISCB CONFERENCES





