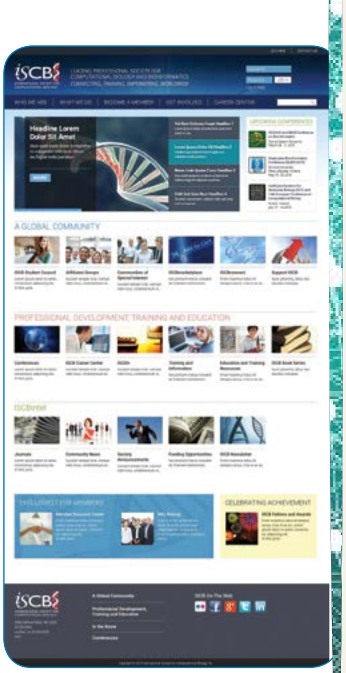
iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

Newsletter

SUMMER 2015 | VOLUME 18 | ISSUE 02

Features

Wooley Memoriam



New face of ISCB

DUBLIN
ISMB
ECCB
2015
JULY 10-14

In this issue:

ISCB the leading professional society for computational biology and bioinformatics community

Dear Members and Colleagues,

It is amazing to look back and see how far ISCB has come over the past seventeen years. We have grown to nearly 3,400 members from more than 70 countries. Through the work of hundreds of volunteers, we continue to bring the community top-rated conferences, training, educational materials, journals, and opportunities to connect, network, and collaborate.

Change is what propels us forward and ISCB continues to embrace change. During ISMB/ECCB 2015 in Dublin, we will be debuting two of our newest initiatives – ISCBconnect and the improved ISCB web portal!

ISCBconnect is an online globally accessible platform designed specifically to provide the community with the ability to forge meaningful connections, access training resources and learn at their own pace, while collaborating with others, and sharing information, expertise and experiences. Developed by the ISCB Communities of Special Interest (COSIs), researchers will have opportunities to flag material as particularly helpful and/or to engage in lively discussions of those that, for whatever reason, particularly pique their interest. These online virtual communities will engage participants in continued conversation around the latest trends, techniques and tools being used in computational research. Within the community, experts in the field will help to manage the conversations, answer questions and provide additional resources and tools. ISCB appreciated the support of the thirteen COSIs that helped to make this vision a reality.

ISCB is proud to announce the release of our newly redesigned website. It has been crafted to reflect what our members told us they need. Immediately you will notice streamlined menus, simple navigation and categorized information to enable quicker access to information. Our new platform is designed to be responsive to any computer, tablet, or smartphone. We hope you find our redesigned site to be helpful and your go to place for information.

This issue of the ISCB newsletter is filled with great information including the celebration of the ISCB Fellows, Award Recipients, the newest addition to the ISCB official journals, The ISCB Community Journal hosted by F1000Research, and much much more.

Again, I would like to personally thank the many volunteers that keep our Society moving forward, the leadership of ISCB for their continued dedication and service, and all ISCB members for their support. On behalf of the many contributing authors of this newsletter, we hope you enjoy.

Diane E. Kovats
ISCB Executive Director

Meeting the Global Thirst for Bioinformatics Training

Written by the GOBLET Executive Board on behalf of the GOBLET Consortium – Terri Attwood, Vicky Schneider, Michelle Brazas and Fran Lewitter

Meeting the Global Thirst for Bioinformatics Training
Written by the GOBLET Executive Board on behalf of the GOBLET Consortium – Terri Attwood, Vicky Schneider, Michelle Brazas and Fran Lewitter

The demand for bioinformatics training (from students, junior faculty, seasoned academics, even high-school teachers) increases globally each year. To meet this growing demand, the Global Organisation for Bioinformatics Learning, Education & Training (GOBLET) has engaged in numerous training programs and initiatives. Presented here is an introduction to GOBLET, a summary of some recent accomplishments and a general call for participation in our efforts.

GOBLET was established in 2012. It is a subscription-based, umbrella organisation for a spectrum of societies, networks, institutions, groups and individuals. (ISCB is one of the founding members of GOBLET.) The Foundation, steered by an Executive Board and 5 Committees *(Figure 1)*, aims to provide a global, sustainable support structure for bioinformatics capacity development.

Figure 1. GOBLET Operational Board Structure

2014-2015 GOBLET Accomplishments

In the past year, GOBLET has achieved a number of notable successes. For example, the Foundation has:

- Published 3 papers [1-3]
- Published a joint training strategy with ELIXIR [4]
- Launched an open survey of training needs
- Held training workshops in Boston [5], Manchester [6], Toronto [7]
- Worked with ISCB to launch the Computational Biology Education Community of Special Interest (CoBE COSI) [8]
- Won funds from the Canadian Institute for Health Research to support the 2014 Annual General Meeting (AGM)
- Hired technical & administrative interns
- Started planning the November 2015 AGM in Cape Town

How to participate?

Currently, 40+ organisations and individual members have joined GOBLET and supported the Foundation's work. Anyone may contribute to the portal by depositing training materials; however, full benefits accrue on becoming a member. Individuals, groups and organisations can join - to find out more, visit www.mygoblet.org and navigate to our membership pages. Once a member, we encourage you to join one of our Committees in order to more actively participate in the Foundation's work, and to help shape and steer its future direction.

Lessons Learned & Impacts

GOBLET is a grass-roots organisation, created by the community for the community. Along the way, we have gained valuable experience not just from organizing and presenting different types of training for different levels of audience, but also from working with trainers from other organisations; this, in turn, has shaped our ongoing outreach efforts, moving forward. Some of the take-home messages from this collective effort include the following:

- *Community*: Participation in a network of bioinformatics trainers and educators is invaluable.
- *Open Science*: Sharing of bioinformatics training materials, data-sets, scripts and best practices helps to improve training globally.
- *More Trainers Needed*: One of the biggest hurdles in bioinformatics training is the availability of trainers. GOBLET is working to train more trainers at all levels, from high-school to post-graduate to seasoned faculty.
- *Collective effort*: Aligning training efforts with like-minded organisations, such as ELIXIR, increases our collective output and reduces redundancy.

Get to know us

Many members of the Operational Board and general membership will be attending ISMB/ECCB 2015 in Dublin. Please visit our booth in the Exhibitor's area.

At ISMB/ECCB 2015, we are involved in organizing a Workshop on Education in Bioinformatics that will be held on Sunday July 12 from 10:10 a.m. to 12:40 p.m. and continue from 2:00 p.m. to 4:30 p.m. The title of the section is "Unlocking the super teacher inside you - Becoming competent in delivering bioinformatics training". This session is a joint effort of the CoBE COSI, the ISCB Education Committee and GOBLET. Please join us for this session.

The GOBLET Consortium will be presenting a poster during Sunday's education poster session. Please stop by our poster to meet us.

Finally, our AGM in November 2015 will be in Cape Town, South Africa, and is open to the community. Please check the GOBLET home page over the next couple of months to see details of the meeting as our planning continues.

We hope to see you at one of the venues mentioned above. We'd love to have you involved in our efforts. There is still a lot to do to bring bioinformatics skills to the global community.

References:

1. Attwood TK et al. (2015) GOBLET: the Global Organization for Bioinformatics Learning, Education & Training. PLoS CB, 11(4), e1004143.
2. GOBLET Consortium (2014) GOBLET: achievements & goals a year on. EMBnet.journal, 20, e751.
3. Corpas M et al. (2015) The GOBLET training portal. Bioinformatics, 31(1), 140-2.
4. https://www.elixir-europe.org/news/elixir-and-goblet-publish-joint-training-strategy
5. https://www.iscb.org/workshop-high-school-teachers-ismb2014
6. http://www.mygoblet.org/sites/default/files/goblet_events/SEBGOBLETWorkshopReport070714.pdf
7. http://www.mygoblet.org/training-portal/materials/stao-2014-understanding-genetic-disease-thanks-bioinformatics
8. http://cosi.iscb.org/wiki/CoBE:Home

2015 ISCB Accomplishment by a Senior Scientist Award: Cyrus Chothia

By Christiana N. Fogg, PhD, Freelance Science Writer, Kensington, Maryland, USA

The International Society for Computational Biology (ISCB; http://www.iscb.org) honors a senior scientist annually for his or her outstanding achievements with the ISCB Accomplishment by a Senior Scientist Award. This award recognizes a leader in the field of computational biology for his or her significant contributions to the community through research, service, and education.

Cyrus Chothia, an emeritus scientist at the Medical Research Council (MRC) Laboratory of Molecular Biology and emeritus fellow of Wolfson College at Cambridge University, England, is the 2015 ISCB Accomplishment by a Senior Scientist Award winner.

Chothia was selected the by Awards Committee, which is chaired by Dr. Bonnie Berger of the Massachusetts Institute of Technology (MIT). He will receive his award and deliver a keynote presentation at 2015 Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) in Dublin, Ireland in July 2015.

Cyrus Chothia: The Structures and Functions of Proteins

Chothia was deeply interested in history as a young student in England but was discouraged from pursuing this subject by teachers. "Because my foreign languages were so bad," Chothia recalled, "my teachers said I couldn't be an historian. I turned to chemistry." As a youth, Chothia remembers being fascinated by a hugely popular BBC television series by Nobel Laureate John Kendrew called series. I knew what I wanted to do, I wanted to be a molecular biologist and go Cambridge. I did it eventually in a roundabout way." Michael Levitt, a 2014 Nobel Laureate and a colleague of Chothia's, was also deeply moved by Kendrew's series as a young man.

Chothia completed his Bachelor of Science degree at Durham University in 1964 and his Master of Science degree at Birkbeck College, University of London, in

1967. He then pursued his PhD under the guidance of Peter Pauling at University College London. Chothia has fond memories of his time under Pauling's supervision. "He was a generous supervisor and we got along extremely well," he said. His PhD research examined the conformations of molecules at nerve receptors. This marked the beginning of his lifelong research interest in protein structures.

After his PhD, Chothia went to the LMB for postdoctoral training, during which time he got to know Joel Janin and Michael Levitt. His experience at LMB was quite different from his time under Pauling, and he and his new supervisor parted after three years. But this presented Chothia with an opportunity to travel abroad to different labs. "[Levitt and Janin] helped me find new places. Kendrew helped me get an EMBO fellowship to come to America to Fred Richards' lab at Yale. America was marvelous scientifically. People were excited about their work. I then went to the Weizmann Institute in Israel for six months and then to Paris to Joel's laboratory for two years. This was my 'Grand Tour' and it was actually very valuable. I went to all these different labs and learned many things that I could use when I got back to Cambridge." This was a very fruitful period for Chothia, and he published numerous papers with Levitt and Janin. Chothia and Levitt developed the "all-a, all-b, a/b and a+b" classification of protein structures, and Chothia and Janin worked out the underlying principles required for protein-protein recognition and packing of protein secondary structures.

In 1976, Chothia came back to England and was affiliated with the University College London and the LMB. He was named the E.P.A. Cephalosporin Fund Senior Research Fellow of the Royal Society in 1980, which offered him stable funding to work as an independent researcher for ten years. Chothia recollected, "During that time, I met Arthur Lesk and we got on enormously well. Lesk was there for more than ten years. Working with him and others was very productive." Their work covered a wide range of topics in structural biology, including how protein structures change to adapt to mutations, mechanisms by which proteins can transmit information to distant sites in a structure, and the observation that a small repertoire of structures exist for the main chain conformation of immunoglobulin hypervariable regions, and these structures can be predicted from the amino acid sequences. By 1990, Chothia recalled how his lab work changed. "I was given a permanent position at Cambridge and begin to have students," he said. "That made things somewhat different and I liked working with them. Before this, I worked with my contemporaries, and they would tell me when I was talking nonsense. Joel Janin and I used to have fierce arguments. When I started taking students the relationship became somewhat different: it was important to explain the terms of the argument."

In 1992, Chothia's work on protein structures led him to propose that most proteins are comprised of domains that come from a limited number of families. Together with Tim Hubbard, Alexei Murzin, and Steven Brenner, he created the Structural Classification of Proteins (SCOP) database. SCOP contains all entries in the Protein Data Bank and provides a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known. More recently, Chothia developed the SUPERFAMILY database with Julian Gough, which is a structural and functional annotation for all proteins and genomes. The SUPERFAMILY annotation is based on a collection of hidden Markov models that represent structural protein domains at the SCOP superfamily level. Superfamilies group together domains with an evolutionary relationship.

Chothia is still active in the lab and is interested in questions related to biological complexity. His recent work has shown that a significant increase in the number of superfamilies in eukaryotes correlates with the complexity of organisms. But he is aware that there are further questions to answer. He said, "The number of proteins about which we have good information as to function is small: we don't know what most proteins do." These questions are sure to keep Chothia and other scientists in this field curious and busy for years to come.

Outstanding Contributions to ISCB Award

By Christiana Fogg, PhD, Freelance Science Writer, Kensington, MD

2015 marks the first year that the International Society for Computational Biology (ISCB) honors one of its members with the Outstanding Contributions to ISCB Award. This award recognizes an ISCB member who has made unique and lasting contributions to ISCB through exemplary leadership, education, service, or a combination of these elements.

Lawrence (Larry) Hunter, Professor at the University of Colorado Medical School, is the inaugural winner of the Outstanding Contributions to ISCB Award. He will receive this award at the 2015 Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) in Dublin, Ireland in July 2015.

Larry Hunter: Founding Father of ISMB and ISCB

Larry Hunter pursued computational biology as a graduate student at Yale University in the 1980s before such a term for the field existed. He built a computer program that used case-based reasoning to diagnose lung tumor pathology, but he felt frustrated by the limits of computation having a noticeable impact on disease outcomes. As a freshly minted PhD with a background in artificial intelligence (AI), Hunter sought out career opportunities that would apply his skills and give him a steady paycheck. He joined the NIH's National Library of Medicine (NLM) in March 1989 as one of its first computer scientists, during a time when NIH was trying to strengthen its influence over the Human Genome Project. Hunter began maintaining a database of AI researchers with interests in molecular biology, and in 1991 he used this list to organize the first workshop that formed the basis of the Intelligent Systems for Molecular Biology (ISMB) meeting. The official "first annual" ISMB conference took place in 1993 on the NIH grounds and sold out almost instantly. Different universities in the US and UK hosted the next several ISMB conferences, and Hunter and others, including Russ Altman, Chris Rawlings, David Searls and Jude Shavlik were the primary meeting organizers. Planning and organizing each meeting presented unique challenges, but moving money for the meeting between institutions became a particularly cumbersome task.

The burgeoning popularity of the early ISMB conferences as well as the financial and logistical challenges of organizing the conferences compelled Hunter and his colleagues to consider establishing a scientific society for those who used computation to investigate biological questions. At the ISMB 1996 conference in St. Louis, MO, Hunter and members of the steering committees from prior ISMB conferences met to discuss the possibilities of organizing a new scientific society, and they voted on a board of directors, including Hunter as president, to guide this effort. Hunter recalled, "I felt a great sense of obligation to make the Society work. There were a growing number of people coming to the field, and the conference was expanding pretty rapidly. I had never run an organization before, and was very concerned about getting it right. There were also some political issues that I felt I had to be very careful to get right. Researchers with a background in computational complexity theory thought of themselves as quite different from the ones who came from a background in artificial intelligence. There was some discussion by people who wanted to form a different society, associated with the RECOMB conference. We had a long dinner on a Greek beach at the ISMB 1997, which was the basis for working out an agreement that kept the community whole." The board agreed on a mission statement for the nascent society at this marathon strategy session in Greece. The original statement was, "The International Society for Computational Biology is dedicated to advancing the scientific understanding of living systems through computation; our emphasis is on the role of computing and informatics in advancing molecular biology," but the second phrase has been dropped to adapt to the Society's broader focus.

The board agreed on the International Society of Computational Biology as a name, and ISCB was officially incorporated as a non-profit organization in 1997. Hunter faced some unexpected challenges as president of the newly formed ISCB, including the unforeseen difficulties of trying to find a bank that would accept a large check that was the underlying funding for this organization. He was keenly aware that scientists with allegiances to ISMB or to RECOMB, a competing conference, had to feel welcome and appropriately represented by ISCB. Most surprisingly, he recalled, "I greatly underestimated the amount of time it would take to make it all work. We had no staff, and everything was done by the executive committee, so I put much more time into it than I thought I was going to." He remembered how computational biology and bioinformatics were considered as peripheral and offbeat fields by many scientists at the time of ISCB's founding. "Hard, logical computer science was seen as having no connection at all to wet, squishy biology," he recounted. "When I mentioned "computational biology," people couldn't even hear the words together, they would often say "confrontational biology, what's that?""

ISCB has grown and evolved as a scientific society since its founding, especially as computational biology and bioinformatics have becoming increasingly vital components of biological research. He has seen ISCB become a critical resource for facilitating interactions and collaborations between scientists across fields, especially via ISMB and its other conferences. "I think my proudest achievement is that the society is still going today," Hunter said. "I booted it up in good enough organizational and financial shape that it looks like it will have a long life. I expect it will outlive me. It's really an honor to have created something of enduring value for so many people."

Hunter envisions that ISCB will adapt and change in the future in order to be of value to its membership. He said, "One interesting possibility would be for ISCB to organize events and activities to provide short-term training in informatics to biomedical researchers. Conferences like VizBi do that very well for biological visualization, and ISCB might be able to meet a need organizing similar conferences or tutorials at non-bioinformatics meetings. Twenty years from now I will be almost 75, so it will have to be the next generation to figure out how the Society evolves to stay relevant and valuable."

References

[1] Gibson TA (2012) "The Roots of Bioinformatics in ISMB." PLoS Comput Biol 8(8): e1002679. doi:10.1371/journal.pcbi.1002679

[2] Ferguson C, Morrison McKay BJ (2006) "History of ISCB." The International Society of Computational Biology. Web. 20 Mar. 2015.

Overton Prize

By Christiana Fogg, PhD, Freelance Science Writer, Kensington, MD

ISCB honors the achievements of an early- to mid-career scientist with the Overton Prize each year. The Overton Prize was instituted to honor the untimely loss of Dr. G. Christian Overton, a respected computational biologist and founding ISCB Board member. Winners of the Overton Prize are independent investigators in the early to middle phases of their careers that are selected because of their significant contributions to computational biology through research, teaching, and service.

ISCB is pleased to recognize Dr. Curtis Huttenhower, Associate Professor of Computational Biology and Bioinformatics at the Harvard T.H. Chan School of Public Health as the 2015 winner of the Overton Prize. Huttenhower will be presenting a keynote presentation at the 2015 Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) in Dublin, Ireland in July 2015.

Curtis Huttenhower: From Linguistics to the Gut

Curtis Huttenhower has vivid memories of his Apple IIe, the tool that first brought him into the world of computer science by way of BASIC programs and text adventure games like Zork. His first research experience was in computational linguistics, and he recalls fondly how the computer games he played as a child were text-driven and quite different than modern games' graphical experiences. Huttenhower's early experiences "talking" with computers drew him to later study computational language processing, and he recalled, "Some of the same tricks those games used to communicate in the 80s are still in use today. It's surprisingly challenging for a computer to understand sentences like, "Pick up the red fruit," in reference to an apple, when a human child has no problem."

Huttenhower graduated from the Rose-Hulman Institute of Technology in 2000, where he majored in computer science, chemistry, and math. He remembers being drawn to the physical sciences as well as computation, but he also admitted that despite his interest in the natural sciences, he was at first discouraged from studying these fields because he was dreadful at memorization. He recounted, "I was, and remain, absolutely terrible at memorizing lists of facts. That kept me out of biology for a long time. It's a rare student who enjoys the toughest parts of general biology or chemistry, memorizing gene and chemical names. Organic chemistry was all about rules rather than facts, though - generalizable principles. That got me into biochemistry, and the combination of problem solving in the wet lab and problem solving in the dry lab, by way of bioinformatics, was a lot of fun."

Although Huttenhower graduated with excellent undergraduate academic performance, he was initially rejected from all the graduate programs he applied to, and he found himself going in a very different direction by taking a software development job with Microsoft. In retrospect, though, he considers his two years at Microsoft as an invaluable experience, during which he learned the importance of management and testing infrastructure and the value of standard operating procedures and standardized methods for organizing computational projects. Huttenhower also sees value in this experience as he advises trainees about career options in academia and industry. "Particularly given the challenges of the modern life science careers," he mentions, "it's important to remember how productive and enjoyable industry work can be, and that neither of the two options are intrinsically better or worse than the other."

Huttenhower was finally accepted into a graduate program in computational linguistics at Carnegie Mellon University after two years of applications, and he has a new perspective of this process now. "Serving on admissions committees a decade later," he said, "I understand better now what a challenging process it is." Dannie Durand was Huttenhower's research advisor, and he credits her for his current career path. He recalled, "She was a joy to work with and tremendously enthusiastic about bioinformatics, and the enthusiasm was catching. By the time I finished my MS, I was applying for PhD programs in computational biology rather than language processing. She and Russell Schwartz were, and still are, fantastic motivators of new students entering the field."

Huttenhower then went to Princeton University to pursue his PhD and postdoctoral studies in computer science under the guidance of Olga Troyanskaya. He credited Troyanskaya's mentorship as elemental to his success, and he described, "[She] created, and has since grown, an exciting and productive lab. In addition to key pieces of basic knowledge in bioinformatics and strategies for a research career, I learned from her how to figure out which scientific problems matter, at least inasmuch as any of us know."

In 2009, Huttenhower accepted a position as an assistant professor of computational biology and bioinformatics in the department of Biostatistics at the Harvard T. H. Chan School of Public Health. He considers himself fortunate to have great mentors, especially Owen White, John Quackenbush, and Ramnik Xavier, as he has launched his academic career. Huttenhower has also considered his friendships and collaborations with other junior faculty has been crucial to early survival. He sees now that this mutual support and guidance has been pivotal to the success of early career computational biologists. "Chad Myers, Matt Hibbs, Florian Markowetz, and Edo Airoldi formed the core of Olga's lab along with me in her first few years as faculty," he recalled, "and they've all gone on to extremely successful research careers."

Huttenhower has established a robust research program in his lab, with a large part of his group working on projects related to the NIH Human Microbiome Project. He considers microbiome research to be an area of particular interest because relatively little is known about microbial communities, the field has a broad and solid foundation in classical microbiology on which to build, and findings in this area may significantly influence human health. He is enthusiastic about translating microbiome research to clinical applications. He said, "The microbiome represents an untapped new source of possible disease biomarkers and therapeutic interventions. In inflammatory bowel disease and type 1 diabetes, we're trying to determine which changes in the microbiome predict disease onset or inflammatory activity. Even in the worst case, knowing when a flare or seroconversion was becoming likely would allow stronger treatments to be introduced to prevent exacerbation or stave off disease activity. In the best case, the microbiome is modifiable, unlike human genetics. It's difficult to modify, since like cancer it represents a complex system that's evolved to be resistant to change, but the potential is there."

Huttenhower is excited about his work, and he shares a good problem to have with other life sciences researchers. "Like many scientists in public health," he said, "we spend our time working both on translational applications and on interesting basic biology, and at this point in the field as a whole there are many findings from both areas that represent ongoing work with a lot of potential." The tools developed for his lab's human microbiome research can also be applied to research on other microbial communities, and there are many open questions in their uses for areas as far-flung as agricultural microbial communities, bioremediation, and the basic biology of microbial interactions. Huttenhower noted, "Saccharomyces cerevisiae has been a great model microbial isolate for decades, and we're still learning how to make better wine, beer, and bread, so research into the complexities of mixed microbial communities is unlikely to run out of challenges any time soon!"

Bioinformatics Update

By Jennifer Boyd, Oxford Journals Oxford University Press

2014 was another busy and successful year for Bioinformatics. Our submission rate continued to increase in 2014, to 2300 papers, of which around 30% were accepted. Of our published papers, around 20% were published open access, with authors choosing between CC-BY-NC and CC-BY licences.

Our software papers continue to attract a high level of usage and citation. In particular, the following papers have been extremely popular with our readership:

- RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies, by Alexandros Stamatakis (doi: 10.1093/bioinformatics/btu033)
- Trimmomatic: a flexible trimmer for Illumina sequence data, by Anthony M. Bolger, Marc Lohse and Bjoern Usadel (doi: 10.1093/bioinformatics/btu170)

In 2014 we also published this paper by Michael Levitt and colleagues – Michael Levitt is the first bioinformatician to receive the Nobel Prize:

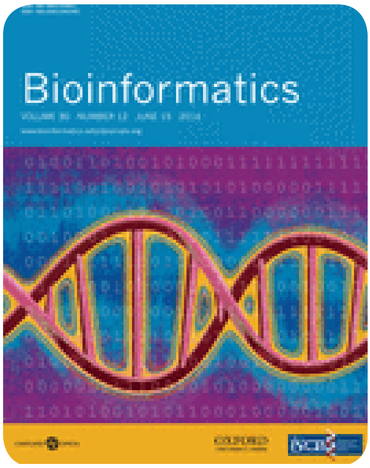
- Redundancy-weighting for better inference of protein structural features, by Chen Yanover, Natalia Vanetik, Michael Levitt, Rachel Kolodny and Chen Keasar (doi: 10.1093/ bioinformatics/btu242)

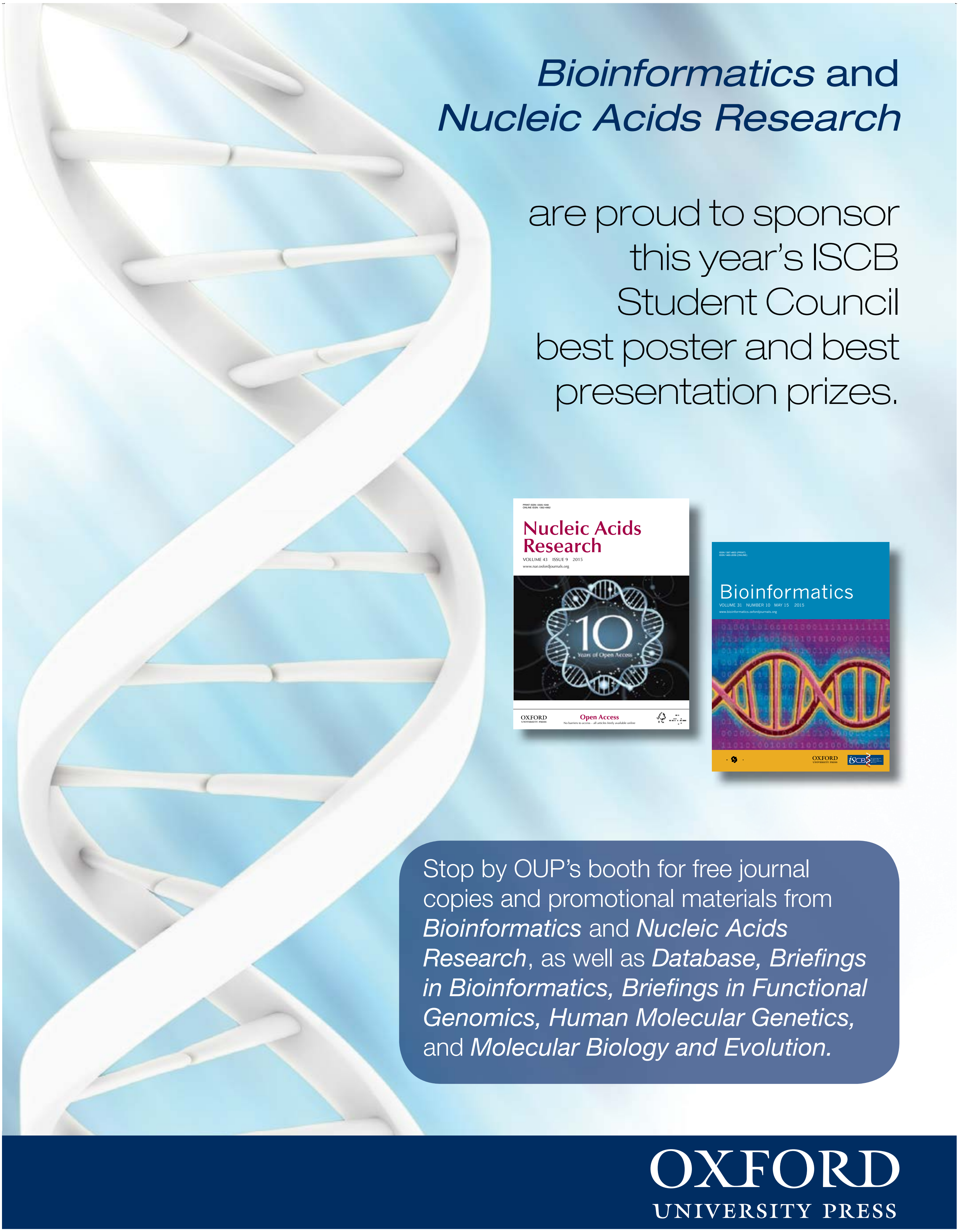
Bioinformatics has an impact factor of 4.261, maintaining its position as one of the top journals in computational biology. Our publication speed remains very fast – accepted articles are online within 5 days and are published in an issue within 7 weeks. Review time is also fast, with first decision 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 (http://www.oxfordjournals.org/our_journals/bioinformatics/iscb_articles.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/ECCB 2015 in Dublin – see you there!

With best wishes,
The Bioinformatics Editorial team





Busy Spring for FASEB's Office of Public Affairs

By Debra Speert, PhD, Director of Communications, FASEB

The Federation of American Societies for Experimental Biology (FASEB) and its Office of Public Affairs provide a policy voice for the 27 FASEB societies and more than 120,000 biological and biomedical researchers from around the world that they represent. We are currently in appropriations season, when the US Congress makes decisions about agency budgets. It is a particularly busy and important time to advocate for predictable and sustainable federal funding of research.

FASEB's Capitol Hill Day provides member societies the opportunity to discuss the challenges facing the research community with members of Congress and their staff. Despite steady rain and gray skies, 50 scientists from 27 states participated in the largest Capitol Hill Day to date for FASEB on April 14. Representatives of 21 FASEB member societies and nearly all of the basic biomedical science chairs associations met with more than 100 congressional offices to advocate for sustainable and predictable funding increases for the National Institutes of Health (NIH), the National Science Foundation, the Department of Energy Office of Science, and the competitive research program at the Department of Agriculture. **Judith Blake, PhD,** who represents the International Society for Computational Biology (ISCB) on the FASEB Board of Directors and provides input as a member of the Data Science and Informatics Subcommittee, participated in the event. Dr. Blake and her colleagues met with congressional offices, offering FASEB's fiscal year (FY) 2016 funding recommendations for the federal science agencies and sharing state and district fact sheets summarizing the impact of federal science investment on local institutions and businesses.

FASEB's president, Joseph R. Haywood, PhD, shared similar messages in meetings with Tom Cole (R-OK), the Chair of the House Labor, Health and Human Services, and Education (L-HHS) Appropriation Subcommittee, which writes the legislation that funds NIH, and Howard Shelanksi, Administrator of the White House Office of Information and Regulatory Affairs (OIRA). While in Washington, DC, Dr. Haywood also met with partners in the research community: Frankie Trull, founder and president of the Foundation for Biomedical Research and president of the National Association for Biomedical Research, and Rush Holt, the new Chief Executive Officer of the American Association for the Advancement of Science.

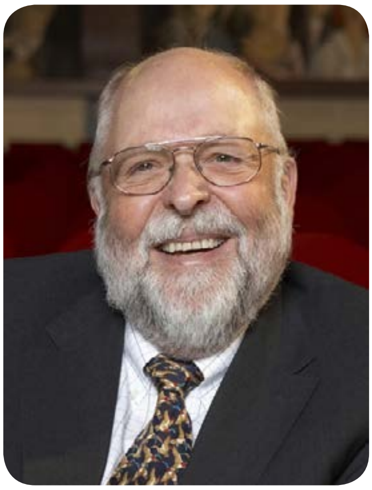
Two weeks later, Dr. Haywood returned to Washington, DC to testify before the House Appropriations L-HHS Subcommittee. He asked the subcommittee to appropriate $32 billion for NIH in fiscal year 2016, explaining that a five year commitment to five percent annual increases would help restore the buying power of the NIH budget, which has declined by more than 22 percent since 2003. "Every one of us is the spouse, parent, child, dear friend, or acquaintance of someone who is relying on our nation's scientists and physicians to develop tomorrow's treatments," Dr. Haywood told the subcommittee. "[NIH] investment is critical to expedite progress toward the cures that are so desperately needed for all of our loved ones, and for developing innovative technologies and new global industries to sustain the nation's continued economic recovery," he said.

FASEB regularly issues comments on agency proposals and policies, which ranged this spring from recommendations on ways to reduce regulatory burden to strategies to improve the impact and sustainability of research. Throughout the spring, FASEB has prioritized work with lawmakers in the House and Senate to help shape bills proposing strategies to increase research funding. With swift moving legislation addressing funding for federal agencies, dialogue with policymakers will be key to ensuring that the voices of our members are heard.

For up-to-date information on FASEB's Public Affairs activities, sign up to receive FASEB's Washington Update at http://washingtonupdate.faseb.org/.

In Memoriam: Klaus Tschira

By Thomas Lengauer



On March 31, 2015 Klaus Tschira suddenly and unexpectedly passed away at the age of 74.

Klaus Tschira, physicist, engineer, entrepreneur and generous sponsor, impacted information technology in Germany and well beyond. But he also did wonders for science in general, for the German foundation system, and for our field — computational biology.

In the beginning of the 70s, together with four colleagues from IBM, Klaus Tschira founded what today is SAP SE, Germany's largest software company with close to 75,000 employees in 130 countries and 280,000 customers in 190 countries. When the five founders started the company, going into the business of pure software development was a global novelty. During the first decade, the founders were the prime developers; in the 80s and 90s, when the company blossomed and went international, they shaped its success through a period of amazing growth. It is by the development in those decades, that Klaus Tschira shaped the face of information technology in Germany and also globally.

SAP AG develops and sells business software. For our field, and for science, the impact of Klaus Tschira really took off in the mid-90s when he founded his foundation, the Klaus Tschira Stiftung. The foundation has as its goal furthering science in the broadest sense, and Klaus Tschira gave the foundation its leverage by supplying it with his immense assets. There are a multitude of projects that the foundation has brought forth in the 20 years of its existence. Among those projects are supporting young children's education in science subjects, funding a multitude of science projects in a wide variety of science and technology disciplines, including mathematics and information technology, funding very innovative science buildings throughout Germany, among them the DNA double-helix shaped Advanced Training Center on the EMBL Heidelberg campus (based on his own design) and the House of Astronomy in Heidelberg, which is shaped like a spiral galaxy. Among the projects which had most direct impact on our field is the foundation of the European Media Laboratory in 1997 and the Heidelberg Institute for Theoretical Science (HITS) in 2010. HITS, located in Heidelberg and harboring over a hundred scientists brings together research groups in such diverse fields as computational biophysics, bioinformatics, mathematics, computer science, computational linguistics, astronomy and astrophysics. EML and HITS have been home to several groups in computational biology. Today, the computational biophysics groups of Rebecca Wade and Frauke Gräter, as well as Siegfried Schloissnig's group working on genome assembly and analysis of NGS data, the group led by Wolfgang Müller providing databases and data management for systems biology projects, and that of Alexandros Stamatakis working on fast phylogenetic methods, belong to the strengths of HITS.

Beyond science, Klaus Tschira has been very active and effective in improving the conditions for establishing and operating private foundations in Germany. It was due to his initiative that a long-standing law preventing foundations from supporting other foundations was finally dismissed in 2014.

I have had the privilege of knowing Klaus Tschira for 20 years. I was always extremely impressed by his openness, richness of new ideas, rejection of status, sincere interest for other people's thoughts, humility and humor. He will continue to be a model for me and for the whole scientific community with his vision, endurance, generosity and empathy.

PLOS Computational Biology Overview, June 2015

By: Gary Beardmore, Publications Manager, PLOS Computational Biology

In 2014-2015, PLOS Computational Biology continued its tradition of publishing high-quality research and enabling members of the community to contribute to scientific communication through the creation of resources for current and future generations of computational biologists. The journal experienced an 11% increase in published articles over a 1% decline in submissions and reported a healthy average of 142 articles submitted per month.

During the period June 2014 to May 2015, PLOS Computational Biology was delighted to be able to publish several Message from ISCB articles. Most notable were the announcement of the award for research on the Ebola virus with an article entitled ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus [1] and the article describing the soft skills young researchers develop at ISCB entitled Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities [2].

Our ever-popular 'Ten Simple Rules' series of articles on professional development, led by Founding Editor-in-Chief Philip Bourne since 2005, continue to be popular articles in the journal. One of our most talked about pieces was a tongue-in-cheek piece kindly written by Richard J. Roberts entitled Ten simple rules to win a Nobel prize [3]. Sir Roberts won the Nobel Prize in Physiology or Medicine himself in 1993 and delivers his message that you cannot aim for a Nobel Prize, merely perform good science and with luck you may reach this peak.

We have been publishing Topic Pages since 2012 and currently have eight in the collection, the most recent article entitled Inferring Horizontal Gene Transfer [4] was released at the end of May. These articles are submitted and undergo an 'open review' process (reviewers' names are known to the authors and the public, and the reviews, along with the authors' rebuttals, are also made public). The articles are then published by PLOS as well as Wikipedia, where the PLOS article remains the article of record but subsequent edits can be made by the public as on other Wikipedia articles. We are very grateful to Spencer Bliven for his help in creating and maintaining the server for this project since its conception. We are in the process of bringing it in-house giving us more flexibility with this exciting project and Spencer continues to volunteer his time to assist us with Topic Pages.

The PLOS Computational Biology 'Topic Pages' collection image. Image credit: PLOS
www.ploscollections.org/topicpages

In February this year all of the PLOS journals thanked reviewers by publishing a list of everyone who reviewed for us in 2014, along with a notice of our appreciation. Reviewers also received an e-mail thanking them for their efforts and pointing them to the published article. Each journal released their own list and PLOS Computational Biology was no exception [5]. PLOS Computational Biology could not exist without the community of volunteer reviewers and editors, we highly value all of the time they give, and continue to give.

PLOS Computational Biology is a 'Community Journal'; we value your ideas and comments, so please do not hesitate to come and visit us at Booth 1 at ISMB or via ploscompbiol@plos.org at any time.

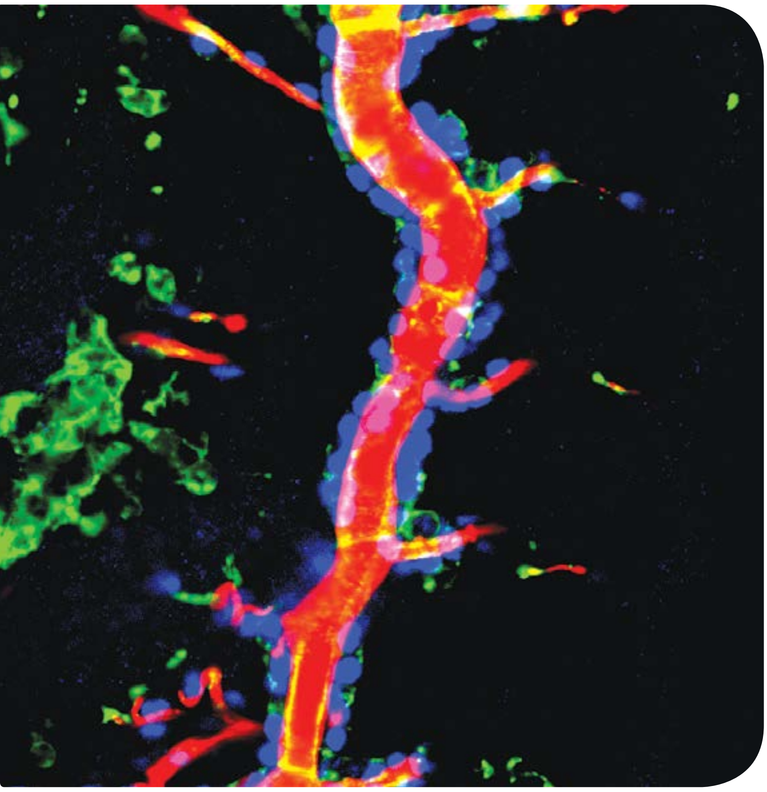
Examples of highly viewed articles in 2014

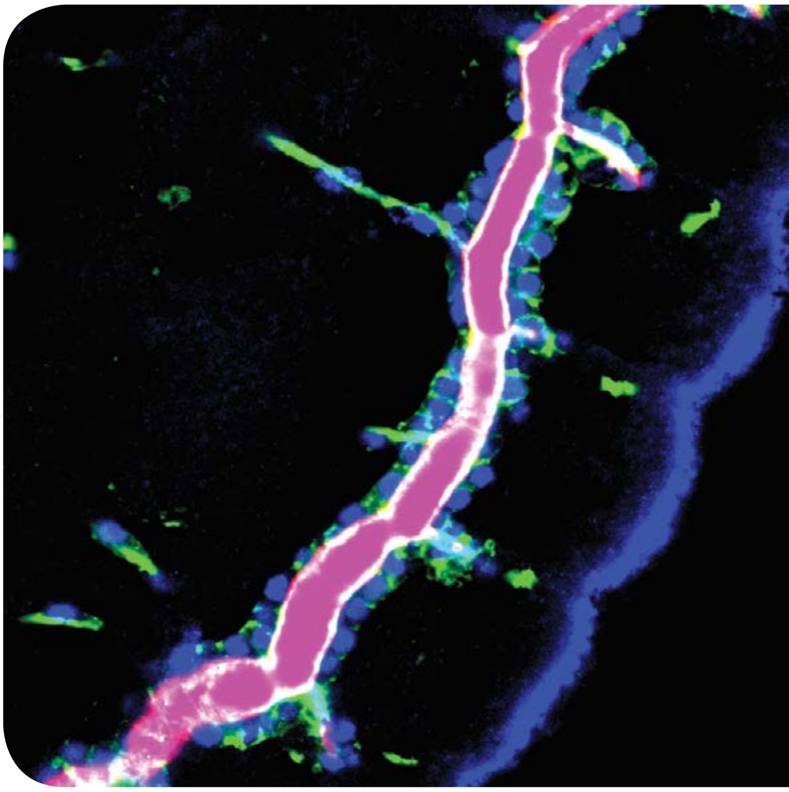
Generous N, Fairchild G, Deshpande A, Del Valle SY, Priedhorsky R (2014) Global Disease Monitoring and Forecasting with Wikipedia. PLoS Comput Biol 10(11): e1003892. doi:10.1371/journal.pcbi.1003892
Chennu S, Finoia P, Kamau E, Allanson J, Williams GB, Monti MM, et al. (2014) Spectral Signatures of Reorganised Brain Networks in Disorders of Consciousness. PLoS Comput Biol 10(10): e1003887. doi:10.1371/journal.pcbi.1003887

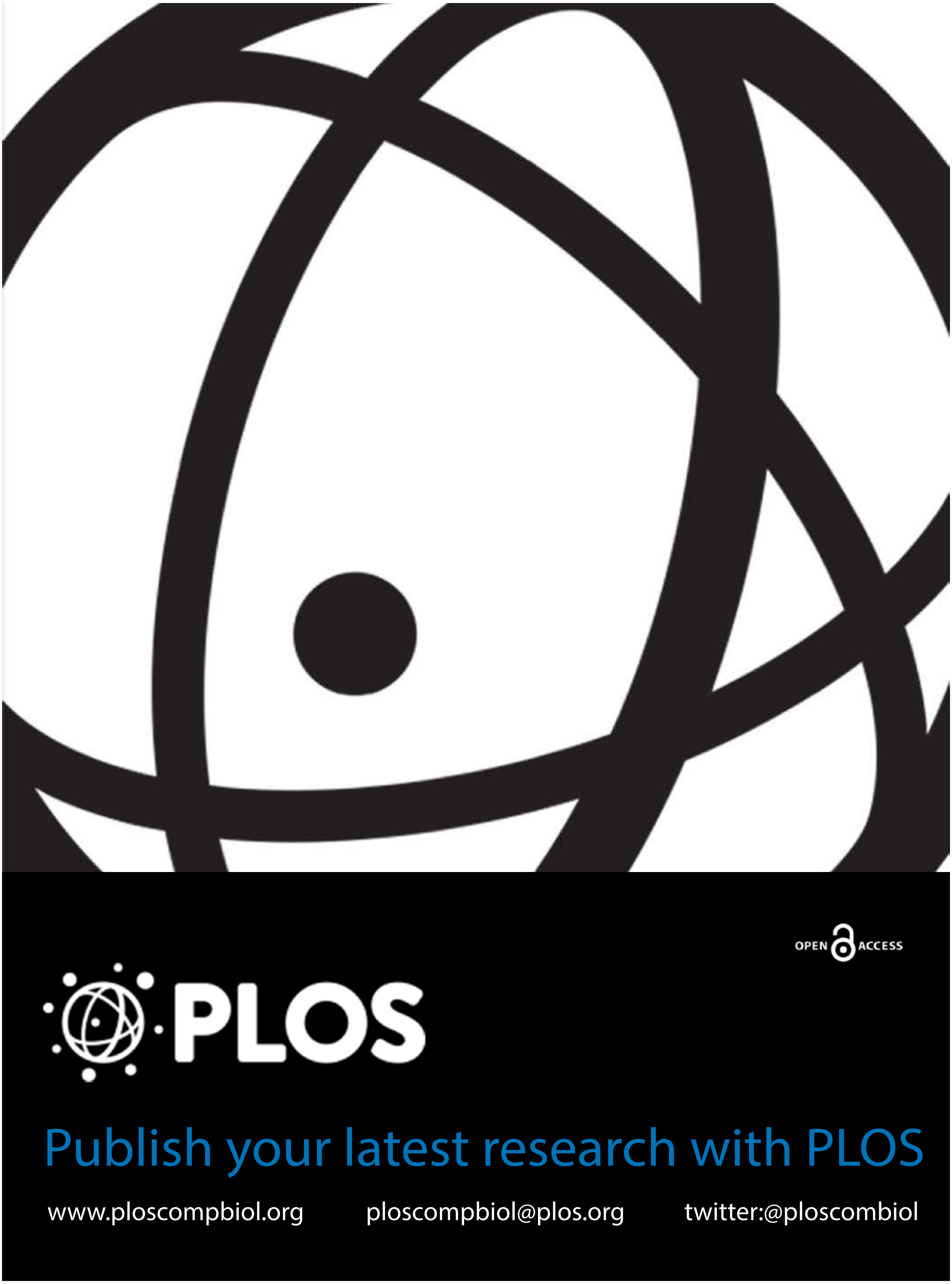
Cadieu CF, Hong H, Yamins DLK, Pinto N, Ardila D, Solomon EA, et al. (2014) Deep Neural Networks Rival the Representation of Primate IT Cortex for Core Visual Object Recognition. PLoS Comput Biol 10(12): e1003963. doi:10.1371/journal.pcbi.1003963

References

1. Karp PD, Berger B, Kovats D, Lengauer T, Linial M, Sabeti P, et al. (2015) ISCB Ebola Award for Important Future Research on the Computational Biology of Ebola Virus. PLoS Comput Biol 11(1): e1004087. doi:10.1371/journal.pcbi.1004087
2. de Ridder J, Meysman P, Oluwagbemi O, Abeel T (2014) Soft Skills: An Important Asset Acquired from Organizing Regional Student Group Activities. PLoS Comput Biol 10(7): e1003708. doi:10.1371/journal.pcbi.1003708
3. Roberts RJ (2015) Ten Simple Rules to Win a Nobel Prize. PLoS Comput Biol 11(4): e1004084. doi:10.1371/journal.pcbi.1004084
4. Ravenhall M, Škunca N, Lassalle F, Dessimoz C (2015) Inferring Horizontal Gene Transfer. PLoS Comput Biol 11(5): e1004095. doi:10.1371/journal.pcbi.1004095
5. (2015) PLOS Computational Biology 2014 Reviewer Thank You. PLoS Comput Biol 11(2): e1004184. doi:10.1371/journal.pcbi.1004184







PLOS Computational Biology Celebrates its First Decade

By Christiana N. Fogg, PhD, Freelance Science Writer, Kensington, Maryland, USA

The first issue of PLOS Computational Biology was published in June 2005 at a time when the computational biology community sought a "home for important biological research driven by computation." PLOS Computational Biology is an official journal of ISCB and has become a well-respected publication for scientists applying computation across diverse fields of biology. PLOS Computational Biology has also become more widely appreciated by scientists in all fields for its unique article collections, particularly, the "Ten Simple Rules" series launched by founding Editor-in-Chief Phil Bourne.

The July 2015 issue of PLOS Computational Biology features several articles commemorating the first ten years of the journal's publication. An article titled, "Computational Biology: Moving into the Future One Click at a Time," includes perspectives by Phil Bourne, Win Hide, Janet Kelso, Scott Markel, Ruth Nussinov, and Janet Thornton. These scientists share their memories of the heady beginnings of computational biology and their thoughts on the field's promising and provocative future. They touch on several themes familiar to the computational biology community, including, the transformation of biology from hypothetical modeling to a data-driven science, the need for collaboration between computational and experimental biologists, the greater public awareness of computational biology (e.g., personalized genomics and precision medicine), and the challenges in dealing with the storage, organization, and appropriate use of the vast amounts of biological data being generated every day.

[1] Bourne PE, Brenner SE, Eisen MB (2005) PLoS Computational Biology: A New Community Journal. PLoS Comput Biol $^{1(1)}$: e4. doi:10.1371/journal.pcbi.0010004 (accessed June 5, 2015).

F1000Research to publish new ISCB Community Journal online

By Diane Kovats

The journal will provide dedicated channel for select ISCB conference research

The International Society for Computational Biology (ISCB) and F1000Research are pleased to announce the formation of an innovative partnership to produce the ISCB Community Journal - a new, dedicated, digital channel on the F1000Research publishing platform.

The ISCB Community Journal will be launched on F1000Research this summer to provide the ISCB's growing membership and conference attendees with an affordable, open publishing platform for all research presented at many official and affiliated ISCB conferences.

Scientists who belong to the ISCB's Communities of Special Interest (COSIs) or who attend its Special Interest Group (SIG) meetings will also be able to take advantage of the new channel.

The initiative will enable ISCB to support the publication of all research in a range of formats in one centralized channel for the first time. Articles based upon the research presented at many official and affiliated conferences will be published using F1000Research's immediate publication and transparent peer review model, without limitation on article size, type, or perceived impact.

Most ISCB conference attendees will also be able to share and publish all the academic posters and slides that are presented at each conference and host them in one easily searchable domain.

Diane E. Kovats, Executive Director, ISCB, said: "F1000Research's platform offers a viable alternative to traditional scholarly society journals."

"A lot of high-quality and valuable science that is shared at conferences, including posters and slide presentations, never gets published, and essentially becomes 'lost' research. In the digital age, it should be possible to share all the science presented at conferences quickly and easily."

Michael Markie, Associate Publisher of F1000Research, said: "There is always a treasure chest of research that is presented at academic conferences that never sees the light of day. This research often contains early findings, in order to obtain feedback or to identify potential collaborators. All this research takes significant time, effort and cost, but may be viewed by only a small number of conference participants before the work disappears. This represents a huge waste of funding and researcher time, leads to studies being needlessly repeated, and slows scientific progress."

Rebecca Lawrence, Managing Director of F1000Research, said: "We are delighted to be collaborating with the ISCB on creating and publishing their innovative ISCB Community Journal. F1000 and the ISCB have always shared closely aligned goals in wanting to find ways to enable the rapid dissemination of all types of research outputs. It is particularly fitting that our first society channel is with the ISCB."

For more information on the ISCB Community Journal, read the F1000Research blog http://blog.f1000research.com/2015/04/30/f1000research-to-publish-the-iscb-community-journal

Report on the ISCB Africa ASBCB Conference on Bioinformatics 2015

By Nicola Mulder, Ph.D.

We received funding from H3ABioNet to support travel fellowships for African students to attend the fifth ASBCB Bioinformatics conference in Africa, which is the fourth ISCB Africa ASBCB Conference on Bioinformatics in conjunction with ISCB. The conference was held at the White Sands Hotel in Dar es Salaam, Tanzania from the 9th-11th March 2015 (http://www.iscb.org/iscbafrica2015). It was preceded by a Student Symposium organised by the ISCB and ASBCB Student Councils and attended by students and junior academics. Two days of workshops, one on "Exploring variation data and variation annotation" and the other on "Genomic data visualization", were held at the University of Dar es Salaam following the conference.

The Bioinformatics conference ran over 3 days and included five excellent keynote presentations from top researchers in their field: Matthew Berrimann, Michele Ramsay, Michal Linial, Tom Gilbert and Roderic Guigo. Sessions were divided into the following topics with a total of 30 accepted oral presentations:

- Host/pathogen systems biology
- Bioinformatics of human genetics
- Molecular epidemiology and evolution
- Functional, structural and comparative genomics
- Database and resource development
- Search and design of vaccines and drugs

The audience agreed that the peer reviewed and keynote talks were of high quality, and we were particularly encouraged the see the majority of presentations coming from African scientists and students. Two poster sessions saw the presentation of >50 posters, again, predominantly from African laboratories. The program included ASBCB and ISCB Society business meetings, where participants discussed new ideas for "Twitter parties" and how to encourage participation in international conferences.

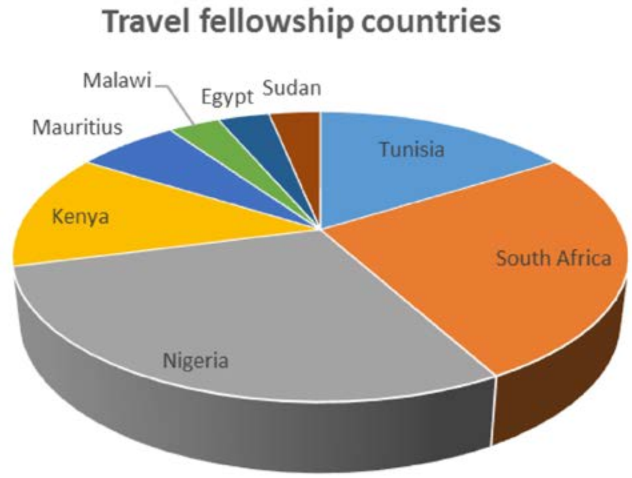


Figure 1. Country distribution of all travel fellowship recipients.

The Conference was attended by ~80 scientists from around the world, with the majority coming from Africa. There were many opportunities for networking and African scientists and students interacted with those who came from Europe and the USA. Through generous sponsorship from the Wellcome Trust and H3ABioNet, we were able to offer a total of 31 full or partial travel fellowships for African students to attend the conference and workshops. Figure 1 shows the distribution of countries of travel fellowship recipients, who are pictured in figure 2. Fifteen of these travel fellowships came specifically from H3ABioNet funding.

H3ABioNet funding enabled us to offer 15 partial or full travel fellowships to students or junior academics who would not otherwise have been able to attend. Table 1 lists the H3ABioNet travel fellowship, some of the recipients have expressed their appreciation below:

"I would like to thank H3ABioNet for the travel fellowship. The travel fellowship provided me with a very rare opportunity to attend an international bioinformatics conference, where high quality cutting edge science was discussed. It also provided an excellent opportunity to meet and network with other scientists from multiple research fields. As a result, I have already actively started communicating and working with contacts/collaborators I met at the ISCB-ASBCB conference. Thanks for this wonderful opportunity."
Benard Kulohoma

"I wish to thank H3ABioNet for funding my trip to the ISCB-Africa. Being from a computing background, I normally have trouble in understanding the bioinformatics requirements of researchers from life Science. Also, at

the University of Mauritius I have little chance to interact with people who are very active in Bioinformatics research. This conference gave me the chance to interact with high-profile researchers in the field. I also had the opportunity to meet people in the field of life science and I have realized that there is a lot yet to be done in terms of bioinformatics tools and research. Also the keynote speeches were really inspiring and motivating. If I did not attend the ISCB-Africa I would never have had the chance to meet such high-profile people. I have also had the chance to do networking and hopefully I can start doing some collaborative work with researchers whom I met at ISCB-Africa. Hence again, I am really thankful to H3ABioNet for this opportunity."
Shakuntala Baichoo

"I thank you for everything you did for us to be able to come to this conference. It was a wonderful experience to meet all these people, hear them and discuss with them. I have made good contacts that I will use for my future works."
Kevin Persand

"I want to thank you and the funders of the travel fellowship of the ISCB Africa ASBCB Conference on Bioinformatics 2015. Tanzania is an amazing country and the conference venue was the ideal scenario to share ideas between peers and to create alliances and future collaborations with researchers from Africa and abroad. The quality of the presentations (oral and poster) was really high and the key notes were incredibly motivating. I really appreciate the opportunity. Thanks."
Gustavo Salazar

"Thank you H3ABioNet for granting me the opportunity to share my project with fellow researchers. Indeed it was a wonderful experience, the feedback that i got from some expects in the field will assist me greatly to finalize and complete my project. It was also a good networking platform and my first time in Dar es Salaam and I thank H3ABioNet for it all."
Darlington Mapiye

"I would like to thank them for helping us to attend this conference. It's very necessary for a student like us to attend such meeting. We listened to comments about our work and suggestions to improve it. And like wise we shared our thoughts about others' work. It was a wonderful event for networking. Thanks a lot indeed for the travel fellowship."
Rehab Ahmed

"I want to acknowledge H3ABioNet for funding my trip, hotel accommodation and conference attendance to Da es Salam, Tanzania in order to expand my scope in the field of Bioinformatics. You have enabled me through your funding to interact and gain better knowledge in my research work. Thanks"
Jumoke Soyemi

"As my part, the conference was really perfect (the venue, the program and the presentations were excellent). Being in the first year PhD, all this is new to me. I really learned many things during the last week that are important for a researcher and it was a memorable experience that I would like to relive. In this context, I would like to take this opportunity to thank H3ABioNet for giving me the chance to attend ISCB Africa ASBCB Conference on Bioinformatics 2015 and for allowing me to live this experience. Thanks to H3ABioNet for his continuous support, I'll never forget that I was trained, became

bioinformatician and my university research career does not stop to change for the better in the frame of this project. I'm so proud to be a part of H3ABioNet project."
Cherif Ben Hamda

"I am writing this letter to express my gratitude for you and for the funders of the project H3ABioNet for their consideration in supporting my work to be presented at the ISCB ASBCB 2015 Conference. I believe that my work can be useful for many people present on this conference from Africa, and you have given me the opportunity to introduce it for them. Your perspective and encouragement mean a lot to me. Thank you for all that you've done."
Mohamed Alibi

List of H3ABioNet travel fellowship recipients and their country of origin

First Name	Last Name	Affiliation	City	Country
Oussema	Souiai	Institut Pasteur de Tunis	Tunis	Tunisia
Darlington	Mapiye	University of the western cape	Cape town	South Africa
Benard	Kulohoma	International Centre for Insect Physiology and Ecology	Nairobi	Kenya
Gustavo	Salazar	University of Cape Town	Cape Town	South Africa
Kevin	Persand	University of Mauritius	Moka	Mauritius
Rosaline	Macharia	International Center of Insect Physiology and Ecology	Nairobi	Kenya
Amel	Ghouila	Institut Pasteur de Tunis	Tunis	Tunisia
Cherif	Ben Hamda	Institut pasteur de tunis	Tunis	Tunisia
Mohamed	Alibi	Institut Pasteur de Tunis	Tunis	Tunisia
Mohamed	Issa	Univesity of Zagazig	Zagazig	Egypt
Benjamin	Kumwenda	Malawi Liverpool Wellcome Trust/University of Malawi	Blantyre	Malawi
Rehab	Ahmed	Center for bioinformatics- Sudan.	Khartoum	Sudan
Trust	Odia	Covenant University	Nigeria	Nigeria
Jumoke	Soyemi	Covenant University	Ota	Nigeria
Shakuntala	Baichoo	University of Mauritius	Reduit	Mauritius

ISCBtv

Science at the Click of the Mouse

Our hectic schedules and lives don't always allow our members to attend the many conferences and workshops that are offered by ISCB. We know how important it is to stay up with the latest research happening in the field. As an ISCB member, you have exclusive access to ISCBtv, your science at a click of the mouse.
From the comfort of your office, home, or airport waiting area, you can enjoy the hundreds of recorded talks from ISCB official meetings.

Check it out by clicking on ISCBtv at www.iscb.org.

In Memoriam: John Wooley

By Terry Gaasterland, PhD, Director, Scripps Genome Center & Philip E. Bourne, Ph.D., FACMI, Associate Director for Data Science (ADDS)

Dr. John Wooley, the long-time associate vice chancellor for research and professor of pharmacology at the University of California, San Diego, passed away in April after a long battle with cancer. Through decades spent launching new initiatives in computational biology that pushed forward discoveries, innovation, and national programs in genomics, protein structure, crystallography, and systems biology, Dr. Wooley shaped policy at the U.S. National Science Foundation and U.S. Department of Energy to pave the way for massive growth and transformation in the field of computational biology.

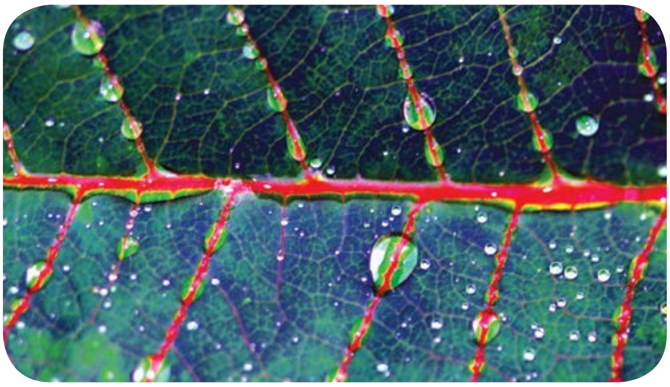
"John was a visionary seeing some 35 years ago the necessity of integrating two of the greatest revolutions of the end of the 20th century and the beginning of the 21st century: that of computing and computer science on the one hand, and biological sciences on the other," recalled longtime colleague Peter Arzberger, now Senior Advisor for Research Cyberinfrastructure at NSF. "As we consider the current biomedical research challenges, we need to look 10 to 20 years into the future, very much as John would have."

Wooley earned his Ph.D. in biophysics from the University of Chicago, working with Albert Crewe to build the first high-resolution, scanning-transmission electron microscope and to study the higher-order structure of the genetic material inside of cells. He had received his bachelor's degree in physics, chemistry and biochemistry from Michigan State University. In 1984, he left a professorship at Princeton to become a program officer at the National Science Foundation (NSF) to take up the challenge of building modern computational biology. While there, he was involved in developing a series of programs for the federal government, from collaborating on the first stages of the genome project to establishing the first federal programs in bioinformatics and in computational biology.

"John Wooley was an inspiration to me and to our community. His vision saw the potential impact of integrating computer science and biology as we entered the 21st Century. Both fields were transforming as new technologies made possible new types of observations at massive scales. Not only did he shape the direction of the field, but he shaped individuals through his mentorship and unflagging optimism. I had great luck to benefit directly from his guidance and leadership during my early years as a post-doctoral Fellow at the Department of Energy and on through my time as a professor in the Bioinformatics & Systems Biology program at UC San Diego. John will be missed by many," said Terry Gaasterland, Director of the Scripps Genome Center at the Scripps Institution of Oceanography and Professor in the Bioinformatics & Systems Biology program at UC San Diego.

In 1988 he became the founding director of NSF's new Division of Infrastructure and Resources (now called the Division of Biological Infrastructure). In that capacity, Wooley managed interdisciplinary biology research infrastructure and training programs funded by the NSF.

At a joint NSF meeting of the advisory committees for both Cyberinfrastructure and for Biological Sciences just days after John Wooley's passing, members remembered his fundamental contributions as a strong advocate for building the interface between all areas of biology and computing broadly. As Arzberger recalls, when Wooley went to the NSF, it was prior to the creation of NSF super-computing centers to serve all disciplines.



Wooley also helped create new NSF programs to grow a community of biologists, computer scientists, and mathematicians that focused on building algorithms, tools, software and databases used by the biological science communities, across all of biology, from structural biology and neuroscience to the ecological sciences. One resource tracing its funding back to these programs is the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (PDB).

As he was ending his eight years at NSF, Wooley co-edited a seminal workshop report, "Computational Biology: An Overview" (1992). In 1994, Wooley joined the Department of Energy as chief of staff and deputy associate director in its Office of Science. He was responsible for biological and environmental sciences, overseeing biotechnology, molecular and cellular biology, the health effects of radiation and energy production, molecular nuclear medicine, and climate change research. Wooley also coordinated major aspects of the human genome project, including bioinformatics, and led efforts in developing programs for microbial genomes and computational structural biology.

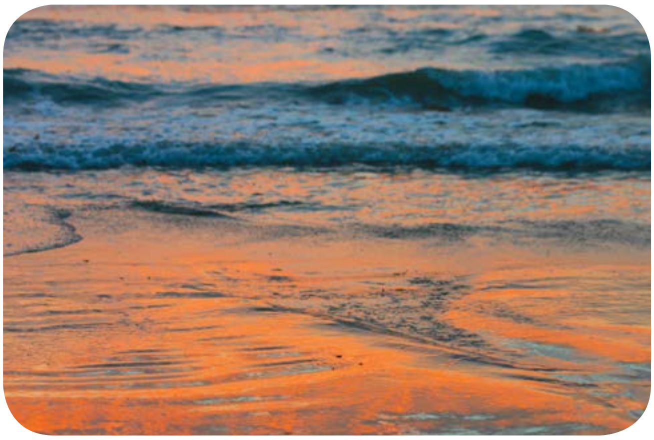
Shortly after he arrived at UC San Diego, Wooley would also be closely affiliated with the effort to win a state competition to create what became the California Institute for Telecommunications and Information Technology (Calit2), whose founding director Larry Smarr had worked closely with Wooley at NCSA. Wooley helped draft portions of the proposal to make biological sciences one of the primary 'layers' for early adoption of new information technologies, naming the two-campus (UCSD/UCI) Calit2 initiative "Digitally Enabled Genomic Medicine."

He was also active and instrumental in several new efforts based at UC San Diego, including the:

- Joint Center for Structural Genomics (JCSG), where, as co-PI, he served as director of the center's Bioinformatics Core;
- xxRCN for Genomic and Metagenomic Standards; the Interoperable Information Infrastructure for Biodiversity Research (I3BR); and others.

In his final weeks, Wooley was confined to a hospital room, but enjoyed being able to log in to walk through a virtual tour of his landscape and flower photographs, secure in the knowledge that his photographs would outlive him, as would the community of experts in computational biology and bioinformatics that did not exist 30 years ago when he joined NSF.

"John gave me my first grant while he was at the NSF. It was the early 90's and the first grant between a biomedical researcher and a computer scientist at Columbia University. What was remarkable was that John gave us more money than we asked for. Many grants later, that has never happened to me again. That was the kind of person John was; breaking rules and tradition to do what he believed in. In that case it was to explore the use of object-oriented database technologies for answering new types of questions of the rapidly growing corpus of macromolecular structure data. What we learnt from that grant ultimately fed into our work on the RCSB Protein Data Bank (PDB) from which many others were to make landmark discoveries in structural biology and bioinformatics. John saw that coming – that was his strength – seeing the future as if it were today. I was thrilled when John joined us at UCSD and he was instrumental, along with Palmer Taylor, in my securing a tenured professorship in the new School of Pharmacy and Pharmaceutical Sciences even before one brick was laid for the building to house the School. I would periodically visit John in his office and be amazed at his command of what was hot (and what was not) in the ever growing field of computational biology. He kept up this encyclopedic knowledge even as his health fluctuated. Frail on the outside there was enormous strength within; a strength which I and many others gained from. Our young field has lost a pioneer to whom we all owe a great debt." Philip E. Bourne, Ph.D., FACMI



John is survived by his wife Su Chung and their son David, both living in La Jolla.

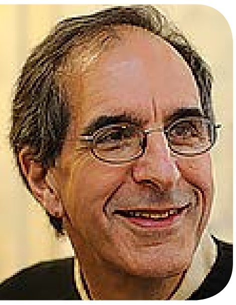
**Credit to CalUTech

Meet the ISCB Fellows Class of 2015

The International Society for Computational Biology (ISCB) confers Fellow status to ISCB members that have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics.

The ISCB Fellows program began in 2009, and 43 members have been conferred with this status to date. Potential Fellows are identified through a call for nominations to the ISCB membership and are chosen by the Fellows Selection committee. Eight fellows have been selected for the 2015 Fellows class, and they will be introduced at the ISMB/ECCB meeting in Dublin, Ireland in July 2015.

Rolf Apweiler Joint Associate Director and Senior Scientist at European Bioinformatics Institute (EBI) of the European Molecular Biology Laboratory (EMBL) in the United Kingdom. Apweiler received his PhD from the University of Heidelberg and has been at EMBL since 1987. He has made many contributions to the field of proteomics, including work on methods for automating annotation of proteins, and development of proteomic data stands. Apweiler has also led the EMBL-EBI team that contributes to the UniProt Consortium. In 2015, Apweiler was appointed Joint Director of EMBL-EBI with Ewan Birnay, and they start in these positions officially on 1 July 2015.



Cyrus Chothia 2015 ISCB Accomplishment by a Senior Scientist Award Emeritus scientist at the Medical Research Council Laboratory of Molecular Biology (the LMB) and emeritus fellow at Wolfson College, University of Cambridge in the United Kingdom. Chothia completed his PhD at University College London and spent much of his career at the LMB. His research has examined key factors that define the structure and function of proteins, particularly how changes in amino acids sequences impact structure. Chothia has contributed to the development of several databases, including SCOP, which includes all protein structures from the Protein Data Bank and their evolutionary relationships, and SUPERFAMILY, a database that includes a structural and functional annotation for proteins and genomes.

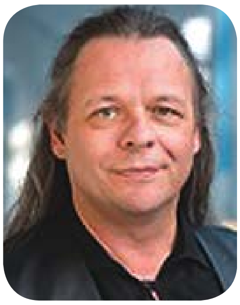
Julio Collado-Vides Professor and Head of the Program of Computational Genomics at the Center for Genomics Sciences, Universidad Nacional Autónoma de México (UNAM). Collado-Vides holds a PhD in biomathematics from the Universidad Nacional Autónoma de México. His research at UNAM is focused on using computational design, genomic prediction, and comparative and evolutionary analyses to understand the regulation of gene expression in bacteria. Collado-Vides has developed several bioinformatics tools, including RegulonDB, the primary database on transcriptional regulation in E. coli K-12.

Mark Gerstein Albert L. Williams Professor of Biomedical Informatics, Molecular Biophysics & Biochemistry, and Computer Science at Yale University in the United States. Gerstein completed his PhD in biophysics/chemistry at Cambridge University. His research uses bioinformatics-based approaches to explore several key areas of personal genomics, particularly in relation to how genomics changes lead to diseases like cancer. Gerstein had developed a diverse number of bioinformatics tools and resources that can analyze changes in protein and nucleic acid structure and investigate structural variations and copy number variations.

Desmond Higgins Professor of Bioinformatics at the School of Medicine & Medical Science, Conway Institute, University College Dublin in Ireland. Higgins completed his PhD at Trinity College Dublin and has spent his career developing bioinformatics tools and algorithms for sequence alignment and molecular evolution. He is one of the developers of the multiple sequence alignment programs Clustal and T-coffee, and his current research includes the analysis of high throughput genomics data, particularly by applying multivariate analysis methods for data integration.

Thomas Lengauer Professor and Director of the Max Planck Institute of Informatics in Saarbrucken, Germany. Lengauer received his PhD in computer science from Stanford University. His research interests include protein structure and function prediction, computational drug screening and design, and developing bioinformatics approaches to the diagnosis and treatment of diseases, including cancer and HIV.

Micheal Levitt Professor of Computational Structural Biology, and Robert W. and Vivian K. Cahill Professor in Cancer Research in the School of Medicine, and Professor (by courtesy) of Computer Science at Stanford University in the United States. Levitt received his PhD from the University of Cambridge. He was one of the earliest developers of computational approaches to study the structure and conformation of molecules. Levitt was awarded the 2013 Nobel Prize in Chemistry with Martin Karplus and Arieh Warshel "for the development of multiscale models for complex chemical systems." He continues to develop computational approaches to predict macromolecular structures and has developed a statistical framework for sequence comparison and structure comparison.

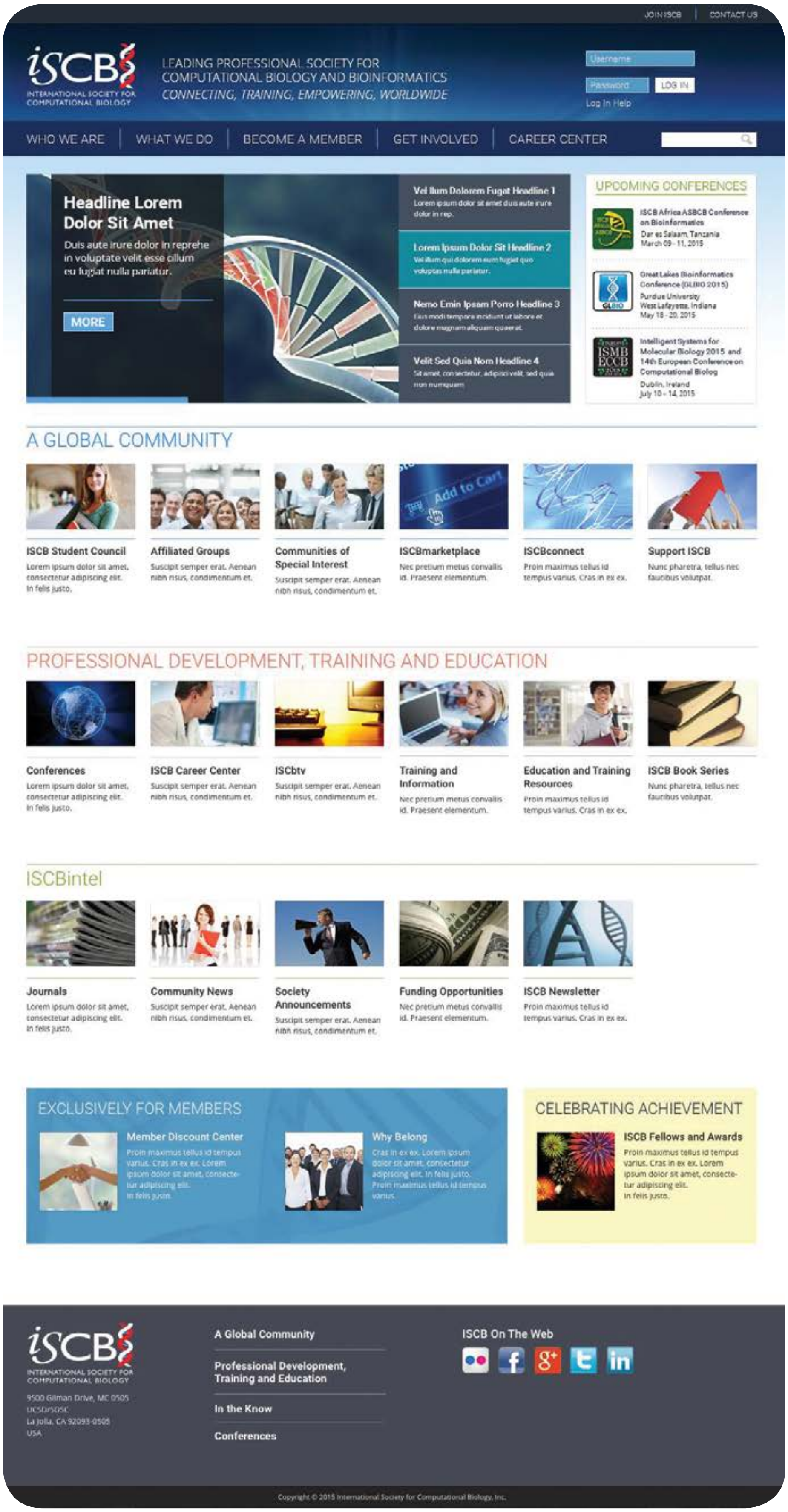


Burkhard Rost Professor and head of Computational Biology & Bioinformatics at the Department of Informatics at the Technical University of Munich in Germany. Rost received his PhD from the University of Heidelberg. His research applies machine learning to biological data, including sequences and evolutionary information to make predictions about protein structure and function and gain novel insights into evolution. Rost recently completed an eight-year term as President of ISCB, during which he oversaw significant improvements to the Society, including growth in membership and the successful organization of several international computational biology conferences.

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

Tolga Can
Sujoy Ghosh
Emna Harigua
Jennifer Weller
Priscila Grynberg
Hrishikesh Deshmukh
Guilherme Oliveira
Jonathan Magasin
Francisco Melo
Daniel Vicarel
Juan Cifuentes
Karen Dowell
Deborah Chasman
Pierre Carrier
Jyothi Thimmapuram
Gabriel Wajnberg
Ezequiel Juritz
Drena Dobbs
Sarah Mukolwe
Janos Binder
Jeffrey Fisk
John Nealon
Michael Bauer
Gustavo Stolovitzky
Jennifer Weller
Derek Aguiar
Conrad Halling
Yuri Ikeda
Karen Dowell
Marco Antoniotti
Konstantinos Papadimitriou
Hengwu Li
Jyothi Thimmapuram
Yaw Nti-Addae
Deborah Chasman
Oz Solomon
Janos Binder
Fiona Nielsen
Alex Slater
Stuart Ray
Marco Manca
Christof Winter
Andrew Warren
Ney Lemke
Diane Kovats
Gabriel Wajnberg
Gloria Franco
Samson Adeyemi
Terence Speed
Yingqian Zhan
Clare Sansom
Fernanda Costa
Nancy Mah
Prashanth Suravajhala
Hector Garcia Martin
Yayoi Natsume-Kitatani
Bonnie Berger
Lothar Richter
Junfang Chen
Olga Botvinnik
Jesus Galaz-Montoya
Robert Edwards
Tsung Fei Khang
Kirk DeLisle
Philip Bourne
Ronald Tepper
Judith Blake
Kirk Jordan

Check out the new face of ISCB at the ISCB Exhibit Booth!



LEADING PROFESSIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY AND BIOINFORMATICS
CONNECTING, TRAINING, EMPOWERING, WORLDWIDE

Headline Lorem Dolor Sit Amet

Duis aute irure dolor in reprehe in voluptate velit esse cillum eu fugiat nulla pariatur.

Vel Ilum Dolorem Fugat Headline 1
Lorem ipsum dolor sit amet duis aute irure dolor in rep.

Lorem Ipsum Dolor Sit Headline 2
Vel illum qui dolorem eum fugiat quo voluptas nulla pariatur.

Nemo Emin Ipsam Porro Headline 3
Eius modi tempora incidunt ut labore et dolore magnam aliquam quaerat.

Velit Sed Quia Nom Headline 4
Sit amet, consectetur, adipisci velit, sed quia non numquam

UPCOMING CONFERENCES

ISCB Africa ASBCB Conference on Bioinformatics
Dar es Salaam, Tanzania
March 09 - 11, 2015

Great Lakes Bioinformatics Conference (GLBIO 2015)
Purdue University
West Lafayette, Indiana
May 18 - 20, 2015

Intelligent Systems for Molecular Biology 2015 and 14th European Conference on Computational Biolog
Dublin, Ireland
July 10 - 14, 2015

A GLOBAL COMMUNITY

ISCB Student Council
Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo.

Affiliated Groups
Suscipit semper erat. Aenean nibh risus, condimentum et.

Communities of Special Interest
Suscipit semper erat. Aenean nibh risus, condimentum et.

ISCBmarketplace
Nec pretium metus convallis id. Praesent elementum.

ISCBconnect
Proin maximus tellus id tempus varius. Cras in ex ex.

Support ISCB
Nunc pharetra, tellus nec faucibus volutpat.

PROFESSIONAL DEVELOPMENT, TRAINING AND EDUCATION

Conferences
Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo.

ISCB Career Center
Suscipit semper erat. Aenean nibh risus, condimentum et.

ISCbtv
Suscipit semper erat. Aenean nibh risus, condimentum et.

Training and Information
Nec pretium metus convallis id. Praesent elementum.

Education and Training Resources
Proin maximus tellus id tempus varius. Cras in ex ex.

ISCB Book Series
Nunc pharetra, tellus nec faucibus volutpat.

ISCBintel

Journals
Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo.

Community News
Suscipit semper erat. Aenean nibh risus, condimentum et.

Society Announcements
Suscipit semper erat. Aenean nibh risus, condimentum et.

Funding Opportunities
Nec pretium metus convallis id. Praesent elementum.

ISCB Newsletter
Proin maximus tellus id tempus varius. Cras in ex ex.

EXCLUSIVELY FOR MEMBERS

Member Discount Center
Proin maximus tellus id tempus varius. Cras in ex ex. Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo.

Why Belong
Cras in ex ex. Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo. Proin maximus tellus id tempus varius.

CELEBRATING ACHIEVEMENT

ISCB Fellows and Awards
Proin maximus tellus id tempus varius. Cras in ex ex. Lorem ipsum dolor sit amet, consectetur adipiscing elit. In felis justo.

9500 Gilman Drive, MC 0505
UCSD/SDSC
La Jolla, CA 92093-0505
USA

A Global Community
Professional Development, Training and Education
In the Know
Conferences

ISCB On The Web

Copyright © 2015 International Society for Computational Biology, Inc.

Mark Your Calendars for ISMB 2016!

Meet Your ISCB Board of Directors

Executive Officers

Alfonso Valencia, Ph.D.
President, ISCB
Spanish National Cancer Research Centre (CNIO)
SPAIN

Burkhard Rost, Ph.D.
Past-President, ISCB
Technical University Munich
GERMANY

Bonnie Berger, Ph.D.
Vice President, ISCB
Mathematics/EECS
USA

Terry Gaasterland, Ph.D.
Vice President, ISCB
University of California, San Diego
USA

Thomas Lengauer, Ph.D.
Vice President, ISCB
Max Planck Institute for Informatics
GERMANY

Christine Orengo, Ph.D.
Vice President, ISCB
University College London
UNITED KINGDOM

Reinhard Schneider, Ph.D.
Treasurer, ISCB
Luxembourg Centre for Systems Biomedicine (LCSB)
LUXEMBOURG

Scott Markel, Ph.D.
Secretary, ISCB
Dassault Systèmes BIOVIA
USA

Board Members

Teresa Attwood, Ph.D.
Professor of Bioinformatics
Faculty of Life Sciences & School of Computer Science
United Kingdom

Alex Bateman, Ph.D.
Informatics
European Bioinformatics Institute
United Kingdom

Judith A. Blake, Ph.D.
Professor
Bioinformatics and Computational Biology
USA

Alan Christoffels, Ph.D.
DST/NRF Research Chair in Bioinformatics and Health Genomics
South African National Bioinformatics Institute
South Africa

Manuel Corpas, Ph.D.
Plant and Animal Genomes Project Leader
The Genome Analysis Centre
United Kingdom

Bruno Gaeta, Ph.D.
Senior Lecturer
Bioinformatics Program Director
Australia

Paul Horton, Ph.D.
Affiliates Committee Representative
Stuckey Professor
Japan

Anupama Jigisha, Graduate Student
Student Council Representative to the ISCB Board of Directors
University College Dublin
Ireland

Janet Kelso, Ph.D.
Bioinformatics Group Leader
Evolutionary Genetics
Germany

Richard H. Lathrop, Ph.D.
Professor, Computer Science
Dept. of Computer Science
USA

Fran Lewitter, Ph.D.
Director, Bioinformatics and Research Computing
Whitehead Institute
USA

Michal Linial, Ph.D.
Professor of Biochemistry
Department of Biological Chemistry
Israel

Francisco Melo Ledermann, Ph.D.
Associate Professor and Director of Innovation
Faculty of Biological Sciences
Chile

Jill P. Mesirov, Ph.D.
Associate Director and Chief Informatics Officer
Director, Computational Biology and Bioinformatics
USA

Nicola Mulder, Ph.D.
Associate Professor
Head of Computational Biology Group and H3ABioNet
South Africa

Predrag Radivojac, Ph.D.
Associate Professor
Informatics and Computing
USA

Anna Tramontano, Ph.D.
Professor
Department of Biochemical Sciences " Rossi Fanelli"
Italy

Olga Troyanskaya, Ph.D.
Assistant Professor
Department of Computer Science & Lewis-Sigler Institute for Integrative Genomics
USA

Lonnie R. Welch, Ph.D.
School of Electrical Engineering and Computer Science
Ohio University
USA

EX OFFICIO DIRECTORS DETAILS

Martin Vingron, Ph.D.
Director at Max Planck Institute for Molecular Genetics, Computational Molecular Biology
Germany

NEW ISCB AWARD!

ISCB's annual awards are the most prestigious international awards designated exclusively to researchers in the field of computational biology/bioinformatics. In addition to the Senior Scientist, Overton Prize, and Outstanding Contribution to ISCB Awards, ISCB is pleased to announce a new annual award, the "Mid-Career" Award.

This award is in recognition of leading scientists who are within two decades post-degree and have consistently made outstanding contributions over time.

Nominations from all regions of the world are encouraged, and the selection of award winners will be selected by the ISCB's awards committee, which is chaired by Dr. Bonnie Berger of the Massachusetts Institute of Technology (MIT). Nominations are due by December 2nd, 2015. The nomination form, as well as a link to the full policies and procedures of ISCB awards, can all be accessed at http://www.iscb.org/iscb-awards.

Please join in nominating members of our community who have who have consistently made outstanding contributions over time, and then proceed to the nomination form to ensure they are considered for this prestigious award.

ECCB 2016
The Hague
September 3-7

15th European Conference on Computational Biology

3-7 September 2016
The Hague, The Netherlands

The Springer-ISCB Computational Biology book series is…SEEKING BOOK PROPOSALS-!!

Sponsored by the International Society for Computational Biology, the Computational Biology series publishes the very latest, high-quality research devoted to specific issues in computer-assisted analysis of biological data. The main emphasis is on current scientific developments and innovative techniques in computational biology (bioinformatics), bringing to light methods from mathematics, statistics and computer science that directly address biological problems currently under investigation.

The series offers publications that present the state-of-the-art regarding the problems in question; show computational biology/bioinformatics methods at work; and finally discuss anticipated demands regarding developments in future methodology. Titles can range from focused monographs, to undergraduate and graduate textbooks, and professional text/reference works. Springer is seeking to publish quality books in the areas including, but not limited to:

- Databases, Data Analysis and Ontologies
Series Editors-in-Chief:
- Functional and Comparative Genomics
* Andreas Dress (CAS-MPG
- Gene Regulation and Transcriptomics
Partner Institute for
- Protein Interactions and Networks
Computational Biology,
- Data, Literature and Text Mining China)
- Molecular Sequence Analysis
* Michal Linial (Hebrew University
- Biological Networks of Jerusalem, Israel)
- Sequencing and Genotyping Technologies
* Olga Troyanskaya (Princeton
- Population Genetics University, USA)
- Systems Biology
* Martin Vingron (Max Planck
- Imaging and Visualization Institute for Molecular
- Computational Proteomics Genetics, Germany)
- Molecular Structural Biology
- Evolution and Phylogenetics
- Metagenomics
- Biomedical Applications
- High Performance Bio-Computing
- Synthetic Biological Systems
==============================
Please contact Wayne Wheeler, Senior Editor for Computer Science at Springer: wayne.wheeler@springer.com

Planning Continues for NSF Big Data Regional Innovation Hubs

By Bethany Drehman, PhD, Office of Public Affairs, FASEB

Recognizing the value of broad collaboration in the data sciences, the National Science Foundation (NSF) is developing several Big Data Regional Innovation Hubs to facilitate new partnerships. Progress continued in May 2015 with a series of regional planning meetings. These charrettes convened stakeholders from business, non-profit, academic, and government institutions in each of four regions of the country for one-day planning and brainstorming workshops.

During the May workshops, NSF staff shared information about the goals and structure of the proposed Hubs network. They explained that Hubs were intended to facilitate new collaborations, but not directly fund research or its infrastructure. Projects developed through Hubs would need to seek external funding from separate sources, including other NSF grant programs. Possible Hub activities suggested at the charrettes include the creation of topical meetings and workshops to bring together diverse groups of researchers and other stakeholders as well as the development of resources, such as directories, to provide additional opportunities to identify potential partners, projects, and funding sources.

Each Hub will be led by a Steering Council of volunteers representing different stakeholder groups, with executive staff overseeing day-to-day operations. The Hubs will focus on self-selected priority areas of regional importance, termed "spokes," with "nodes" representing the actual partnerships within a priority area. The spoke topics are expected to change as the Hubs evolve and new research areas emerge. NSF also plans to develop a national network across Hubs to share and extend the reach of successful projects, as suggested in comments submitted (https://www.faseb.org/Portals/2/PDFs/opa/2014/11.4.14%20FASEB%20comments%20on%20Accelerating%20the%20Big%20Data%20Innovation%20Ecosystem.pdf) by the Federation of American Societies for Experimental Biology (FASEB).

NSF will award one Hub grant per region. After nine to ten years, NSF expects the Hubs to become independent non-profit organizations that secure funding through other mechanisms. Currently, individuals and institutions are collaboratively developing applications, which are due by June 24, 2015.

Those interested in becoming more involved with the Hubs should visit https://bdhub.info/ to join in the discussion. FASEB will continue to monitor the development of this new program and encourage the inclusion of scientific societies in Hub activities.

INVEST IN YOU AND YOUR FIELD – BECOME AN ISCB MEMBER TODAY!

ISCB Members enjoy:

DISCOUNTS

Take advantage of ISCB member discounts and attend just one official ISCB meeting, and your membership pays for itself!

- Up to $175 savings on ISCB Official Conferences, and at least 10% on affiliated conferences
- 25% or more savings on Journal Subscriptions
- Up to 25% savings on books published by Springer, CRC Press and Cambridge University Press
- $200 savings on publications in the *ISCB Community Journal*

ISCB CAREER CENTER

Looking for your first position, exploring a career change or need to hire someone within the field? The career center offers members

- Complimentary Job Postings (valued at $275)
- Unlimited access to the ISCB Resume Repository
- An opportunity to Upload Your Resume (a $75 annual saving)
- YOU@iscb.org email address

CONNECTIONS TO COMMUNITIES & SCIENCE AT YOUR FINGERTIPS

Connecting, collaborating, and training are the lifeblood of research. Members can

- Access the ISCB Member Directory
- Get training and science at the click of the mouse through ISCBtv – recordings of talks from official ISCB conferences
- Browse educational materials and curriculum development tools

LEADERSHIP, RECOGNITION, AWARDS & TRAVEL FUNDING

ISCB celebrates scientific achievement and supports the development of emerging researchers. Members are eligible for:

- ISCB Travel Fellowships, supporting travelto ISCB conferences, ECCB, PSB and RECOMB
- ISCB Awards
- The opportunity to become part of ISCB leadership, and influence the field by serving on committees, task forces and conference steering groups

Members who are 10 years beyond their postdoctoral fellowships may also take advantage of the Senior Member Designation.

OUR COLLECTIVE VOICE PROMOTES, REPRESENTS & ADVOCATES FOR SCIENCE

3,400 members strong, ISCB works diligently to promote the field of computational biology and bioinformatics by having an influential voice with governments and agencies responsible for scientific funding. Our partnership with FASEB strengthens our voice, allowing us to continue to push for better scientific research funding.

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

www.iscb.org/iscb-membership-benefits

News From ISCB Student Council

By Anupama Jigisha (SC Representative to the ISCB Board of Directors),
Alexander Junge (SC Vice Chair), Farzana Rahman (SC Secretary and ISCB Student Council Symposium Co-Chair, 2015),
Avinash Shanmugam (Former SC Representative to the ISCB Board of Directors)

The ISCB Student Council

The ISCB Student Council (SC), the student organization of the ISCB, is composed of students and young researchers that strive to promote the professional development of the next generation of computational biologists. We organize scientific events like the Student Council Symposiums, provide networking opportunities through our social events and career opportunities through soft skills workshop, facilitate internships and connect with student communities at the local level through our Regional Student Groups initiative. As an addition to our symposiums preceding ISMB and ECCB, the SC introduced African and Latin American editions of the Student Council Symposium in the past year. These events were organized in close collaboration with local Regional Student Groups and took place in Tanzania and Brazil, respectively.

You can read more about the SC at http://iscbsc.org/ or look us up on Facebook, LinkedIn, and Twitter. Of course, the best way to learn about the SC is to talk to our leaders. If you have a few minutes between sessions or if you are feeling lost in the crowd, stop by the ISCB Student Council booth (booth 25). We will show you how we are making a difference in the computational biology student community. In addition, we are always looking for volunteers that would like to become a part of our team. So come see us!

The ISCB Student Council Symposium 2015

The ISCB Student Council Symposium, our flagship event, is a congregation of students and young researchers in the field of Computational Biology. Organised by student volunteers from all over the world, the event provides young researchers and students the opportunity to present their work to an international audience, share and exchange ideas, build network with other members of the community, and develop vital soft skills for a promising career.

This year we are holding the 11th edition of the Student Council Symposium where we will highlight 12 student talks and more than 85 student poster presentations on topics ranging from comparative genomics, bioinformatics tools to bioinformatics education. Our delegates will have the opportunity to hear encouraging and thought-provoking keynotes from Prof. Des Higgins (University College Dublin, Ireland) and Prof. Ruth Nussinov (Tel Aviv University, Israel). With the help of our generous sponsors and independent peer reviewers, we will be awarding three travel fellowships. The SC looks forward to welcoming you in Dublin, Ireland on 10 July 2015 for the symposium.

Internship program

The SC has recently facilitated the recruitment of the ninth intern to the SC Internship Program since its inception in 2009. We are thankful to Dr. Reinhard Schneider who has offered this internship at his group at Luxembourg Centre for Systems Biomedicine (LCSB) at the University of Luxembourg and Dr. Venkata Satagopam for coordinating with us on behalf of the research group. The SC continues to strive to bring internship opportunities to students from developing nations to increase their exposure to research and facilitate scientific and cultural exchange between the interns and host labs.

"I am highly thankful to Dr. Bateman who has guided me so well throughout the internship period. Working in the group improved my skills and proficiency that a researcher requires to excel in his field" - Rohit Thakur, Intern in the SC Internship Program with the group of Alex Bateman, Ph.D.

Uniting many scientists across the globe, ISMB/ECCB is a unique platform to interact with the SC and to learn more about the Internship Program that helps students to have an invaluable experience in an international research environment. We furthermore encourage group leaders to offer internships through the SC and help more students benefit from learning in an established research environment with plenty of resources. We are also searching for additional sponsors for this initiative to reduce the financial burden on the host laboratory. Interested group leaders and sponsors are highly encouraged to contact us at internships@iscbsc.org to learn more about the Internship Program.

Regional Student Groups initiative

Our regional student groups (RSG) initiative is an effort to connect directly with local computational biology student communities around the world. Our RSGs organize workshops, talks, hackathons and other events specifically tailored to the needs of the student community. RSGs have also been a major driving force behind the regional Student Council Symposiums that have been organized in Europe, Latin America and Africa .

Since its beginning in 2006, the RSGs initiative has grown to include over 30 RSGs around the world and continues to grow. Check if there is an RSG in your country or region at http://rsg.iscbsc.org or stop by the SC booth to chat with RSG leaders. If there is no RSG in your country, talk to us about how you can start an RSG there!

SC Activities @ ISMB/ECCB 2015

- **Student Council Booth:** Visit the SC at booth 25 and find out what all the fuss is about.
- **ISCB Student Council Symposium:** A full day of student presentations, keynote lectures and a student poster session on Friday, July 10.
- **Student Council Social Event:** Come socialize with fellow students at the official SC Social Event on July 10. Please ask people at our booth for more details.
- **AKES - How to navigate a bioinformatics career path:** The SC is co-organizing this session focusing on career development. Saturday, July 11, 1:30 pm - 5:30 pm.
- **Job posting board:** Located next to the SC booth, you can come advertise your position or search for a job. We provide this service to connect job seekers with job advertisers at ISMB/ECCB 2015.
- **Student Council Social HQ:** Each evening SC members will be gathering in an informal setting to sit back and continue discussions. Come visit the SC Booth to find out more.

iSCB Student COUNCIL
11
SYMPOSIUM 2015

Events/Conferences of interest

Upcoming Conferences

RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2015
November 16 - 18, 2015
Philadelphia, Pennsylvania, USA www.iscb.org/recomb-regsysgen2015 Now in its eighth 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.

13th Annual Rocky Mountain Bioinformatics Conference United States - Colorado - Aspen/ Snowmass
December 10 - 12, 2015 www.iscb.org/rocky2015
13th 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.

Affiliated Conferences

GIW/InCoB-Asia 2015
Japan – Tokyo
Sep 09 through Sep 11
GIW/InCoB 2015 is the first joint conference between GIW and IncoB, two prominent international bioinformatics conferences in East Asia with a combined history of 40 years.
Event Registration: 2015-05-20 through 2015-09-02
ISCB Member Discount: 15 Percent

NETTAB & Integrative Bioinformatics 2015 Joint Conference
Italy – BA – Ruvo di Puglia
Oct 14 through Oct 16
The 15th NETTAB Workshop and the 11th Integrative Bioinformatics conference are joining their forces for a synergistic event able to attract even more researchers than in the past on their traditional topics.
Event Registration: 2015-06-01 through 2015-10-06
ISCB Member Discount: 30 EUR

VI Argentinian Conference on Bioinformatics and Computational Biology (CAB2C 2015)
Argentina – Province of Buen – Bahia Blanca
Oct 14 through Oct 16
The CAB2C is a multidisciplinary forum for the presentation and discussion of research in computational biology, bioinformatics and their applications. The CAB2C welcomes academic and professional contributions, from various scientific disciplines (Computer Science, Statistics and Mathematics, Molecular Biology, Biochemistry, Genetics, Medicine Microbiology and others).
Event Registration: 2015-07-17 through 2015-09-25
ISCB Member Discount: 10 percent

Big Data in Healthcare - Challenges, Innovations and Implementation
Luxembourg – Munsbach
Oct 28 through Oct 29
The main objective of the Symposium is to bring together worldwide experts from academia, industry, doctors, policy makers and patient organisations in the field of Big data in Health Care to exchange about state-of-the-art research and technologies. The aim is to critically review the current scientific knowledge and the entire life cycle of Big Data in Health Care.
ISCB Member Discount: 10 percent

Pacific Symposium on Biocomputing (PSB) 2016
United States – HI – Kohala Coast
Jan 04 through Jan 08
The Pacific Symposium on Biocomputing (PSB) 2016 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.
Event Registration: 2015-08-03 through 2016-01-08
ISCB Member Discount: 50 USD

Other Conferences & Events of Interest

NIMBios Investigative Workshop: Many-cell System Modeling
United States – TN – Tennessee – Knoxville
Hosted by: National Institute for Mathematical and Biological Synthesis (NIMBioS)
Jul 07, 2015 through Jul 09, 2015
http://nimbios.org/workshops/WS_manycell

Lipari School on BioInformatics and Computational Biology
Italy - Lipari Island
Hosted by: Jacob T. Schwartz International School for Scientific Research
Jul 19, 2015 through Jul 25, 2015
http://lipari.cs.unict.it/LipariSchool/Bio/

The 29th Annual Symposium for the Protein Society
United States - Barcelona
Hosted by: The Protein Society
Jul 22, 2015 through Jul 25, 2015
http://www.barcelocongresos.com.es/protein2015/welcome.html

Protein Interactions and Networks
United Kingdom – Cambridge – Hinxton
Hosted by: Wellcome Trust Advanced Courses
Aug 03, 2015 through Aug 11, 2015
http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/WTVM049891.htm

AlCoB 2015
Mexico - Mexico City
Hosted by: National Autonomous University of Mexico and Rovira i Virgili University, Tarragona, Spain
Aug 04, 2015 through Aug 06, 2015
http://grammars.grlmc.com/alcob2015/

Structural bioinformatics (SBI) microsymposium at the 29th European Crystallographic Meeting
Croatia – Rovinj
Hosted by: ECA (European Crystallographic Association)
Aug 23, 2015 through Aug 28, 2015
http://ecm29.ecanews.org/programme/microsymposia/#ms10

NIMBioS Investigative Workshop: Morphological Plant Models
United States - TN – Knoxville
Hosted by: National Institute for Mathematical and Biological Synthesis (NIMBioS)
Sep 02, 2015 through Sep 04, 2015
http://www.nimbios.org/workshops/WS_plantmorph

HSB 2015: The 4th International Workshop on Hybrid Systems Biology
Spain – Madrid
Hosted by: Madrid Meet 2015
Sep 03, 2015 through Sep 04, 2015
http://hsb2015.fi.muni.cz

Systems Biology of Infection Symposium - 2nd Edition
Switzerland - Ascona
Hosted by: Universität Basel – Switzerland
Sep 06, 2015 through Sep 10, 2015
http://www.targetinfectx.ch/SysBioInf/

The Sixth International Workshop on Static Analysis and Systems Biology (SASB 2015)
France - Saint-Malo
Hosted by: SAS conference
Sep 08, 2015 through Sep 08, 2015
https://www.lri.fr/sasb2015/

EMBL Conference: Protein Synthesis and Translational Control
Germany – Heidelberg
Hosted by: EMBL Heidelberg
Sep 09, 2015 through Sep 13, 2015
http://www.embl.de/training/events/2015/TRC15-01/index.html

2015 ACM International Workshop on Big Data in Life Sciences (BigLS)
United States - GA – Atlanta
Hosted by: ACM-BCB conference
Sep 09, 2015 through Sep 09, 2015
http://www.bigls.org/

ACM-BCB 2015
United States - GA – Atlanta
Hosted by: ACM, Atlanta, GA
Sep 09, 2015 through Sep 12, 2015
http://acm-bcb.bme.gatech.edu/2015/

ACM International Workshop on Big Data in Life Sciences
United States - GA – Atlanta
Hosted by: Georgia Tech
Sep 09, 2015 through Sep 09, 2015
http://www.bigls.org

WABI 2015
United States - GA – Atlanta
Hosted by: ISCB, ACM SIGBio, EATCS
Sep 10, 2015 through Sep 12, 2015
http://wabi.gatech.edu/

Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB2015)
Italy – Naples
Hosted by: CNR
Sep 10, 2015 through Sep 12, 2015
http://bioinfo.na.iac.cnr.it/cibb2015/

NIMBioS Investigative Workshop: Evolution and Warfare
United States - TN - Tennessee – Knoxville
Hosted by: National Institute for Mathematical and Biological Synthesis (NIMBioS)
Sep 16, 2015 through Sep 18, 2015
http://www.nimbios.org/workshops/WS_warfare

EMBO | EMBL Symposium: The Mobile Genome: Genetic and Physiological Impacts of Transposable Elements
Germany – Heidelberg
Hosted by: European Molecular Biology Laboratory
Sep 16, 2015 through Sep 19, 2015
http://www.embo-embl-symposia.org/symposia/2015/EES15-05/index.html

Circulating Biomarkers 2015
United Kingdom – Glasgow
Hosted by: Biotexcel
Sep 30, 2015 through Oct 01, 2015
https://biotexcel.com/event/circulating-biomarkers-2015/

OFFICIAL CONFERENCES OF ISCB

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

www.iscb.org

Open Call for Research coming soon!

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

NOVEMBER 16 - 18, 2015
PHILADELPHIA, PENNSYLVANIA, USA

JOIN US!

for the premier meeting for computational and experimental scientists in the areas of regulatory genomics and systems biology

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

www.iscb.org/recomb-regsysgen2015

Photo Credit: Pennsylvania Convention Center North Broad Street
Photo by bklphoto.com for Philadelphia Convention & Visitors Bureau (PHLCVB)

13th ANNUAL CONFERENCE

ROCKY 2015
Bioinformatics Conference

ROCKY MOUNTAIN BIOINFORMATICS

DECEMBER 10 - 12, 2015
VICEROY HOTEL
ASPEN/SNOWMASS, COLORADO

SHARE science, networking, and the spectacular scenery of the Rocky Mountains!

The Rocky Conference attracts people from around the world to an affordable luxury resort to share in a small and intimate conference. You will experience synergistic relationships, great presentations, and free time to explore and have fun. The program includes 10-minute flash talks, keynote speakers, a poster session and plenty of scheduled social time for informal discussions.

Mark your calendar and join us in the spectacular setting of the Colorado Rocky Mountains.

LAB RETREAT

Plan an off-site retreat, bring your colleagues to Rocky and SAVE!

This is the perfect opportunity to roll your conference attendance funds into a very affordable academic group retreat experience in the spectacular setting of the Colorado Rocky Mountains - during ski season!

KEYNOTE SPEAKERS

LARRY GOLD, Ph.D.
Chairman and Founder of SomaLogic
Professor, University of Colorado
Boulder, Colorado, USA

KIRK E. JORDAN, PhD
IBM Distinguished Engineer
IBM T.J. Watson Research, USA

KARIN VERSPOOR, PhD
Associate Professor
University of Melbourne
Australia

iSCB Official Conference

www.iscb.org/rocky2015

NGS'16

CRG Centre for Genomic Regulation

April 4 - 6 • Barcelona, Spain

GENOME ANNOTATION

iSCB Official Conference

www.iscb.org/ngs2016

GLBIO 2016

GREAT LAKES BIOINFORMATICS CONFERENCE

May 2016
Toronto, Canada

iSCB Official Conference

www.iscb.org/glbio2016

ISMB 2016

ORLANDO
FLORIDA • USA
JULY 16 - 19

iSCB

2016

ISCB-Latin American Conference

ARGENTINA

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

ISCB-Asia Conference

2016

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
Official Conference

DUBLIN
ISMB
ECCB
2015
JULY 10-14

Thank you to our generous Sponsors!

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

QIAGEN
BIOINFORMATICS

F1000Research
Open for Science

THE ROYAL SOCIETY
PUBLISHING

BioMed Central
The Open Access Publisher

GPB
Genomics, Proteomics & Bioinformatics

DNA genotek

amazon

Fáilte Ireland
National Tourism Development Authority

Genentech
A Member of the Roche Group

CCB | CENTER FOR COMPUTATIONAL BIOLOGY
UNIVERSITY OF CALIFORNIA, BERKELEY

Akamai

ECCB

BITS Società di Bioinformatica Italiana
Bioinformatics ITalian Society

H3ABioNet

intel

DU PONT

3S BIOVIA