ISCBNewsletter

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iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
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FEATURING THE ISMB 2016 CONFERENCE PROGRAM!

ISMB
2016

ORLANDO
FLORIDA•USA
JULY 8 to 12, 2016

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

Beyond the Limits of Standard Computation

Discover ➤ Innovate ➤ Engage

CONFERENCE PROGRAM

LETTER FROM THE PRESIDENT

Dear Members and Colleagues,

It is amazing to look back and see how far ISCB has come over the past eighteen years. We have grown to over 3,200 members from nearly 80 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.

So far 2016 has been a banner year for ISCB, and we are only half way through! Here at ISMB 2016 we celebrate these accomplishments of our Society and those involved. We have introduced the Senior Member designation, the ISCB Innovation Forum, welcomed nominations for the mid-career award, celebrated our first Member-get-a-member campaign winner – Catherine Putout from Loyola University Chicago, seen the great accomplishments of the diversity task force, and recognized the winner of ISCB's first Ebola Award competition and introduced a new annual ISCB challenge for best computational solution to emerging global health threats.

ISCB is excited at the prospect of its new Innovation Forum. The ISCB Innovation Forum is a unique and productive opportunity for industry to contribute in a sustained manner to the ISCB mission and to gain prominence in its expert and influential constituency. We look to the ISCB Innovation Forum to provide our corporate and industry partners the opportunity to influence directly and actively the future of ISCB and its growing membership. We hope to continue to see this grow with help from members like you!

Your involvement with ISCB proves first hand the value of a membership in the society. Because of that known value, ISCB released its new and exciting Member-Get-a-Member Campaign in late 2015. As proven, the success of our society is directly linked to its members. With this knowledge the society is offering a chance to win a free registration to a conference of your choice all by recruiting your colleagues to be ISCB members today! Spread the knowledge! Through increased membership participation, we can do even more! Imagine more travel fellowships to ISCB conferences, online training, complimentary e-books, or even recorded talks from all of the official ISCB conferences. The possibilities are numerous and without limitation.

During ISMB, we will announce the winner of the Fight Against Ebloa award, and introduce an on-going annual ISCB challenge for the best computational solution to emerging global health threats. This award goes beyond just Ebola and calls for papers on all global threats facing the world today.

In an age of Zika, Ebola and numerous other diseases, new approaches are needed to address such threats. ISCB is excited at the prospect of engaging new ideas, collaborative efforts and discovering potential cures for such destructive illnesses facing so many around the world.

This issue of the ISCB newsletter is filled with great information including the celebration of the ISCB Fellows, ISCB Award Recipients, the ISMB 2016 Conference Program, an update on 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.

Sincerely,

Alfonso Valencia
President, ISCB

2016 ISCB INNOVATOR AWARD
SERAFIM BATZOGLOU

2016 marks the awarding of the inaugural ISCB Innovator Award, which honors an ISCB scientist who is within two decades of receiving a graduate degree, and has consistently made outstanding contributions to the field and continues to forge new directions. The inaugural winner is Dr. Serafim Batzoglou, Professor in the Department of Computer Science at Stanford University. Batzoglou will receive his award and deliver a keynote address at ISMB 2016 in Orlando, Florida on July 12th, 2016 to mark this honor.

Batzoglou remembers having an early fascination with numbers and a sense of wonder about the universe around him as a young child. He recalled,"I was interested in math and science for as long as I can remember. Before going to preschool, I remember counting and adding large numbers, as well as wondering how big space is and where it ends." Batzoglou's curiosity was stoked by other cultural touchstones, including the novels of Jules Verne and Carl Sagan's captivating Cosmos television series. These early experiences nurtured his interests in math, physics and computer science, and Batzoglou went on to earn two bachelor of science degrees in mathematics and computer science at the Massachusetts Institute of Technology (MIT). Batzoglou also encountered computational biology for the first time as an undergraduate. He said, "Upon entering college, I was deciding between two fields of study that had fascinated me during high school: astrophysics and artificial intelligence (AI). However, during the early nineties I felt that neither physics nor artificial intelligence was experiencing any exciting growth. At least that was my impression around 1995, when I had been admitted to a PhD program in computer science at MIT and was deciding on an area to focus on. I took Bonnie Berger and David Gifford's class on computational biology and felt that this was a research area with great potential where I could apply my computer science background to do science (rather than engineering)." Batzoglou credits his early mentors for giving him invaluable undergraduate research experiences, including Sorin Istrail, with whom he had a very enjoyable research summer during 1997, and his undergraduate research supervisor, David McAllester.

Batzoglou went on to earn his PhD in computer science at MIT under the mentorship of his advisor Bonnie Berger and co-mentor Eric Lander. During his early career, he was the lead algorithms designer and implementer of ARACHNE, one of the first programs for whole genome shotgun sequence assembly that was used for assembling several genomes including the mouse and dog genomes. Batzoglou's early work included using comparative genomics for human gene identification. Together with his collaborators he developed multiple genome alignment tools, including LAGAN, and applied these tools to predict human genes from similar mouse genes. This work was significant to the emergence of the field of comparative genomics and its applications for identifying genes, regulatory regions, and evolutionary events, as well as other features across species.

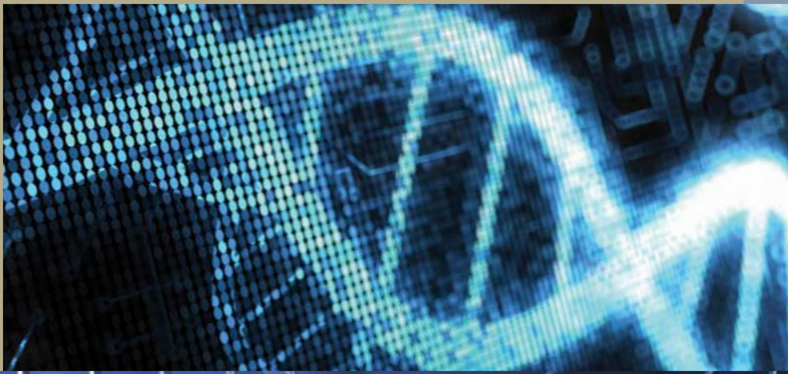
Batzoglou and his lab focus currently on the development of algorithms, machine learning methods and systems for the analysis of genomic data. He recalls one of his more surprising research moments that stands out in his memory. "It was unexpectedly good news to me back in 2005 that Conditional Random Fields (CRFs) and similar flexible models that can learn very large parameter sets, could be so successful in a large variety of classic computational genomics problems including RNA secondary structure prediction, gene finding, and sequence alignment. My line of work on CRFs, together with my PhD students at the time, Chuong Do and Sam Gross, who led the effort, was when we began applying machine learning in earnest to genomics problems."

Batzoglou aims to follow the example of his PhD mentor as he mentors students and post-docs in his lab. "I think I follow a similar style and philosophy as my PhD advisor, Bonnie Berger, in that I am supervising my students in a relatively hands-off, "first do no harm" manner, and to the extent possible allow them to define new research topics and directions." He also looks forward to a time when more novel research can be supported through the grant system, and said, "The most talented and motivated students will do their best research when given freedom, encouragement and some resources. I would be supportive of a large fraction, say 25%, of the government funds to be earmarked for work on new directions – i.e., work on which the proposing PIs have no other funds and no related papers."

Batzoglou's novel research contributions have been recognized through several awards including being named among the Top 100 Young Technology Innovators in 2003 by MIT's Technology Review Magazine and a 2004 NSF CAREER Award. His research publications alone also show his impact on the field, and his purely bioinformatics-based publications have been cited hundreds of times. Batzoglou has also served the computational biology community in numerous capacities, especially through his service as a member of the steering committee, program chair, session chair, and organizing committee member for various RECOMB and ISMB meetings.

Looking forward, he said, "The topic I am most fascinated by right now, although it hasn't majorly influenced my research yet, is deep learning. Like many of my AI colleagues, I subscribe to the opinion that we are witnessing a major breakthrough in our ability to replicate (and improve on) a large fraction of the intellectual and perceptual capacity of humans. The victory of AlphaGo against Lee Sedol is a historic moment. From a personal perspective, I learned Go in 2003, and back then I considered it a midpoint in AI between where we were and full-blown human-level intellectual capacity (excluding emotions and human experiences, which AI hasn't been focusing on as much). The significance of advances in AI cannot be overstated. I believe that AI will transform medicine, finance, construction, manufacturing, commuting and transport, and almost every other sector in society, over the next 20 years. I also believe that a large fraction of jobs in these fields will be made redundant. Re-education is great, but it is not clear at all what the new marketable human skills will be 20 years down the line. Perhaps anything involving human interaction, although that's not clear. In terms of computational genomics and biomedicine, to the extent that we will be able to collect and agglomerate large genomic and biomedical datasets, application of AI will lead to breakthroughs that will start by vastly improving health care, agriculture and biotechnology, and continue to places that are hard to imagine today."

Batzoglou feels greatly honored to be selected as the inaugural winner of the ISCB Innovator Award, and said, "Innovation in computational biology – and in general – is largely a community process. I thank the committee for recognizing my work, and more importantly I thank my colleagues, mentors and foremost my students, with whom I should be sharing this Award."



2016 OVERTON PRIZE AWARDED TO DEBORA MARKS

The International Society for Computational Biology (ISCB) recognizes the achievements of an early- to mid-career scientist with the Overton Prize each year. The Overton Prize was established 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 who are selected because of their significant contributions to computational biology through research, teaching, and service.

ISCB is pleased to recognize Debora Marks, Assistant Professor of Systems Biology and director of the new the Raymond and Beverly Sackler Laboratory for Computational Biology at Harvard Medical School. She will accept this honor and present a keynote talk at ISMB 2016 in Orlando, Florida, on Sunday, July 10th.

As a child and young adult, Marks never considered becoming any sort of scientist. She was fairly confident that she was either going to travel in time around the universe in the tardis with Dr. Who or be a professional political protester and save the world. However, math was a constant that captured Marks's attention since she was a little girl and she recalls spending far too much time with math puzzle books, "math was one of the only activities that forced me to focus and calmed my brain".

After school, Marks went to study medicine at the University of Bristol (in England) but left - now with some regret - after her 2nd MBChB degree as she was "more interested in theatre and politics than Latin names for bones". Many years later, after babies and a variety of interesting jobs, Marks felt the pull back to academia and her first love, mathematics, and went on to complete an honors degree in mathematics at Manchester University. She recalled the focused scope of her mathematics studies during a time when students were not allowed to attend other courses, and interdisciplinary studies were not yet en vogue. "In England, when you did a math degree, it was a math degree and you were not supposed to dilute it with 'lower value' subjects like biology, computer science or even physics. I did however manage to attend an odd course on chaos and fractals that sparked my interest in the intersection of math and biology that continues to drive me today."

Marks considers her introduction to computational biology somewhat unorthodox and recalled, "I came to computational biology by jumping in the deep end. After my math degree I won an award from the Wellcome Trust to research drug design for *Leishmania* and trypanosomiasis. I was given a Silicon Graphics machine and told to get to work. I hadn't got a clue. I'd never used a computer. Because I had a math degree, they thought I was a computer scientist of sorts."

In the wake of the Human Genome project, Marks went on to get a bioinformatics position at Harvard at a time when interest in the potential for computation in biological research intensified. MicroRNAs first captured her attention in mid-2000, and her work on these was eventually submitted as a PhD thesis at the Humboldt University in Berlin under the guidance of Reinhard Heinrich and, after Heinrich's untimely passing, completed with Hanspeter Herzl as thesis mentor.

She recalled, "I accidently read an article in a biology journal lying around about what was then a semi-obscure discovery about small RNAs regulating development in worms. I couldn't stop thinking about it. Do these little RNAs stick to more than one gene? Maybe humans have them?" MicroRNAs were obscure at the time, only two were known, not the category. The floodgates only opened after the discovery of tens (at the time) of the now named "microRNAs", nearly identical in sequence across worms, flies and humans, published in three back-to-back papers in October 2001 and suggesting strong selection across many species. "So, what are they doing in all these organisms?" As more identified more and more of these microRNAs, it became obvious to Marks that a way needed a way to find out what processes they regulated. Unlike the much more complicated task of identifying targets of proteins, the chemistry of base-pairing suggested an obvious way to explore what microRNAs might stick to."

Marks was the first, concurrently with the Cohen and Bartel labs, to publish genome-wide targeting by microRNAs, first in fly, then in human, having developed the miRanda algorithm that is still used today for target prediction. "Although many groups have now published papers on how to discover microRNA targets," Marks said "At best, the science of microRNA target prediction is still imprecise, presenting an unmet challenge for the computational community". These early papers highlighted the potential genomic scope of microRNA targeting across large pools of mRNAs and their many-to-many, cooperative and combinatorial regulation of protein expression, something we now take for granted. Struck by these indications of potential system-wide effects, Marks undertook work to investigate the function of small RNAs in the context of the cellular environment by using mathematical modeling, re-analysis of previously published experiments, and additional in vitro experiments.

She made several key findings that included demonstrating that mRNA half-life influences the effects of microRNA and siRNA targeting for thousands of gene targets and that mRNA and microRNA abundance impacts microRNA targeting (now thought of as the mRNA sponge effect, and, controversially, "ceRNAs"). She also showed that introducing siRNAs or microRNAs into cells results in attenuation of endogenously regulated genes. Marks explained, "This is a really important consideration for the interpretation of gene knock-down experiments and for therapeutic uses of small RNAs". Her more recent work showed that for a given level of protein, adding microRNA regulation can reduce protein noise or fluctuations, especially for transcripts with low expression.

Quite by chance, Marks's postdoctoral work shifted sharply away from microRNAs to the field of ab *initio* 3D structure prediction of proteins. Together with Chris Sander, they revisited an older idea that had been advanced independently by the groups of Sander, Neher and Taylor in the mid-1990s of using covariation of residues in proteins across evolution to identify residues that might be in contact in 3D. They reasoned that if these inferred contacts were accurate enough, one should be able to fold a protein sequence using simple methods such as distance geometry and restrained molecular dynamics. The key advances were to use a statistically global model of covariation across the sequences that removes transitive correlations in the data, by using a probability model for entire proteins in the sequence family, not unlike a suggestion made by Gary Stormo and Alan Lapedes in 1999. She said, "We stumbled across statistical physics models that are used to determine inhomogeneous interactions in Ising models from observed data that contain transitive correlations. Listening to the team of Riccardo Zecchina, including Andrea Pagnani and Martin Weigt, in Torino, Italy made us think that their approaches to the analysis of correlated mutations could be important for the 3D structure-from-sequence problem. Working with their team in collaboration, I set off in the spring of 2010 to see if the maximum entropy method could work to find truly interacting co-evolved residues. If the computation was correct then co-evolved residue pairs should match contacts in known 3D structures, and they did nearly to the ceiling. I then cajoled a friend, Lucy Colwell who, like me, was also recent graduate, to join the project. What fun we had! Well, that is until it was time to try and publish it. Reviewers found it difficult to believe, but eventually we published the results at the end of 2011, and the EVfold community has grown ever since. Marks explained,

2016 OVERTON PRIZE AWARDED TO DEBORA MARKS, CONT.

"The method is very democratic. It is fast and can be run on a laptop, even the folding, and relies only on gene sequences. Immediate applications were to proteins that are challenging experimentally such as large membrane proteins and to protein-protein complexes. More than five of the transmembrane proteins have since been crystallized and agree well with the predicted structures, such as the adiponectin receptor". "A very effective mini-CASP," she added with a smile.

After the protein folding breakthrough in the fall of 2010, implementation of similar methodology led her to the solution, published in 2016, of another hard and unsolved problem in computational biology, that of computing RNA 3D structures and of RNA-protein complexes just from sequence information.

Currently, Marks has a newly formed lab at Harvard Medical School and is building the Raymond and Beverly Sackler Laboratory for Computational Biology. She is continuing the "3D from sequence" work, including new types of biomolecular interactions and their conformational flexibility. The Marks lab is also going back to math and developing the core algorithms for sequences, and model inference for multidimensional biological data. At the same time, Marks is branching out with new applications that include the challenge of predicting the effects of genetic variation on disease risk and drug response, especially combinations of events, and particularly in antibiotic resistance "It may seem we are promiscuous in our choice of biological questions, but the underlying thread is one of solving problems that are hard to solve experimentally. One far-reaching question that I am increasingly less embarrassed to admit being interested in is: What makes us all different? With genomes in hand, surely we can now find out how much is nature, how much is nurture and how much is stochastic?"

Marks is grateful to her mentors and her "wonderful" Systems Biology department who have supported her throughout her unusual career path and feels greatly honored to be recognized with the Overton Prize. She is especially thankful to her new group members and her long-time scientific collaborator Chris Sander. She said, "I want to share the prize in spirit with all those who have tolerated and encouraged me despite the odds."

Marks's final message to young scientists (young in spirit, that is) is to "go big, go risky, and learn statistics (!)"

2016 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD: BURKHARD ROST

The Outstanding Contributions to ISCB Award was launched in 2015 to recognize individuals who have made lasting and valuable contributions to the Society through their leadership, service, and educational work, or a combination of these areas. Burkhard Rost is the 2016 winner of the Outstanding Contributions to ISCB Award and will be recognized at the 2016 Intelligent Systems for Molecular Biology (ISMB) meeting in Orlando, Florida on July 8-12, 2016.

Rost is the Alexander von Humboldt Professor and chair of bioinformatics and computational biology at the Technical University Munich. His research interests focus on using machine learning and artificial intelligence to predict the structures and functions of proteins and genes.

Rost has served ISCB in numerous positions throughout his career, including being co-chair of the largest annual meeting in computational biology, Intelligent Systems in Molecular Biology (ISMB), during 2007 (Vienna), 2008 (Toronto), 2011 (Vienna), 2012 (Long Beach), and 2013 (Berlin). Rost served as ISCB president from 2007-2014. When he assumed the leadership position, the Society was in financial turmoil. He recalled, "All I wanted to do was clean up," and sought out colleagues who would help steer ISCB in their right direction through their leadership roles on the Executive Committee and the Board of Directors, and as committee chairs. He attributes the flourishing of ISCB under his leadership to these colleagues and said, "I have found a way to motivate the people who are passionate about what they do. I can motivate people and I found the right people."

Rost strove to broaden the international reach of ISCB beyond Europe and the United States and said, "We wanted ISCB to have conferences in many places, outside the realm of what we typically do. I believe we found a way of making it sustainable." During Rost's term as president, he led the effort to organize several international meetings in Africa, Asia, and Latin America. These truly international meetings included ISCB Africa (2010: Bamako, Mali; 2011: Cape Town, South Africa; 2013: Tunis, Tunisia; 2015: Dar es Salaam, Tanzania) in cooperation with the African Society for Computational Biology and Bioinformatics (ASBCB), ISCB Latin America (2010: Montevideo, Uruguay; 2012: Santiago de Chile, Chile; 2014: Belo Horizonte, Brazil), and most recently ISCB Asia (2011: Kuala Lumpur, Malaysia; 2012: Shen Zhen, China; 2013: Seoul, South Korea). ISCB continues to organize these international meetings and is developing other virtual platforms, like ISCBconnect, to help ISCB members from around the globe connect with each other outside the confines of a conference.

Rost wanted to find ways for students and trainees to become involved with ISCB in a meaningful way and helped advocate for and support the ISCB Student Council (ISCB SC). The ISCB SC has blossomed since its inception in 2004, and student members organize and manage the SC's year round activities including scientific events, networking opportunities, soft-skills training, educational resources and career advice.The ISCB SC hosts a popular annual symposium at ISMB and has become the voice of the rising generation of computational biologists. Rost said, "Young people see ISCB as a society that does something and they are more active than ever before."

Rost was concerned about the lack of diversity in ISCB's leadership at the beginning of his term and focused on getting more women on the Executive Committee (EC) because he believed diversity is essential for the success of "how important decisions are made." Now women hold many leadership roles across ISCB and are being honored in growing numbers for the scientific contributions to computational biology through ISCB awards and recognition as ISCB Fellows.

Rost will be remembered as one of ISCB's most devoted presidents through his tireless service to connect the international computational biology community through multiple platforms and being a strong united voice for a very broad field. He will continue to support the ISCB community as a past-president and lifetime ISCB member.

THE ISCB COMMUNITY JOURNAL: MEET THE EDITORS!

At ISMB 2015 we were pleased to announce the launch of the ISCB Community journal, a fully open access online publication that is freely available to everyone. To work alongside our affiliate journals Bioinformatics and PLoS Computational Biology, the ISCB Community Journal is intended to support our growing conference program and Communities of Special Interest (COSIs) by providing a platform to disseminate not just research articles, but all of the presented conference research in one centralised place.

However, the ISCB Community Journal is different compared to a journal in the traditional sense. Articles are published under a post publication peer review model, where papers are published immediately (after some pre-publication checks) followed by an invited, open peer review process. The journal also has a robust data sharing policy; all primary research articles must include the submission of the data underlying the results, together with details of any software used to process results. Within the journal there are individual "channels" for each conference or community, and in these channels researchers can publish a range of articles types such as research paper, method papers, software tools, data only papers and any other piece of research that is written up to be peer-reviewed. In addition to peer-reviewed articles, the channel also enables attendees to share and publish all the academic posters and slides that are presented at the various ISCB conferences.

We believe the new publishing model of the ISCB Community Journal enables us to go further in supporting all of the society's publishing needs. It will allow us to help support and showcase research from all regions, including our US and European conferences, but also those in Africa, Asia and Latin America. It also helps us build communities around our conferences by providing a place to further the discussion through the publication of the presented research enabling others who were unable the meeting sees the latest work that was discussed. Each conference, event and workshop related to the ISCB will be able to extend the visibility of everything presented at a meeting and therefore broadcast their research beyond the conference hall to the wider scientific community.

The Executive Officers of the ISCB recently published their reaction (http://f1000research.com/articles/5-157/v1) to a controversial editorial published in the New England Journal of Medicine around data-sharing. Open data is something as a society we fully support and so the ISCB Community Journal is dedicated to making sure that underlying data is open to allow others to see the raw data to be able to replicate a study and analyse the data, and as in some circumstances, reuse it.

Over the past few months we have been working on how best to integrate the ISCB Community Journal with our conferences and communities, and soon we will see our first articles being published.

During this time, we have appointed four Chief Editors, who will oversee the development of the journal, and help us support our global community. We are pleased to introduce them to you below:

Christine Orengo: My group is based at University College London and manages the CATH-Gene3D classification of domain structure superfamilies. We develop algorithms for structural and functional annotation of proteins and for functional genomics. For example we are collaborating with several UK groups using proteomics studies to understand how splicing rewires protein networks in the different stages of fly development. We also participate in a functional effects domain of Genomics England which is seeking to interpret the effects of mutations linked to rare diseases and certain cancers. We are involved in a number of UK and European structural bioinformatics training initiatives. The ISCB Community Journal is a very exciting opportunity to publicise all the activities of communities in ISCB – one of the most established societies in computational biology. It will be wonderful to have a record of the exciting new work presented in the ISCB-X and Affiliated conferences and in the annual meetings of the Communities of Special Interest (COSIs) who run the SIGs and satellite meetings at ISMB.

Christos Ouzounis: Was recently appointed as a Director of Research at the Centre for Research & Technology Hellas (CERTH) in Thessalonica, Greece – following his return from the UK. His research interests encompass computational genomics, systems and synthetic biology. Experimenting with a new publishing model, he thinks that the ISCB Community Journal can provide an ideal conduit for fast publication of scientific reports, conference proceedings and opinion articles, in a single space with an identical look-and-feel for the ISCB community.

Michael Sammeth: My group is affiliated with the Federal University of Rio de Janeiro (UFRJ), where we are mainly doing research on transcriptomics and functional genomics across multiple organisms, including human and also an increasing amount of relevant tropical species such as pathogens of neglected diseases and their corresponding vectors. As a professor at the Institute of Biophysics Carlos Chagas Filho (IBCCF), I am also giving regular classes in bioinformatics to under-/graduate students. When the ISCB as one of our communities with the longest tradition in computational biology recently implemented the idea of a dedicated publication platform in form of the Community Journal, I felt that this will be a great chance to increase the visibility of all contributions from the numerous conferences and Special Interest Group satellites.

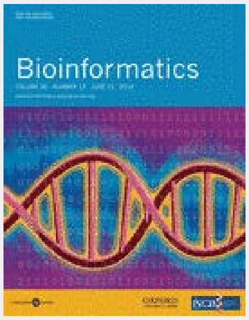
Louxin Zhang: He is currently an Associate Professor at the National University of Singapore. My research interests lie in bioinformatics in comparative and evolutionary genomics. With adopting the post publication peer review policy, the ISCB Community Journal is perfect complement to other affiliate journals of the ISCB.

As the name reflects, the new society journal is for the ISCB community and we want to be inclusive to all of our society members and allow them to have a say in the direction we go. We have created the foundations but we are more than happy to receive input on the journal and new ideas on how we can make it as valuable as possible with regards to publishing and communicating research in computational biology.

We are keen to create a pool of peer reviewers for the journal to help review any published articles, and we will soon be sending out a request to all of our members to volunteer to be a part of this reviewing board. All the reviews in the ISCB Community Journal are completely open, citable and include the name and affiliation of the reviewer, so it will be a chance for all participating reviewers to receive credit for the work they have done, and will enable others to see the contributions you have made to the society.

If you have any questions about the ISCB Community Journal or would like to be more involved, please feel free to contact our Editors.

2016 BIOINFORMATICS UPDATE


Bioinformatics

Bioinformatics has had a very busy and successful 2015. We continue to serve ISCB members and the wider computational biology community and we thank our authors, reviewers, and readers for the continued support.

Our submission rate for 2015 was around 2000 papers, of which in the region of35% were accepted. Of our published papers, around 20% were published open access, with authors choosing between CC-BY-NC and CC-BY licences.

Our levels of online readership and citation remain high, reflecting the value of our papers to the field. In particular, the following papers from 2015 have been extremely popular with our readership:

- **repDNA: a Python package to generate various modes of feature vectors for DNA sequences by incorporating user-defined physicochemical properties and sequence-order effects**, by Bin Liu, Fule Liu, Longyun Fang, Xiaolong Wang and Kuo-Chen Chou,doi:10.1093/bioinformatics/btu820
- **HTSeq—a Python framework to work with high-throughput sequencing data**, by Simon Anders, Paul Theodor Pyl and Wolfgang Huber, doi:10.1093/bioinformatics/btu638

We now track and display article-level metrics and Altmetrics alongside journal articles. The following articles have had particularly high Altmetric scores:

- Bioinformatics programs are 31-fold over-represented among the highest impact scientific papers of the past two decades, by Jonathan D. Wren, doi:10.1093/bioinformatics/btw284 84
- On genomic repeats and reproducibility, by Can Firtina and Can Alkan, doi:10.1093/bioinformatics/btw139 66

At the time of writing (prior to the release of the 2015 Journal Citation Report), Bioinformatics has an impact factor of 4.981, and is 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 several years (**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 2016 in sunny Orlando – see you there!

With best wishes,
The Bioinformatics Editorial team

Tweet Alert – ISCB moves all Twitter handles under @ISCB

ISCB is working to streamline our Twitter communication and hash tags. Instead of having individual accounts for each major event, ISCB is going to use one main twitter handle - @ISCB. Each event will have it's own hash tag like #ISMB16, #GLBIO, #ISCBNGS, #Rocky. This will allow us to track the conversation and keep you better informed.

Follow us today!

FASEB PUBLIC AFFAIRS
BUSY SPRING!

Science policy issues took center stage this winter at the Federation of American Societies for Experimental Biology (FASEB). Through active consensus-building, FASEB represents the values and viewpoints of the member societies, whose ranks grew to 30 on January 1 as the Society for Experimental Biology and Medicine, American Aging Association, and US Human Proteome Organization joined the Federation.

On January 14, FASEB issued recommendations on Enhancing Research Reproducibility, culminating six months of effort to address a growing issue in the scientific community. The recommendations were timed to assist researchers in complying with new requirements to address rigor and reproducibility in National Institutes of Health (NIH) grant applications and incorporated input from stakeholders within and beyond the FASEB.

The report addressed general factors that impede the ability to reproduce experimental results as well as factors that specifically affect the use of two key tools critical to basic research: mouse models and antibodies. Actions for stakeholders across the research enterprise—including scientists, institutions, professional societies, journals, and federal agencies—were suggested. It was approved by FASEB's Science Policy Committee and Board of Directors. **Harel Weinstein**, **DSc**, is ISCB's delegate to both groups.

Dr. Weinstein also chairs FASEB's Data Science and Informatics subcommittee. In March, the subcommittee spearheaded a broad statement on data access and management in the biological and medical sciences. The statement offered a set of guiding principles that balance the costs and benefits of increased access, taking into consideration dataset utility, resource needs, and administrative burden.

Recognizing the diversity of data types and research areas, the statement advocated flexible and customizable approaches to data management. As research sponsors expand data access requirements, FASEB called upon them to provide corresponding financial and staff support, including investments in underlying infrastructure.

The statement also addressed the use and contents of data management plans, which are increasingly required by funding agencies in the United States. FASEB advised that they remain short summary documents focused on the most essential aspects of data management and that sponsors delay requests for compliance until major barriers are lifted and requirements are well-vetted and harmonized. FASEB's statement offered specific recommendations for research sponsors, investigators, scientific journals, and research institutions, but also encouraged integrated community-based solutions.
Also in March, ISCB's **Judith Blake**, **PhD**, participated in FASEB's annual Capitol Hill Day. The event drew 46 scientist participants from 25 states for meetings with 100 congressional offices. Notable this year was the enthusiastic bipartisan support for biomedical research that greeted FASEB's advocates in offices across Capitol Hill.

FASEB aims to capitalize on that good will to push for increased funding for research at NIH, the National Science Foundation, Veterans Affairs Medical and Prosthetic Research Program, United States Department of Agriculture, and the Department of Energy Office of Science. FASEB's funding recommendations for fiscal year 2017 are available online and were distributed to congressional offices during Hill Day. For up-to-date information on FASEB's Public Affairs activities, sign up to receive FASEB's Washington Update at http://washingtonupdate.faseb.org/.

EFFECTIVE JANUARY 14, 2016

Enhancing Research Reproducibility:

Recommendations from the
Federation of American Societies for Experimental Biology

FASEB
Federation of American Societies for Experimental Biology

HED: WIKIPEDIA’S COMPUTATIONAL BIOLOGY COVERAGE IS MISSING

Improving Wikipedia’s science coverage is an unprecedented opportunity for public engagement. Here’s how you, and your students, can help.

by: Eryk Salvaggio, Wiki Education Foundation

When Martin Karplus, Michael Levitt, and Arieh Warshel won the Nobel Prize in 2013, scientists around the world cheered. Many laypeople, however, scratched their heads. One headline asked, “What the Heck Is Computational Biology and Why Did It Win a Nobel Prize?” The internet is the first place most Americans turn for information about scientific topics. According to the Pew Research Center, 70% turn to the web to learn more about scientific topics, and 90% use a search engine. Usually, that means they end up on Wikipedia. Wikipedia reaches more than 450 million readers around the world. More people turn to Wikipedia’s site on mobile devices than turn to CNN, Fox News, and the Washington Post combined.

Missing pieces

That’s an enormous opportunity for computational biologists. Consider Martin Karplus’ Wikipedia entry. It’s two short paragraphs, none of which describe his contribution to the Nobel Prize. Michael Levitt’s page has a C-class article rating. Arieh Warshel’s biography focuses on his military career.

It’s not only biographies. Computational biology articles are in need of improvement across the board. That includes “classical” bioinformatics, such as sequence analysis or genomics, but also information on computational neuroscience and immunology, and the integration of biological concepts and data. Much of this type of content is missing or underdeveloped.

When people try to get a sense of the work you do, the information is all too often missing or unclear. That’s a huge gap in public knowledge.

How can experts in this field with limited time make an impact on Wikipedia? One way is attending an Edit-a-thon at this year’s ISMB 2016 meeting: Monday, July 11, 7:00 PM - 9:30 PM, America’s Seminar Room, Dolphin Hotel, Orlando, FL. Or consider participating in ISCB’s Wikipedia competition for computational biology, with awards sponsored by the Simons Foundation.

Yet another — and perhaps more sustainably impactful — way experts can make an impact is by working with the Wiki Education Foundation to assign students to write Wikipedia articles instead of a term paper. As one instructor told us, teaching with Wikipedia offers “the same outcomes that a research paper assignment does, with added benefits.”

Wikipedia Year of Science

Millions of people turn to the encyclopedia every day. It’s time to embrace Wikipedia as a powerful ally in science communication. At this year’s ISCB conference, the Simons Foundation and the Wiki Education Foundation are working to make Wikipedia a better, more reliable source of scientific knowledge.

The Wikipedia Year of Science initiative is an unprecedented effort to improve Wikipedia’s communication of scientific knowledge and history. We’re working with instructors in higher education who assign Wikipedia articles to their students. Instead of a term paper, students contribute their knowledge to Wikipedia.

The Wiki Education Foundation is a nonprofit organization dedicated to improving Wikipedia’s missing coverage, such as those in the sciences. Along the way, we’re providing students with a valuable learning opportunity to practice science communication with an audience larger than the New York Times’ readership.

Many students have learned how to write a paper overnight that achieves exactly the grade they need. Wikipedia challenges them to think bigger. They have to do the same research they would for a term paper, but they also have to develop a clear way to communicate what they’ve learned. Writing for the public isn’t just a way of bringing better information to the lay reader in the short term. Students begin thinking about science communication as a skill they need to cultivate. That can prepare them for grant writing, public speaking, and press engagement.

A student perspective

One student, Conor Zeer-Wanklyn, had a Wikipedia assignment in a medical mycology course at the University of Toronto.

“To write an effective Wikipedia article you have to really appreciate context,” he said. “For instance, chemistry students who want to prepare a complete Wikipedia article on a bioinorganic compound need to appreciate the biological, environmental and historical context of that compound. We are forced to acknowledge aspects of the story that we may have otherwise ignored.”

MARK YOUR CAALENDARS ISCB LA

ISCB
LATIN AMERICA
A2B2C
Bioinformatics Conference
2016
NOVEMBER 21-23

ISCB-LA A2B2C Bioinformatics Conference inspires and fosters collaboration between scientists and students to advance research in the areas of Bioinformatics and Computational Biology. The scientific program showcases exceptional keynote speakers, original research scientific talks, and poster sessions.

KEYNOTE SPEAKERS

Ana Amador, PhD
University of Buenos Aries, Argentina
Soren Brunak, PhD
Novo Nordisk Foundation Center for Protein Research, Denmark
Emilio Kropff, PhD
Leloir Institute IIBBA, Argentina
Ruth Nussinov, PhD
National Cancer Institute, United States
Sean O’Donoghue, PhD
Commonwealth Scientific & Industrial Research Organisation , Australia

CONFERENCE TOPICS

- Bioinformatics of Disease and Treatment
- Computational aspects
- Comparative Genomics
- Epigenetics
- Functional Genomics
- Genome Organization and Annotation
- Genetic Variation Analysis
- Metagenomics, Ecology and Environmental Genomics
- Pathogen informatics
- Population Genetics, Variation and Evolution
- Protein Structure and Function Prediction and Analysis
- Proteomics
- Sequence Analysis
- Systems Biology and Networks

KEY DATES
Oral Abstract Submissions Close
2 SEPTEMBER 2016
Poster Abstract Submissions Close
16 SEPTEMBER 2016
Early Registration Closes
14 OCTOBER 2016

http://www.iscb.org/iscb-latinamerica2016

A2B2C Asociación Argentina de Bioinformática y Biología Computacional

iSCB International Society for Computational Biology

HED: WIKIPEDIA'S COMPUTATIONAL BIOLOGY COVERAGE IS MISSING, CONT.

Writing for Wikipedia encouraged him to expand his literature search not only deeper, but wider.

Get involved

Wiki Ed is looking for science instructors in higher ed classrooms to take advantage of this powerful science communications assignment. Even if you've never edited Wikipedia on your own, we can help. We have online orientations, training modules for students, and printed guides and handbooks. One guide focuses specifically on writing about genes and proteins on Wikipedia.

If you're interested in participating, we can help. Visit us at http://www.wikiedu.org/yearofscience, or send us an email: contact@wikiedu.org.

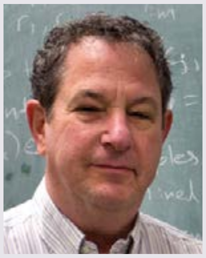
The Wiki Education Foundation (Wiki Ed) is an independent, grant-supported non-profit institution supporting the use of Wikipedia and Wikimedia projects in higher education contexts across the United States and Canada.

MEET THE 2016 ISCB FELLOWS

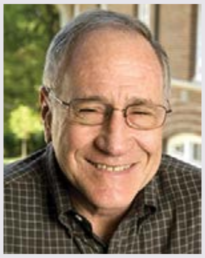
The ISCB Fellows program recognizes members that have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. The program was launched in 2009 and includes recognition of the Fellows at ISMB, the flagship conference of ISCB. This year, thirteen Fellows have been elected and will be honored at ISMB in Orlando, Florida.

Helen Berman Distinguished Professor / Board of Governors Professor of Chemistry and Chemical Biology, Department of Chemistry and Chemical Biology, Rutgers University, USA. Berman is a structural biologist and began her career as a crystallographer. She has studied the structures of protein/nucleic acid complexes, including collagen, and was an instrumental founder and leader of the Protein Data Bank (PDB) and Nucleic Acids Database. Berman's innovations in computational biology include methods, standards, and tools to make these databases more robust and searchable, and she coordinated the effort to form a partnership between global PDB entities to create and maintain a worldwide PDB.

Steven E. Brenner Winner of the 2010 Overton Prize. Professor, Department of Plant and Microbial Biology, University of California, Berkeley, USA. Brenner's research interests span computational biology from individual genome interpretation to understanding RNA-based gene regulation, protein structure evolutionary analysis, and developing better methods for protein function prediction. Brenner is an organizer of the Critical Assessment of Genome Interpretation (CAGI) project and has contributed to the ISCB and open-source software communities through various leadership roles.



Dan Gusfield Professor, Department of Computer Science, University of California, Davis, USA. Gusfield has made many seminal contributions to computational biology since the field was in its infancy. His research focuses on efficiency of algorithms, particularly for combinatorial optimization and graph theoretic problems in the context of bioinformatics data. His present research is focused on optimization problems related to population genetics and population-scale genomics. Gusfield has served the computational biology community in multiple capacities as an educator, administrator, book author and founding Editor-in-Chief of the journal *IEEE/ACM* Transaction on Computational Biology and Bioinformatics.



Barry Honig Professor, Department of Biochemistry and Molecular Biophysics, Columbia University, USA. Honig has made many foundational contributions to computational biology, especially in the fields of protein structure prediction and molecular electrostatics. His diverse research program includes fundamental theoretical work and combines biophysical and bioinformatics methods to gain insight into protein function prediction, protein-DNA recognition, and cell-cell adhesion.

Janet Kelso Group Leader, Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Germany. Kelso's leads topnotch research that uses computational approaches to study the genomes of archaic and modern humans, and to gain insights into genome evolution, gene expression and gene expression regulation. Kelso has also distinguished herself through devoted scientific service through leadership roles in ISCB and bioinformatics journals, support for bioinformatics education, and involvement in the global development of bioinformatics.

Michal Linial Professor, Biological Chemistry / Director, Sudarsky Center for Computational Biology / Director, Institute for Advanced Studies, Hebrew University of Jerusalem, Israel. Linial has made numerous significant research contributions to the field of computational biology through her pioneering work on automatic classification of protein sequences and function prediction, by originating the use of Bayesian networks for expression data analysis, and through the application of compressed sensing to expression data. Linial has also served the ISCB and greater computational biology communities in a variety of leadership roles and has promoted the advancement of computational biology education.

Christine Orengo Professor, Division of Biosciences, University College London, UK. Orengo has made seminal contributions to protein structure classification through her work establishing the CATH resource, and the development of novel robust algorithms to determine structural and functional relationships between proteins. Orengo has served ISCB in a number of leadership roles and has made invaluable contributions to computational biology education and training.

ISMB 2016

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

Beyond the Limits of Standard Computation

ORLANDO
FLORIDA • USA
JULY 8 to 12, 2016

Discover ➤ Innovate ➤ Engage

CONFERENCE PROGRAM

Welcome to Orlando!

On behalf of the organizing committee of ISMB 2016, and the Board of Directors of the International Society for Computational Biology (ISCB), we wish you a very warm welcome. ISMB takes place in the United State this year and promises to be the key meeting for Computational Biology in 2016, and the largest annual computational biology and bioinformatics event worldwide. Attendees will have the opportunity to participate in a multi-track program presenting cutting-edge research in a wide-ranging set of topics and to network with other members of our community.

The steering and scientific organizing committees have prepared a program including a variety of scientific offerings for the meeting and we hope the diversity of options and depth of presented research affords you a stimulating and productive time in Orlando. Following the practice introduced at ISMB 2015 in Dublin last year, all presentations have been organized into one of five Themes: Data, Disease, Proteins, Genes, and Systems. This helps both to logically organize the presentations as well as help you to decide which sessions to attend.

The program includes:

- 3 renowned Keynote speakers.
- 3 Keynote addresses from the 2016 ISCB Award Winners.
- 111 Theme Talks consisting of:
    - 42 Proceedings presentations based on peer-reviewed, original research papers;
    - 36 Highlights Track presentations on recently published work of high impact; and,
    - 33 Late Breaking Research Track papers.
- 4 Special Sessions on current and emerging hot topics.
- 1 ISMB 2016 Industry Session
- 38 Oral Poster presentations.
- 30 Technology Track demonstrations and presentations.
- 3 Workshops, including a full day Junior Principal Investigator program.
- 11 Special Interest Group (SIG) and 2 Satellite Meetings in one- and two-day formats.
- 1 pre-conference Student Council Symposium organized by and for students.
- 3 pre-conference Applied Knowledge Exchange Sessions (AKES)

In addition there are more than 500 posters on display throughout the conference and presented by their authors in two sessions.

We wish to acknowledge all the members of the Scientific Organizing Committee, the Theme Chairs, the Area Chairs, the Applied Knowledge Exchange Sessions Chairs, the Poster Chairs, the Special Interest Groups Chairs, the Special Sessions Chair, the Technology Track Chair, the Travel Fellowship Chairs, the Art and Science Chair, and the Student Council Symposium Chairs. Their dedication and leadership in working with their committees have been invaluable. Over the course of the conference please take a moment to thank them for their efforts and dedication to the success of ISMB 2016.

As Conference Chairs we also appreciate the support of the very many volunteers that have helped guide the development of the conference and of course all the Reviewers who have played an essential role towards forging the scientific program of the conference. A special thanks to our colleagues from the Steering Committee: Janet Kelso, Diane Kovats, Steven Leard, Christine Orengo, and Alfonso Valencia and also to the staff and volunteer leadership of the ISCB organization.

As many of you know, without Steven Leard, the ISMB Conferences Director, there would be no ISMB! We are immensely grateful to Steven and his team for the dedication and effort that they put into organizing all the logistics of this very parallel and complex meeting.

We thank our conference sponsors and exhibitors for their ongoing support. This year's exhibition features commercial and non-profit providers of bioinformatics tools, technologies and publications. We hope you take advantage of everything the conference has to offer, especially the endless opportunity to meet, network, and connect with your fellow researchers.

Finally, we thank the city of Orlando for its welcoming hospitality.

We wish you all a great conference!

Yours sincerely,

Teresa Przytycka,
Conference Co-Chair

Pierre Baldi,
Conference Co-Chair

ISMB 2016 ORGANIZATION

CONFERENCE CHAIRS

Pierre Baldi, *Conference Co-chair, University of California, Irvine, United States*
Teresa Przytycka, *Conference Co-chair, NCBI/NLM/NIH, Bethesda, United States*

STEERING COMMITTEE

Pierre Baldi, *Conference Co-chair, University of California, Irvine, United States*
Teresa Przytycka, *Conference Co-chair, NCBI /NLM/ NIH, Bethesda, United States*
Janet Kelso, *Conferences Committee Co-chair, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany*
Diane E. Kovats, *ISCB Executive Director, Bethesda, United States*
Steven Leard, *ISMB Conference Director, Edmonton, Canada*
Christine Orengo, *ISCB Conferences Committee Co-chair, University College London, United Kingdom*
Alfonso Valencia, *Spanish National Cancer Research Centre (CNIO), Madrid, Spain*

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Co-chair: Fran Lewitter, *Whitehead Institute for Biomedical Research, Cambridge, United States*
Co-chair: Patricia M. Palagi, *SIB Swiss Institute of Bioinformatics, Switzerland*

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Jason McDermott, *Pacific Northwest National Laboratory (US Dept of Energy), United States*
Magali Michaut, *Netherlands Cancer Institute*
James Morton, *University of California, San Diego, United States*
Leighton Pritchard, *The James Hutton Institute, United Kingdom*
Jonas Reeb, *Technical University of Munich, Germany*
Surya Saha, *Boyce Thompson Institute, United States*
Venkata Pardhasaradhi Satagopam, *University of Luxembourg*
Avner Schlessinger, *Mount Sinai School of Medicine, United States*
Eric Talevich, *University of California, San Francisco, United States*
Jie Tan, *Dartmouth College, United States*
Peter Ung, *Icahn School of Medicine at Mount Sinai, United States*
Aaron Wong, *Princeton University, United States*
Victoria Yao, *Princeton University, United States*
Yan Zhang, *Yale University, United States*
Jian Zhou, *Princeton University, United States*
Chengsheng Zhu, *Rutgers University, United States*

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Jill Mesirov, *UC San Diego, United States*
Guilherme Oliveira, *Vale Technology Institute, Brazil*

SPECIAL SESSIONS

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Desmond Higgins, *Conway Institute, Dublin, Ireland*
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Ricardo de Matos Simoes, *Dana-Farber Cancer Institute, Boston, United States*

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Co-Chair: Ben Siranosian, *Broad Institute of MIT and Harvard, Brown University, United States*
Venkata Satagopam, *Luxembourg Centre For Systems Biomedicine (LCSB), University of Luxembourg*
Finance Chair: Ashley Mae Conard, *Brown University, DePauw University, United States*
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Outreach Chair: Nazeefa Fatima, *University of Huddersfield, United Kingdom*
Outreach Committee: Pankhuri Wanjari, *The University of Texas at El Paso, United States*
Travel Fellowships Chair: Melissa Woghiren, *University of Windsor, Canada*
Student Council Executive Team Representative: Anupama Jigisha, *University of Geneva, Switzerland*

ISMB 2016 Keynote Presentations

Northern Hemisphere BCD, Dolphin Hotel

Sunday, July 10

9:00 AM – 10:00 AM

ISCB FELLOWS KEYNOTE

KN01: RUTH NUSSINOV

Leidos Biomedical Research, Inc., National Cancer Institute, Frederick, United States;
Sackler School of Medicine, Tel Aviv University Israel

Ras signaling: A challenge to the biological sciences

4:40 PM – 5:40 PM

ISCB 2016 OVERTON AWARD KEYNOTE

KN02: DEBORA MARKS

Department of Systems Biology, Harvard Medical School Boston, United States

Molecular structure and organism fitness from genomic sequences

Monday, July 11

9:00 AM – 10:00 AM

KN03: SANDRINE DUDOIT

Division of Biostatistics and Department of Statistics, University of California, Berkeley, United States

Identification of novel cell types in the brain using single-cell transcriptome sequencing

4:40 PM – 5:40 PM

KN04: SARAH TEICHMANN

EMBL-EBI and Head of Cellular Genetics at Wellcome Trust Sanger Institute Hinxton, United Kingdom

Understanding cellular heterogeneity

Tuesday, July 12

9:00 AM – 10:00 AM

ISCB 2016 INNOVATOR AWARD KEYNOTE

KN05: SERAFIM BATZOGLOU

Department of Computer Science, Stanford University, United States

Computational challenges in personalized genomics

4:40 PM – 5:40 PM

ISCB 2016 ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE

KN06: SØREN BRUNAK

Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark

Creating disease trajectories of time-ordered comorbidities from big biomedical data covering millions of patients

Walt Disney World Swan and Dolphin Resort

Restaurants

1	Shula's Steak House
2	Lobby Lounge
3	Cabana Bar and Beach Club
4	Picabu
5	The Fountain
6	Todd English's bluezoo
7	Fresh Mediterranean Market

Other

8	Lobby/Front Desk
9	Concierge
10	Disney Guest Services
11	Business Center
12	Shipping Desk
14	Health Club
15	Camp Dolphin
16	Guest Laundry
17	Game Room
18	Mandara Spa

Outdoor

WT	Disney Water Taxi
20	Grotto Pool and Beach
WP	Whirlpools
21	Children's Playground
22	Cabana Beach Hut
23	Pacific Terrace
24	Cabana Deck
25	Lap Pool
26	Spring Pool
27	Kiddie Pool
SA	Smoking Area

Restaurants

A	Splash
B	Splash Terrace
C	Garden Grove
D	Kimonos
E	Java Bar
F	IL Mulino New York Trattoria

Other

G	Lobby/Front Desk
H	Concierge/Disney Guest Services
I	Business Center/Shipping Desk
J	Convention Registration Desk
K	Shopping
L	Health Club
M	Game Room
N	Bakery Display

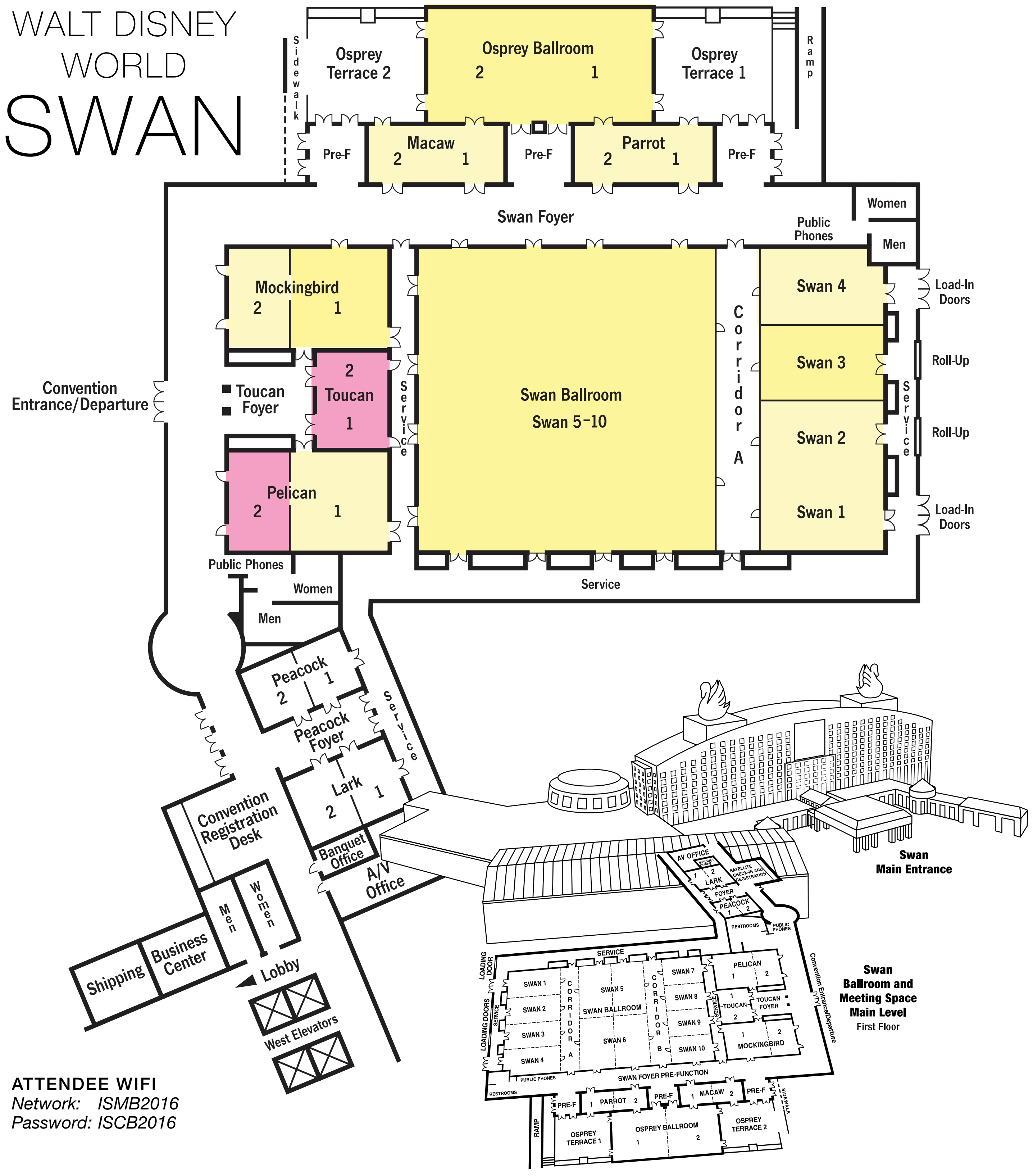
Outdoor

O	Disney Shuttle Bus
WT	Disney Water Taxi
P	Lake Terrace
Q	Swan Terrace
R	Lap Pool
WP	Whirlpool
S	Crescent Terrace
T	Osprey Terrace 1
U	Osprey Terrace 2
SA	Smoking Area

ATTENDEE WIFI
Network: *ISMB2016*
Password: *ISCB2016*

SIGs, Satellites, SCS12 and AKES Schedule

Swan Hotel Conference Centre



ATTENDEE WIFI

Network: ISMB2016

Password: ISCB2016

SIGs, Satellites, SCS12 and AKES Schedule

Swan Hotel Conference Centre

Thursday, July 7

3:00 PM – 6:00 PM	**REGISTRATION** • *Dolphin Hotel Convention Foyer (near Dolphin Hotel guest desk)*

Friday, July 8

ROOMS	OSPREY 1/2	MACAW 1/2	SWAN 3	MOCKING-BIRD 1	SWAN 1/2	PELICAN 2	MOCKING-BIRD 2	SWAN 4	PELICAN 1	PARROT 1/2
8:30 AM - 10:15 AM	**3Dsig (Two Day)**	**CAMDA (Two Day)** *Starts at 4:00 pm*	**BOSC (Two Day)**	**Bio-Ontologies (Two Day)**	**HitSeq: High Throughput Sequencing Algorithms & Applications (Two Day)**	**BioVis: Biological Data Visualization (One Day)**	**Integrative RNA Biology (One Day)**	**Network Biology SIG (One Day)**	**TransMed SIG (One Day)**	**Student Council Symposium 12 (One Day)**
10:15 AM - 10:45 AM	**COFFEE BREAK** • *Swan Foyer*									
10:45 AM - 12:30 PM										
12:30 PM - 1:30 PM	**LUNCH (WITH POSTERS)** • *Swan 5–10*									
1:30 PM - 3:30 PM	**3Dsig** *Continued*		**BOSC** *Continued*	**Bio-Ontologies** *Continued*	**HitSeq: High Throughput Sequencing Algorithms & Applications** *Continued*	**BioVis: Biological Data Visualization** *Continued*	**Integrative RNA Biology** *Continued*	**Network Biology SIG** *Continued*	**TransMed SIG** *Continued*	**Student Council Symposium 12** *Continued*
3:30 PM - 4:00 PM	**COFFEE BREAK** • *Swan Foyer*									
4:00PM - 6:00 PM		**CAMDA (Two Day)** *Starts at 4:00 pm*								
6:00 PM - 8:00 PM	**POSTERS • VARIOUS SIGs (FINISH TIMES MAY VARY)** • *Swan 5–10*									

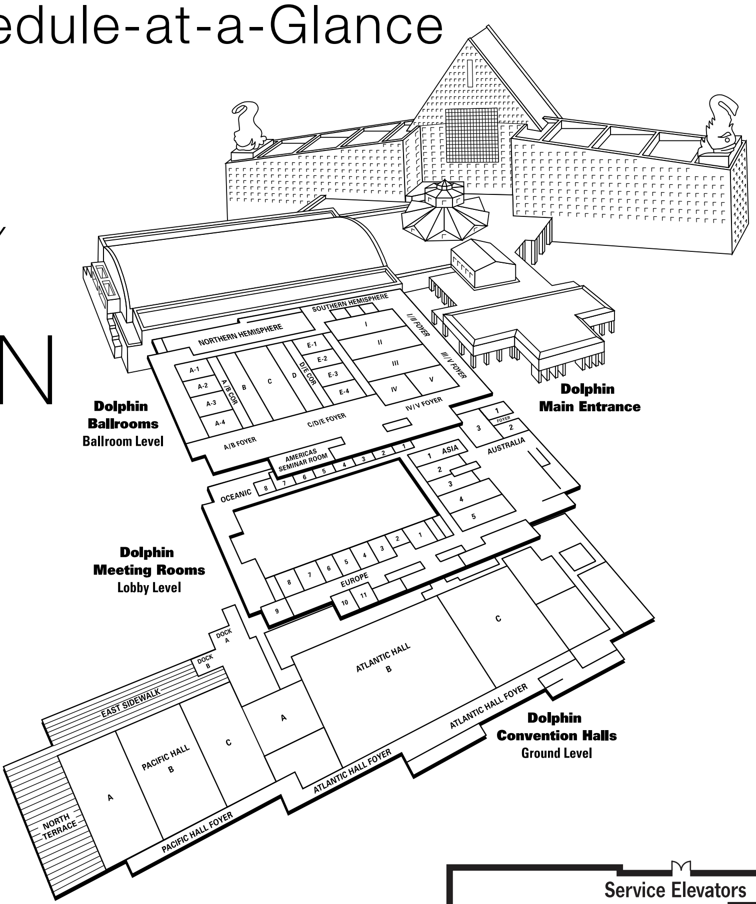
Saturday, July 9

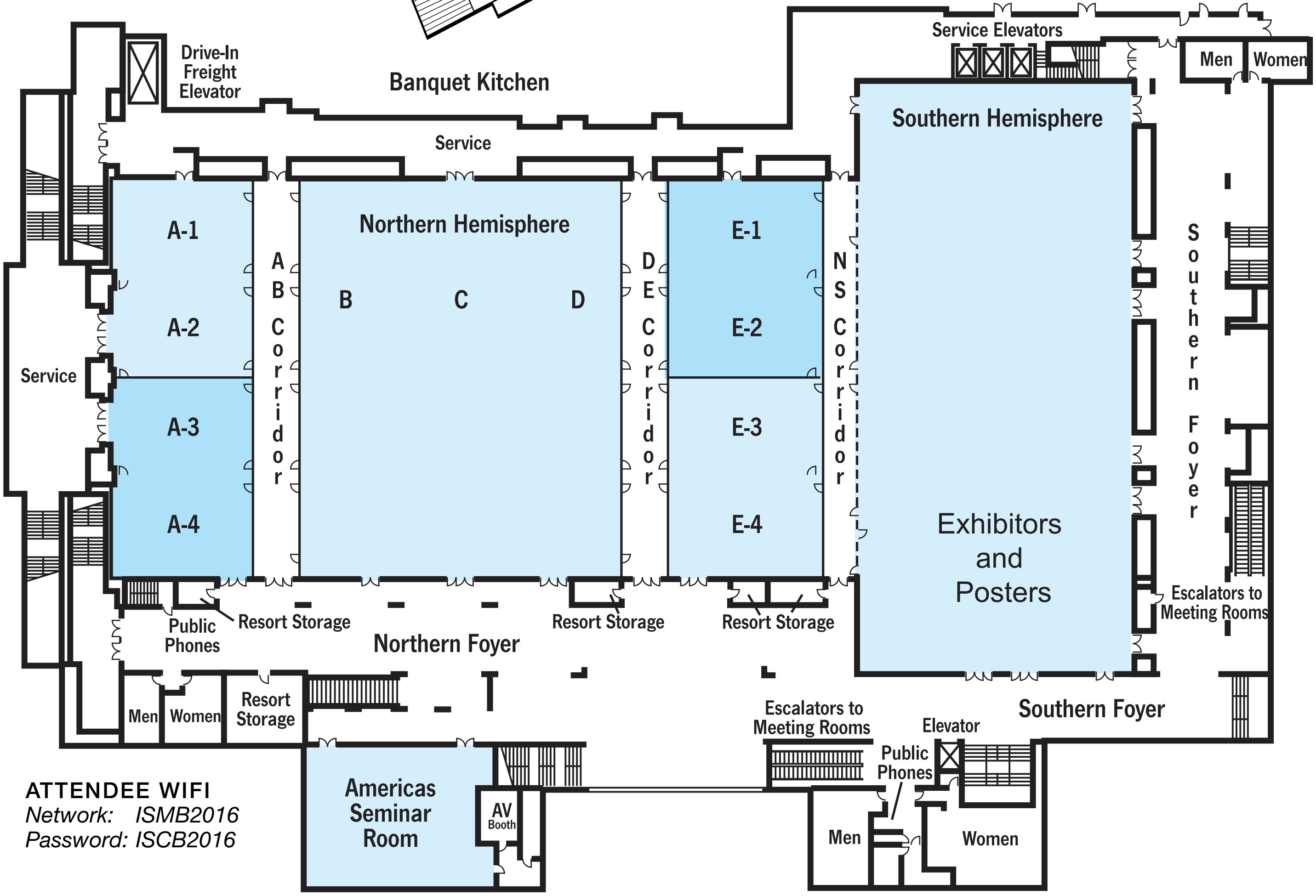
ROOMS	OSPREY 1/2	MACAW 1/2	SWAN 3	MOCKING-BIRD 1	SWAN 1/2	PARROT 1/2	SWAN 4	PELICAN 1	MOCKING-BIRD 2	PELICAN 2	TOUCAN 1/2
8:30 AM - 10:15 AM	**3Dsig (Two Day)**	**CAMDA (Two Day)** *Starts 9:00 am*	**BOSC (Two Day)**	**Bio-Ontologies (Two Day)**	**HitSeq: High Throughput Sequencing Algorithms & Applications (Two Day)**	**Function SIG (One Day)**	**Regulatory Genomics SIG — RegGenSIG (One Day)**	**SysMod SIG (One Day)**	**VarI-SIG (One Day)**	**AKES01: Clouds, Clusters, and Containers**	**AKES02: Community Efforts to Enable Data Analyses**
10:15 AM - 10:45 AM	**COFFEE BREAK** • *Swan Foyer*										
10:45 AM - 12:30 PM											
12:30 PM - 1:30 PM	**LUNCH (WITH POSTERS)** • *Swan 5–10*										
1:30 PM - 3:30 PM	**3Dsig** *Cont'd*	**CAMDA** *Cont'd*	**BOSC** *Cont'd*	**Bio-Ontologies** *Cont'd*	**HitSeq: High Throughput Sequencing Algorithms & Applications** *Cont'd*	**Function SIG** *Cont'd*	**Regulatory Genomics SIG — RegGenSIG** *Cont'd*	**SysMod SIG** *Cont'd*	**VarI-SIG** *Cont'd*	**AKES01** *Cont'd*	**AKES04: Living on the Edge (of Translational Informatics)**
3:30 PM - 4:00 PM	**COFFEE BREAK** • *Swan Foyer*										
4:00PM - 6:00 PM											
5:30 PM - 7:30 PM	**OPENING RECEPTION WITH EXHIBITORS** • *Southern Hemisphere — Dolphin Hotel*										

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

WALT DISNEY
WORLD
DOLPHIN





ATTENDEE WIFI

Network: ISMB2016

Password: ISCB2016

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

🧬 Genes 💊 Disease 🧪 Protein 🕸 Systems 101 Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Saturday, July 9

5:30 PM - 7:30 PM | **OPENING RECEPTION WITH EXHIBITORS** • *Southern Hemisphere — Dolphin Hotel*

Sunday, July 10

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
8:45 AM - 9:00 AM	**Opening Welcome** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**ISCB FELLOWS KEYNOTE** **KN01: Ras signaling: a challenge to the biological sciences** **Ruth Nussinov,** *National Cancer Institute, United States and Tel Aviv University, Israel*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**COSI: Common NetBio/SysMod.** *Chairs: Nicolas Le Novere and Alex Pico. Presenters: Lars Juhl Jensen, Nathan Price*	**TP001: Robust Detection of Alternative Splicing in a Population of Single Cells.** *Joshua Welch* **H** 🧬	**TP002: DFLpred: High throughput prediction of disordered flexible linker regions in protein sequences.** *Fanchi Meng* **P** 🧪	**TP003: Functionally profiling metagenomes and metatranscriptomes at species-level resolution.** *Eric Franzosa* **H** 🧬 🕸	**Oral Presentations** **OP01: Leslie D. Seitz** **OP03: Joseph Crawford** **OP04: Alon Diament** **OP05: Nicolle Witte** **OP06: Nguyen Vo** **OP07: Deepthi Rajagopalan** **OP08: Wen-Chang Lin** **OP09: Hosna Jabbari** **OP10: Hans-Ulrich Klein**	**WK01: JPI (Junior Principal Investigator)** *Organizers: Manuel Corpas, Lucia Peixoto, Washington State; Geoff Macintyre* **Part A: Welcome and icebreaker.** *Lucia Peixoto* **Part B: How to outline an individualized career development plan to become a successful PI.** *Sandrine Dudoit*
10:30 AM - 10:50 AM		**TP004: Scalable latent-factor models applied to single-cell RNA-seq data separate biological drivers from confounding effects.** *Florian Buettner* **L** 🧬	**TP005: Unexpected Features of the Dark Proteome.** *Nelson Perdigão* **H** 🧪	**TP006: Integrating very large multi'omics data by hierarchical all-against-all association testing.** *Gholamali Rahnavard* **L** 🧬 🕸		
10:50 AM - 11:10 AM		**TP007: Lightweight transcriptomics.** *Surojit Biswas* **L** 🧬	**TP008: Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing.** *Yu Xia* **H** 🧪	**TP009: Single molecule-level characterization of bacterial epigenomes, heterogeneity and gene regulation.** *Gang Fang* **H** 🧬		
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS** • *Southern Hemisphere Ballroom*					
11:40 AM - 12:00 PM	**COSI: Common NetBio/SysMod** *Continued* **Joint Community Discussion with** *Natasa Przulj and Jonathan Karr* **Closing Comments by Co-chairs**	**TP010: Analysis of aggregated cell-cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells.** *Alfred Schissler* **P** 💊 🕸	**TP011: Large-scale Text Mining Web Services for Bioinformatics Research.** *Zhiyong Lu* **H** 101	**TP012: Genetic Architectures of Quantitative Variation in RNA Editing Pathways.** *Tongjun Gu* **H** 🧬	**OP11: Francislon Silva de Oliveira** **OP12: Loukia Lili** **OP13: Sophia Banton** **OP14: Lilah Toker** **OP15: Seungyeul Yoo** **OP16: Hui Liu** **OP17: Urszula Czerwinska** **OP18: Taejeong Bae** **OP19: Chia-Jung Chang** **OP20: Manuel Zahariev**	**WK01: JPI** *Continued* **Climbing the grant ladder: The importance of establishing a record of funding early in your career** **Part A: Outline of funding opportunities for early career scientists by stage.** *Lucia Peixoto* **Part B: Climbing the tenure ladder: strategic decisions for promotion.** *Yana Bromberg* **Structured Discussion**
12:00 PM - 12:20 PM		**TP013: Development of a Bayesian tensor factorization model to predict drug response curves in cancer cell lines.** *Nathan Lazar* **L** 💊 101	**TP014: Text as Data: Using text-based features for proteins representation and for computational prediction of their characteristics.** *Hagit Shatkay* **H** 🧪 101	**TP015: A novel algorithm for calling mRNA m6A peaks by modeling biological variances in MeRIP-seq data.** *Yufei Huang* **P** 🧬		
12:20 PM - 12:40 PM		**TP016: DrugE-Rank: Improving Drug-Target Interaction Prediction of New Candidate Drugs or Targets by Ensemble Learning to Rank.** *Shanfeng Zhu* **P** 💊 101	**TP017: Good news: we are getting better at predicting protein function.** *Iddo Friedberg* **L** 🧪 101	**TP018: RNAiFold2T: Constraint Programming design of thermo-IRES switches.** *Juan Antonio Garcia-Martin* **P** 🧬		

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

BoF: Birds of a Feather
OP: Oral Poster
SST: Special Sessions Track
TP: Themed Presentations
TT: Technology Track
WK: Workshop

Sunday, July 10

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE** • *Hotel and Exhibition Hall*					
12:45 PM - 1:45 PM	*"Birds-of-a-feather" (BoFs) are open meetings for participants to meet and talk about topics of mutual interest.*	**BoF01: Exploring and Refining Core Competencies for Bioinformatics (ISCB Curriculum Task Force)** *Leader: Lonnie Welch*	**BoF02: Commons Credits Pilot — Exploring New Ways to Pay for Biomedical Computing** *Leader: David M. Tanenbaum*	**BoF03: Cytoscape Q&A for Users and Developers** *Leaders: Alex Pico, Scooter Morris*	**BoF04: Equal Opportunity in Science — Overcoming Challenges, Increasing Diversity: Gender Balance** *Leader: Bonnie Berger*	**BoF05: Student Council Career Central** *Leader: Student Council*
2:00 PM - 2:20 PM	**SST01: Lost in ribosome profiling,** *Organizer: Tamir Tuller* **Part A: Lost in ribosome-profiling.** *Tamir Tuller* **Part B: The hidden code behind the genetic code.** *Antonio J. Giraldez*	**TP019: Temporal dynamics of collaborative networks in large scientific consortia.** *Daifeng Wang* H	**TP020: Integrative computational modeling across tumors reveals context specific impact of mutations.** *Hatice Osmanbeyoglu* L	**TP021: Boosting alignment accuracy through adaptive local realignment.** *Dan Deblasio* L	**Oral Posters**	**WK01** *Continued* **Strategies to generate data: wet-lab, collaborations and consortia.** *Chair: Logan Everett. Presenter: Trey Ideker* **Structured Discussion** **Roundtable Discussion:** *Sandrine Dudoit, Trey Ideker, Curtis Huttenhower* **Part C: Questions & Wrap up**
2:20 PM - 2:40 PM		**TP022: Positive and negative forms of replicability in gene network analysis.** *Jesse Gillis* H	**TP023: COSMOS: accurate detection of somatic structural variations through asymmetric comparison between tumor and normal samples.** *Jun Sese* H	**TP024: The Post-Genomic Era of Biological Network Alignment: Latest Insights.** *Vipin Vijayan* L	**OP21: Amir Karger** **OP22: Francesca Rizzato** **OP23: Zebulun Arendsee** **OP24: Fan Zheng** **OP25: Varsha D. Badal** **OP26: Zhouxi Wang** **OP27: Maria Anna Rapsomaniki** **OP28: Jing Wang** **OP29: Ying Jin** **OP30: Qingyu Chen**	
2:40 PM - 3:00 PM		**TP025: Efficient Data-Driven Model Learning for Dynamical Systems.** *Ermao Cai* L	**TP026: intSKAT, an integrated Sequence Kernel Association Test, to identify novel clinically impactful somatic mutations in melanomas.** *Y. Ann Chen* L	**TP027: Covariation Is a Poor Measure of Molecular Coevolution.** *David Talavera* H		
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS** • *Southern Hemisphere Ballroom*					
3:30 PM - 3:50 PM	**SST01** *Continued* **Part C: Uncovering tumor-specific amino acid vulnerabilities by differential ribosome codon reading.** *Reuven Agami* **Part D: Statistical Methods for the Analysis of Ribosome Profiling Data.** *Adam Olshen* **Part E: Understanding Biases in Ribosome Profiling Experiments Reveals Signatures of Translation Dynamics in Yeast.** *Jeff Hussmann*	**TP028: Quantitative analysis of microRNA mediated regulation on competing endogenous RNAs.** *Xiaowo Wang* H	**TP029: A Weighted Exact Test for Significance of Mutually Exclusive Mutations in Cancer.** *Mark Leiserson* L	**TP030: CMsearch: simultaneous exploration of protein sequence space and structure space improves not only protein homology detection but also protein structure prediction.** *Xin Gao* P	**OP31: Catherine Snow** **OP32: Stefano Ceri** **OP33: Marcel Grunert** **OP34: Yin Tang** **OP35: Hao Sun** **OP36: Lina Zheng** **OP37: Megan Crow** **OP38: Amrita Roy Choudhury** **OP39: Alastair M. Kilpatrick**	**WK01** *Continued* *Chair: Curtis Huttenhower* **Part A: How to get involved in the ISCB as a JPI.** *Diane Kovats* **Part B: Roundtable Discussion:** *Sandrine Dudoit, Trey Ideker, Curtis Huttenhower*
3:50 PM - 4:10 PM		**TP031: Reconstructing the temporal progression of HIV-1 immune response pathways.** *Siddhartha Jain* P	**TP032: Clonal evolution inference and visualization in metastatic colorectal cancer.** *Ha X. Dang* L	**TP033: Ensemble-Based Evaluation for Protein Structure Models.** *Daisuke Kihara* P		
4:10 PM - 4:30 PM		**TP034: Identification of essential molecular and cellular processes controlling the response time and intensity of inflammation.** *Alexander Mitrophanov* H	**TP035: Robust discrimination of cell types from tissue expression profiles.** *Aaron M. Newman* H	**TP036: Investigating molecular determinants of ebolavirus pathogenicity.** *Mark Wass* L		

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🧬 Genes 🦠 Disease 🧪 Protein 🕸 Systems 🔢 Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Sunday, July 10

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4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB OVERTON AWARD KEYNOTE** *Room: Northern Hemisphere BCD* **KN02: 3D Structure and Fitness of Proteins and RNA from Evolutionary Sequences** **Deborah Marks,** *Harvard Medical School, United States*					
5:40 PM - 7:30 PM	**Poster Session (odd numbered posters)** **SOUTHERN HEMISPHERE BALLROOM**					
6:00 PM - 7:00 PM	*Room: American Seminar* **TT01: Transparent toxicology via enhanced peer review platform,** *Stephanie Boue, Philip Morris International R&D*					

Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
8:45 AM - 9:00 AM	**Morning Welcome — ECCB 2016 Presentation/PhRMA Award Presentations** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**KEYNOTE PRESENTATION** **KN03: Identification of Novel Cell Types in the Brain Using Single-Cell Transcriptome Sequencing** **Sandrine Dudoit,** *University of California, Berkeley, United States*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**SST02: DATA: Compressive Omics: Making Big Data Manageable through Data Compression,** *Organizer(s): Peter Rose, Olgica Milenkovic* **Part A: Computational Biology in the 21st Century: Scaling with Compressive Algorithms.** *Bonnie Berger* **Part B: Trends and Methods in Genomic Data Compression.** *Idoia Ochoa* **Part C: Meaningful Data Compression and Reduction of High-Throughput Sequencing Data.** *Alexander Schliep*	**TP037: LINEs between species: Evolutionary dynamics of LINE-1 retrotransposons across the eukaryotic tree of life.** *David Adelson* **L** 🧬	**TP038: Convolutional neural network architectures for predicting DNA-protein binding.** *Haoyang Zeng* **P** 🧪 🔢	**TP039: What Time is It? Deep Learning Approaches for Circadian Rhythms.** *Forest Agostinelli* **P** 🧬 🕸	**TT02: Chemical Exposure Response Markers Identification in Blood and Genomic-based Diagnostics - Lessons Learned from the sbv IMPROVER Systems Toxicology Computational Challenge,** *Carine Poussin, Philip Morris International R&D*	**WK02: Workshop on Education in Bioinformatics (WEB): Exploiting Cloud and Virtual Resources for Training.** *Organizers: Mainá Bitar, Michelle D. Brazas, Fran Lewitter, Patricia M. Palagi* **Part A: Getting the Best Training in Computational Biology in an Era of Cloud Computing and Big Data.** *Phil Bourne* **Part B: How to Scale Science and People Using the Cloud.** *Nirav Merchant*
10:30 AM - 10:50 AM		**TP040: phRAIDER: Pattern-Hunter Based Rapid Ab Initio Detection of Elementary Repeats.** *John Karro* **P** 🧬	**TP041: RCK: accurate and efficient inference of sequenceand structure-based protein-RNA binding models from RNAcompete data.** *Yaron Orenstein* **P** 🧬 🔢	**TP042: Core Regulatory Circuitry of the Plant Circadian System.** *Pan-Jun Kim* **H** 🧬 🕸		
10:50 AM - 11:10 AM		**TP043: DNA editing of LTR retrotransposons reveals the impact of APOBECs on vertebrate genomes.** *Binyamin Knisbacher* **H** 🧬	**TP044: Predicting the sequence specificities of DNA- and RNA-binding proteins by deep learning.** *Hannes Bretschneider* **H** 🧪 🔢	**TP045: A Framework for Integrating Co-expression Networks with GWAS to Prioritize Candidate Genes in Maize.** *Chad Myers* **H** 🧬 🕸		
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS** • *Southern Hemisphere Ballroom*					

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Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
11:40 AM - 12:00 PM	**SST02:** *Continued* **Part D: Compressive Structural Bioinformatics: High Efficiency 3D Structure Compression.** *Peter Rose*	**TP046: Read-Based Phasing of Related Individuals.** *Shilpa Garg* P	**TP047: Revisiting the computational analysis of DNase sequencing.** *Ivan G. Costa* H	**TP048: Novel Applications of Multi-task Learning and Multiple Output Regression to Multiple Genetic Trait Prediction.** *Dan He* P	**TT02:** *Continued*	**WK02: WEB** *Continued* **Part C: Packaging computational biology tools for broad distribution and ease-of-reuse.** *Matthew Vaughn* **Part D Panel: Experience Exchange: Ideas for Exploiting the Cloud in Bioinformatics Training.** *Moderator: Michelle Brazas* *Panelists: Phil Bourne, Nirav Merchant, Annette McGrath, Matthew Vaughn*
12:00 PM - 12:20 PM	**Part E: Theoretical Foundations and Software Infrastructure for Biological Network Databases.** *Mehmet Koyuturk* **Part F: Task-Specific Compression for Biomedical Big Data.** *Ali Bilgin*	**TP049: An Algorithm for Computing the Gene Tree Probability under the Multispecies Coalescent and its Application in the Inference of Population Tree.** *Yufeng Wu* P	**TP050: The Role of Genome Accessibility in Transcription Factor Binding in Bacteria.** *Antonio Gomes* L	**TP051: A Network-driven Approach for Genome-wide Association Mapping.** *Seunghak Lee* P		
12:20 PM - 12:40 PM		**TP052: Deciphering evolutionary strata on plant sex chromosomes and fungal mating-type chromosomes through compositional segmentation.** *Rajeev Azad* H	**TP053: Predicting effects of noncoding variants with deep learning-based sequence model.** *Jian Zhou* H	**TP054: Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions.** *Haiquan Li* H		
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE** • *Hotel and Exhibition Hall*				**ISCB Town Hall 12:45 – 1:50 PM**	
2:00 PM - 2:20 PM	**TP055: DeepMeSH: Deep Semantic Representation for Improving Large-scale MeSH Indexing.** *Shanfeng Zhu* P	**TP056: Alignment-free scaffolding of large genome drafts using long sequences and jumping library MPET reads.** *Rene Warren* H	**TP057: A Cross-Species Bi-Clustering Approach to Identifying Conserved Co-regulated Genes.** *Jiangwen Sun* P	**TP058: Candidate gene prioritization with Endeavour.** *Amin Ardeshirdavani* L	**TT03: Repeatable Science at Scale: Using Common Workflow Language and Docker for science on AWS,** *Angel Pizarro, Amazon Web Services*	**WK03: Bioinfo-Core Workshop** *Organizers: Charlie Whittaker, Jian-Liang (Jason) Li, Madelaine Gogol* **Part A: Big Data.** *Presenters: Yury Bukhman, Alberto Riva* **Big Data Panel** *Moderator: Madelaine Gogol* *Panelists: Yury Bukhman, Alberto Riva, Hua Li, Jyothi Thimmapuram*
2:20 PM - 2:40 PM	**TP059: Translation of Genotype to Phenotype by a Hierarchy of Cell Subsystems.** *Michael Ku Yu* H	**TP060: Genome assembly from synthetic long read clouds.** *Volodymyr Kuleshov* P	**TP061: Most of the tight positional conservation of transcription factor binding sites near the transcription start site is due to their co-localization within regulatory modules.** *John Spouge* L	**TP062: Furthering understanding of human diseases through integrative cross-species analysis.** *Victoria Yao* L		
2:40 PM - 3:00 PM	**TP063: Jumping across biomedical contexts using compressive data fusion.** *Marinka Zitnik* P	**TP064: Multi-Genome Scaffold Co-Assembly Based on the Analysis of Gene Orders and Genomic Repeats.** *Sergey Aganezov* L	**TP065: Structure-Based Prediction of Transcription Factor Binding Specificity using an Integrative Energy Function.** *Alvin Farrel* P	**TP066: SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets.** *Jie Zheng* H		
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS**					**SOUTHERN HEMISPHERE BALLROOM**

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

🧬 Genes 🦠 Disease ∫ Protein ⬡ Systems 101 Data
H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Monday, July 11

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
3:30 PM - 3:50 PM	**TP067: CellCODE: a robust latent variable approach to differential expression analysis for heterogeneous cell populations.** *Maria Chikina* **H** ⬡ 101	**TP068: deBWT: parallel construction of Burrows-Wheeler Transform for large collection of ge-nomes with de Bruijn-branch encoding.** *Bo Liu* **P** 🧬 101	**TP069: Finding correct protein-protein docking models using ProQDock.** *Sankar Basu* **P** ∫	**TP070: Gene essentiality and synthetic lethality in haploid human cells.** *Jacques Colinge* **H** 🧬 ⬡	**TT04: Biological interpretation of 'omics data: The power of causal analysis,** *Andreas Kraemer, QIAGEN Bioinformatics*	**WK03: Bioinfo-Core Workshop** *Continued* **Part B: Big Compute.** *Presenters: Sergi Sayols Puig, Jingzhi Zhu* **Big Compute Panel.** *Moderator: Brent Richter* *Panelists: Sergi Sayols Puig, Jingzhi Zhu, Sara Grimm*
3:50 PM - 4:10 PM	**TP071: Solving the influence maximization problem on biological networks; a case study involving the cell cycle regulatory network in Saccharomyces cerevisiae.** *David Gibbs* **L** ⬡ 101	**TP072: Compacting de Bruijn graphs from sequencing data quickly and in low memory.** *Rayan Chikhi* **P** 🧬 101	**TP073: Human Protein Complex Map: integration of 10K mass spectrometry experiments.** *Kevin Drew* **L** ∫	**TP074: Influence maximization in time bounded network identifies transcription factors regulating perturbed pathways.** *Kyuri Jo* **H** 🧬		
4:10 PM - 4:30 PM	**TP075: Scalable Tools for Quantitative Analysis of Chemical-Genetic Interactions from Sequencing-Based Chemical-Genetic Interaction Screens.** *Scott Simpkins* **L** ⬡ 101	**TP076: Succinct Colored de Bruijn Graphs.** *Martin Muggli* **L** 🧬 101	**TP077: An Integer Programming Framework for Inferring Disease Complexes from Network Data.** *Konrad Klockmeier* **P** ∫	**TP078: Mogrify: a predictive system for cell reprogramming.** *Julian Gough* **H** 🧬 ⬡		
4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB 2016 Outstanding Contributions Award Presentation to Burkhard Rost** *Room: Northern Hemisphere BCD* **KEYNOTE PRESENTATION** **KN04: Understanding Cellular Heterogeneity** **Sarah Teichmann,** *Wellcome Trust Sanger Institute, Hinxton, United Kingdom*					
5:40 PM - 7:30 PM	**POSTER SESSION (EVEN NUMBERED POSTERS)** • *Southern Hemisphere Ballroom*					

ROOMS	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	AMERICA'S SEMINAR
6:00 PM - 6:20 PM	**TT05: Bisulfite sequence analysis on CyVerse Discovery Environment,** *Jawon Song, Texas Advanced Computing Center*	**TT06: GenePattern Notebook: An integrated analytical environment for genomic research,** *Michael Reich, UC San Diego*	**TT07: BioSchemas: schema.org development for the Life Sciences,** *Niall Beard, University of Manchester*
6:20 PM - 6:40 PM	**TT08: The bioBakery: a platform for comprehensive analysis of microbial community shotgun sequencing data,** *Eric Franzosa, Harvard T. H. Chan School of Public Health*	**TT09: Introducing N-of-1-pathways transcriptome analytic tools: Enabling precision medicine through single-subject studies,** *Yves Lussier, University of Arizona*	**TT10: FAIRDOM: Publishing FAIR Data and Models in Interdisciplinary Life Sciences,** *Natalie Stanford, University of Manchester*
6:40 PM - 7:00 PM	**TT11: PISKa: a HPC tool for stochastic agent and rule-based modeling of spatially explicit complex biological systems,** *Tomas Perez-Acle, Fundacion Ciencia & Vida*		
7:00 PM - 9:00 PM			**ET01: ISCB Wikipedia and Wikidata Edit-a-thon** *Leader: Wiki Foundation Group*

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WK: Workshop
IS: Industry Session

Tuesday, July 12

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
08:45 AM - 9:00 AM	**Morning Welcome and Announcements: ISMB/ECCB 2017 Presentation** *Room: Northern Hemisphere BCD*					
9:00 AM - 10:00 AM	**ISCB INNOVATOR AWARD KEYNOTE** **KN05: Computational Challenges in Personalized Genomics** **Serafim Batzoglou,** *Stanford University, United States*					
10:00 AM - 10:10 AM	**MOVEMENT TO SESSIONS**					
10:10 AM - 10:30 AM	**SST03: Genomic Big Data Management, Modeling and Computing,** *Organizer(s): Stefano Ceri, Marco Masseroli, Emanuel Weitschek* **Part A: Genomic big data management and the GenoMetric Query Language.** *Stefano Ceri* **Part B: TCGA2BED and CAMUR for cancer NGS data processing.** *Emanuel Weitschek* **Part C: Searching patterns in genomic feature regions.** *Ilaria Bartolini*	**TP079: Compressive Mapping for Next-Generation Sequencing.** *Deniz Yorukoglu* **H**	**TP080: Interactome based drug discovery and disease-disease connections.** *Gaurav Chopra* **L**	**TP081: Classifying Cancer Samples by microRNA Profiles: Read the Fine Print!** *Roni Rasnic* **L**	**TT12: Big data technology for designing high-quality oligonucleotides via exhaustive homology tests.** *Min-Soo Kim, DGIST*	**IS01: Computational Opportunities and Challenges from Leading Companies in Industrial Biotechnology (IB),** *Leader: Jean-Francois Tomb*
10:30 AM - 10:50 AM		**TP082: RapMap: A Rapid, Sensitive and Accurate Tool for Mapping RNA-seq Reads to Transcriptomes.** *Avi Srivastava* **P**	**TP083: A convex optimization approach for identification of human tissue-specific interactomes.** *Shahin Mohammadi* **P**	**TP084: RNA sequencing-based cell proliferation analysis across 19 cancers identifies a subset of proliferation-informative cancers with a common survival signature.** *Brittany Lasseigne* **L**	**TT13: MyGene.info and MyVariant.info: high-performance web services for querying gene and variant annotation.** *Chuniel Wu, The Scripps Research Institute*	**Introduction to Industrial Biotechnology: Effective Strategies for Protein Engineering and Economical Large Scale Protein Production.** *David Estell, DuPont Industrial Biosciences*
10:50 AM - 11:10 AM		**TP085: ADAGE-Based Extraction of Biological Context from Public Gene Expression Data.** *Jie Tan* **H**	**TP086: Precision drug repurposing and multi-target drug design using structural systems pharmacology.** *Thomas Hart* **H**	**TP087: Data-Driven Analysis of Lymphocyte Infiltration in Breast Cancer Development and Progression.** *Ruth Dannenfelser* **L**	**TT14: Exploring Open-Access Genetic Variants & Clinical Associations: The European Variation Archive at EMBL-EBI.** *Cristina Gonzalez Garcia, EMBL-EBI*	**Bioinformatics in the Biotech Industry – Tales from the Trenches.** *Bastien Chevreux, DSM Nutritional Products* **Computational Biology Challenges at an Industrial Biotech.** *Amoolya Singh, Amyris*
11:10 AM - 11:40 AM	**COFFEE BREAK WITH EXHIBITORS •** *Southern Hemisphere Ballroom*					
11:40 AM - 12:00 PM	**SST03** *Continued* **Part D:** *Alfonso Valencia* **Part E: Semi-automated human genome annotation using chromatin data.** *Michael Hoffman*	**TP088: SHARAKU: An algorithm for aligning and clustering read mapping profiles of deep sequencing in non-coding RNA processing.** *Yasubumi Sakakibara* **P**	**TP089: Nucleotide sequence composition adjacent to intronic 5' end improves translation costs in fungi.** *Zohar Zafrir* **L**	**TP090: Phenotype Stratification from the Electronic Health Record using Autoencoders.** *Brett K Beaulieu-Jones* **L**	**TT15: GenomeSpace: An environment for frictionless bioinformatics.** *Sara Garamszegi, The Broad Institute of MIT and Harvard*	**IS01** *Continued* **Beyond Silos: Knowledge Management as the Key to Operational Excellence — the BioXM System, a Universal Framework.** *Sascha Losko, Biomax Informatics AG*
12:00 PM - 12:20 PM		**TP091: Analysis of differential splicing suggests different modes of short-term splicing regulation.** *Hande Topa* **P**	**TP092: Prediction of Ribosome Footprint Profile Shapes from Transcript Sequences.** *Tzu-Yu Liu* **P**	**TP093: Leveraging electronic medical records for systematic drug repositioning.** *Hyojung Paik* **H**	**TT16: Recent Developments in the Pathway Tools Software and BioCyc Databases.** *Peter Karp, SRI International*	**Scaling up of Renewable Chemicals.** *Karl Sanford, DuPont Industrial Biosciences*
12:20 PM - 12:40 PM		**TP094: Fast and accurate computation of differential splicing across multiple conditions.** *Eduardo Eyras* **H**	**TP095: Rapid Translation Initiation Prevents Mitochondrial Localization of mRNA.** *Paul Horton* **L**	**TP096: Comparative Analyses of Population-scale Phenomic Data in Electronic Medical Records Reveal Race-specific Disease Networks.** *Benjamin S. Glicksberg* **P**	**TT17: Open PHACTS now offers patent information and interactions from pathways.** *Chris Evelo, Maastricht University*	
12:40 PM - 2:00 PM	**LUNCH AVAILABLE FOR PURCHASE •** *Hotel and Exhibition Hall*					

ISMB 2016 Schedule-at-a-Glance

Dolphin Hotel

🧬 Genes 💊 Disease 🌀 Protein 🕸 Systems 🔢 Data

H Highlights Track **L** Late Breaking Research **P** Proceedings Track

Tuesday, July 12

ROOMS	NORTHERN HEMISPHERE BCD	NORTHERN HEMISPHERE A1/A2	NORTHERN HEMISPHERE A3/A4	NORTHERN HEMISPHERE E1/E2	AMERICA'S SEMINAR	NORTHERN HEMISPHERE E3/E4
12:45 PM - 1:45 PM			**BoF07: Synthetic Biology & SBOL** *Leader: Kevin Clancy*		**BoF06: Navigating the Industry Career Path** *Leader: ISCB Industry Advisory Council*	
2:00 PM - 2:20 PM	**SST04: Molecular Communication and Networking with Applications to Precision Medicine,** *Organizer: Radu Marculescu* **Part A: Biological Basis for Modeling Bacterial Communities.** *Luisa Hiller* **Part B: Molecular Tweeting: Bacteria Network Formation, Dynamics, and Control with Healthcare Applications.** *Radu Marculescu*	**TP097: Using genomic annotations increases statistical power to detect eGenes.** *Dat Duong* **P** 🧬	**TP098: Simultaneous prediction of enzyme orthologs from chemical transformation patterns for de novo metabolic pathway reconstruction.** *Masaaki Kotera* **P** 🌀 🕸	**TP099: Classifying and Segmenting Microscopy Images with Deep Multiple Instance Learning.** *Oren Kraus* **P** 🔢	**TT18: Integrating 3D Structure with Protein, Gene, and Validation Information at the RCSB PDB.** *Peter Rose, UC San Diego*	**TT19: Accelerated NGS Interpretation via the GeneCards Suite.** *Marilyn Safran, Weizmann Institute of Science*
2:20 PM - 2:40 PM		**TP100: GeneiASE: Detection of condition dependent and static allele-specific expression from RNA-seq data without haplotype information.** *Daniel Edsgärd* **H** 🧬	**TP101: Fast metabolite identification with Input Output Kernel Regression.** *Céline Brouard* **P** 🕸 🔢	**TP102: PHOCOS: Inferring Multi-Feature Phenotypic Crosstalk Networks.** *Yue Deng* **P** 🔢	**TT20: Phyre2: Protein modeling and analysis made easy.** *Mark Wass, University of Kent, United Kingdom*	**TT21: Read-Based Phasing Using WhatsHap.** *Marcel Martin, SciLifeLab*
2:40 PM - 3:00 PM		**TP103: Data-driven mechanistic analysis method to reveal dynamically evolving regulatory networks.** *Jukka Intosalmi* **P** 🧬 🕸	**TP104: Faster and More Accurate Graphical Model Identification of Tandem Mass Spectra using Trellises.** *Shengjie Wang* **P** 🌀	**TP105: CD30 cell graphs of Hodgkin lymphoma are not scale-free—an image analysis approach.** *Tim Schäfer* **H** 💊 🔢	**TT22: Using CATH-Gene3D to predict the structure and function of novel protein sequences.** *Christine Orengo, University College London*	**TT23: Large Scale Analyses with Galaxy.** *John Chilton, Galaxy Project*
3:00 PM - 3:30 PM	**COFFEE BREAK WITH EXHIBITORS •** *Southern Hemisphere Ballroom*					
3:30 PM - 3:50 PM	**SST04** *Continued* **Part C: Data-Driven Modeling and In Silico Simulation of Cell Signaling Pathways.** *Diana Marculescu* **Part D: On Scaling Graph Algorithms for Microbiome Applications.** *Ananth Kalyanaraman* **Part E: Panel**	**TP106: A novel method for discovering local spatial clusters of genomic regions with functional relationships from DNA contact maps.** *Kevin Yip* **P** 🧬	**TP107: BioASF: A Framework for Automatically Generating Executable Pathway Models Specified in BioPAX.** *Reza Haydarlou* **P** 🕸 🔢	**TT24: Images for Massively Parallel Drug Discovery.** *Blake Borgeson, Recursion Pharmaceuticals*	**TT25: bio.tools – life science software registry.** *Jon Ison, ELIXIR Denmark*	**TT26: IOBIO: interactive, visually-drive, real-time analysis of genomic big data.** *Alistair Ward, University of Utah*
3:50 PM - 4:10 PM		**TP108: Tracking the Evolution of 3D Gene Organization.** *Alon Diament* **L** 🧬	**TP109: PSAMM: A Portable System for the Analysis of Metabolic Models.** *Ying Zhang* **H** 🕸		**TT27: Visualizing and analyzing protein data with UniProt.** *Sangya Pundir, EMBL-EBI*	**TT28: BACNET: An interactive platform for analysis and publication of multi-omics study.** *Christophe Bécavin, Institut Pasteur*
4:10 PM - 4:30 PM		**TP110: A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data.** *Alexander Butyaev* **H** 🧬 🔢	**TP111: Linear effects models of signaling pathways from combinatorial perturbation data.** *Ewa Szczurek* **P** 🕸		**TT29: Linking literature and data through text mining in Europe PMC: SciLite — An annotation platform for biocuration.** *Senay Kafkas, EMBL-EBI*	**TT30: GeneWeaver.org A system for cross-species heterogeneous functional genomic data integration.** *Elissa Chesler, The Jackson Laboratory*
4:30 PM - 4:40 PM	**MOVEMENT TO KEYNOTE**					
4:40 PM - 5:40 PM	**ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE** *Room: Northern Hemisphere BCD* **KN06: Creating Disease Trajectories of Time-Ordered Comorbidities from Big Biomedical Data Covering Millions of Patients** **Søren Brunak,** *University of Copenhagen, Denmark*					
5:40 PM - 6:00 PM	**Conference Awards and Closing**					

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Akamai

www.akamai.com

As the global leader in Content Delivery Network (CDN) services, Akamai makes the Internet fast, reliable and secure for its customers. In the world of healthcare, life sciences, and bioinformatics, computational big data is consuming more and more bandwidth, placing increased load on online infrastructure. Leveraging the world's largest distributed computing platform, Akamai speeds Internet transactions and transmission of big data by placing cloud storage and computing power closer to the end user. Akamai's advanced web performance, mobile performance, and cloud security solutions are revolutionizing how companies in the field of healthcare and life sciences collaborate, conduct research and drive new discoveries.

PhRMA

http://www.phrmafoundation.org

The PhRMA Foundation supports young scientists in disciplines important to the pharmaceutical industry by awarding them competitive research fellowships and grants at a critical decision point at the outset of their careers. The aim is to encourage young scientists who will be the leaders of tomorrow to pursue careers in research and education related to drug discovery.

BRONZE SPONSORS

F1000Research **BOOTH 4**

http://f1000research.com

F1000Research is an Open Science publishing platform offering immediate publication of posters, slides and articles with no editorial bias. All articles benefit from transparent peer review and the inclusion of all source data. F1000Research publishes the ISCB Community Journal.

Recursion Pharmaceuticals **BOOTH 30**

http://www.recursionpharma.com

Recursion is a 2-year-old startup with fewer than 20 people, but we generate rich biological data at a pace comparable to some of the biggest institutions doing biology and disease research. We combine high-throughput cellular imaging experiments with intelligent computational methods, rapidly testing thousands of drugs against hundreds of diseases.

COPPER SPONSORS

Amazon Web Services **BOOTH 7**

http://aws.amazon.com/health

Amazon Web Services (AWS) provides life sciences and genomics organizations with secure, reliable, low-cost, easy-to-scale, global IT infrastructure "in the cloud." Hundreds of thousands of customers in 190 countries, rely on AWS for their bioinformatics needs, whether it is working with large public data sets or conducting clinical research that combines medical records with genomic information at population scale. Learn more: http://aws.amazon.com/health.

Oxford University Press **BOOTH 25**

http://www.oup.com

Oxford University Press publishes some of most respected and prestigious computational biology journals in the world. They include Bioinformatics, an official journal of ISCB, Database: The Journal of Biological Databases and Curation, and Nucleic Acids Research, among many others. Visit our stand to browse books and to pick up sample copies of journals.

Iowa State University, Bioinformatics and Coputational Biology

http://www.bcb.iastate.edu

The BCB Graduate Program offers interdisciplinary PhD training at the intersections of Biological, Computing and Information Sciences. More than 70 nationally and internationally known faculty - biologists, computer scientists, mathematicians, statisticians, and physicists - participate in a wide range of collaborative research projects. BCB's 100+ alumni have achieved exceptional outcomes.

QIAGEN Bioinformatics **BOOTH 31**

https://www.qiagenbioinformatics.com

QIAGEN Bioinformatics is powered by CLC bio, Ingenuity, and BIOBASE. We offer bioinformatics software tools for next generation sequencing (NGS) data analysis and interpretation. Our solutions are designed to be universal, so you can mix and match the technologies best suited to your needs.

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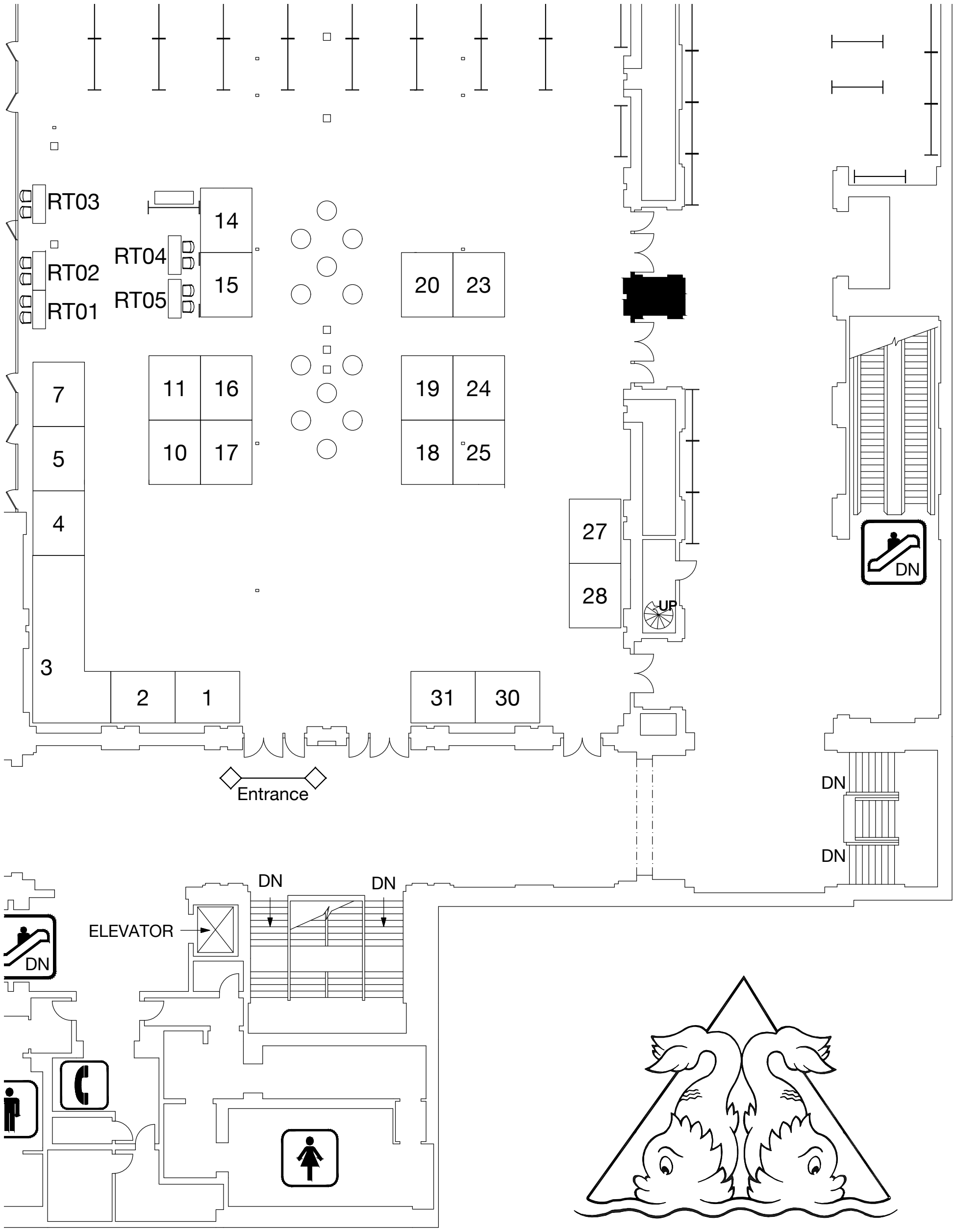
Exhibition Floor Plan

Southern Hemisphere Ballroom



BOOTH	EXHIBITOR
1	ISCB COMMUNITIES OF SPECIAL INTEREST
2	ISCB AFFILIATED GROUPS
3	ISCB STUDENT COUNCIL (ISCB-SC)
3	INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY (ISCB)
4	F1000RESEARCH
5	EMBL — AUSTRALIA
7	AMAZON WEB SERVICES
10	EUROPEAN BIOINFORMATICS INSTITUTE
11	SPRINGER
14	ST. JUDE CHILDREN'S RESEARCH HOSPITAL
15	SBV IMPROVER
16	NDEX PROJECT
17	CAMBRIDGE UNIVERSITY PRESS
18	PLOS
19	GOBLET
20	CRC PRESS
23	ECCB 2016
24	TRAVEL FELLOWSHIP DESK
25	OXFORD UNIVERSITY PRESS
27	ELIXIR DENMARK
28	ELSEVIER
30	RECURSION PHARMACEUTICALS
31	QIAGEN BIOINFORMATICS

RECRUITER TABLES

RT01	THE JACKSON LABORATORY
RT02	UNIVERSITY OF NEBRASKA AT OMAHA
RT03	DUKE UNIVERSITY
RT04	BIOINFORMATICS AND COMPUTATIONAL BIOLOGY @ ISU
RT05	SYLVESTER COMPREHENSIVE CANCER CENTER AT UNIVERSITY OF MIAMI, MILLER SCHOOL OF MEDICINE

WALT DISNEY WORLD
DOLPHIN

Art and Science Exhibition 2016

The Art & Science Exhibition 2016 presents artworks that have been generated as part of research projects. The prize for Best Art & Science work is 200USD. Winners will be announced online following ISMB 2016.

Vote for your favorite work at www.iscb.org/artsciencevote

Exhibitors

Booth 1

ISCB Communities of Special Interest (COSI)

https://www.iscb.org/iscb-cosis

COSIs are Communities of Special Interest. They have been built around major research themes within computational biology, or important activities such as networks of training, mentoring or support. COSIs hold regular meetings usually as SIGs or workshops in the main ISMB meeting. The ISCB COSI Connect web-portal displays information on COSI themes and activities.

Booth 2

ISCB Affiliated Groups

The booth will showcase the ISCB Affiliates program, which links ISCB and regional non-profit membership groups, centers, institutes and networks within specific geographic regions. Come to learn about the meetings and activities of ISCB's current Affiliates, and to discuss the possibility of affiliating your regional group with ISCB.

Booth 3

ISCB Student Council (ISCB-SC)

www.iscbsc.org

ISCB Student Council (SC) is an international network of young researchers in the broader disciplines of the field of Computational Biology. SC provides opportunities for networking, career enhancement and skills development for the next generation of Computational Biology leaders. The SC Symposium (symposium.iscbsc.org) is organized as a part of the annual ISMB conference with student presentations, keynotes, panel discussions and a poster session. Come visit our friendly SC representatives at the booth for more information.

Booth 3

International Society for Computational Biology

http://www.iscb.org

ISCB The International Society for Computational Biology (ISCB) (www.iscb.org) was the first and continues to be the only society representing computational biology and bioinformatics worldwide. ISCB serves a global community of nearly 3,400 scientists dedicated to advancing the scientific understanding of living systems through computation by:

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

ISCB has three official journals – OUP Bioinformatics, PLOS Computational Biology and F1000Research ISCB Community Journal, and has affiliations in place with several other publications for the benefit of our members.

Booth 4

F1000Research

http://f1000research.com/

F1000Research is an Open Science publishing platform offering immediate publication of posters, slides and articles with no editorial bias. All articles benefit from transparent peer review and the inclusion of all source data. F1000Research publishes the ISCB Community Journal.

Booth 5

EMBL Australia Bioinformatics Resource

http://embl-abr.org.au

The EMBL Australia Bioinformatics Resource (EMBL-ABR) is a distributed national research infrastructure providing bioinformatics support to life science researchers in Australia. It was set up as a collaboration with the European Bioinformatics Institute (EMBL-EBI) to maximise Australia's bioinformatics capability. This close partnership is made possible in the context of Australia's associate membership of EMBL. Its Hub is hosted at VLSCI through a funding agreement between the University of Melbourne and Bioplatforms Australia.

Booth 7

Amazon Web Services

http://aws.amazon.com/health

Amazon Web Services (AWS) provides life sciences and genomics organizations with secure, reliable, low-cost, easy-to-scale, global IT infrastructure "in the cloud." Hundreds of thousands of customers in 190 countries, rely on AWS for their bioinformatics needs, whether it is working with large public data sets or conducting clinical research that combines medical records with genomic information at population scale.

Booth 10

European Bioinformatics Institute

https://www.ebi.ac.uk

At the European Bioinformatics Institute (EMBL-EBI), we help scientists realise the potential of 'big data' in biology, helping them exploit complex information to make discoveries that benefit mankind. We manage the world's public biological data and make it freely available to the scientific community via a range of services and tools, perform basic research and provide professional training in bioinformatics. We are part of the European Molecular Biology Laboratory (EMBL), a non-profit, intergovernmental organisation funded by 21 member states and two associate member states. Our 570 staff represent 57 nationalities, and we welcome a regular stream of visiting scientists throughout the year. We are located on the Wellcome Genome Campus in Hinxton, Cambridge in the United Kingdom.

Booth 11

Springer

http://www.springer.com/

Looking to publish your research? Discover Springer's print and electronic publication services, including Open Access! Get high-quality review, maximum readership and rapid distribution. Visit our booth or springer.com/authors. You can also browse key titles in

Exhibitors

your field and buy (e)books at discount prices. With Springer you are in good company.

Booth 14

St. Jude Children's Research Hospital

https://www.stjude.org

A non-profit biomedical research institution where mathematics and computer science are applied to the study of genomics, epigenetics, systems biology, biological image analysis, and structural & chemical biology. Our high-performance computing facility allows seamless integration of computational scientists with experimentalists. Visit our booth to discuss postdoctoral fellowship opportunities.

Booth 15

sbv IMPROVER

http://www.sbvimprover.com

The scope of the sbv IMPROVER project, funded by PMI, is the verification of methods and concepts in systems biology research. It already successfully demonstrated that crowdsourcing is a viable strategy to verify scientific methods and concepts in an industrial context. The latest challenge is the Systems Toxicology Computational Challenge and aims to to verify that robust gene signatures predictive of exposure status to chemical mixtures can be extracted from blood gene expression data.

Booth 16

The NDEx Project

http://www.ndexbio.org

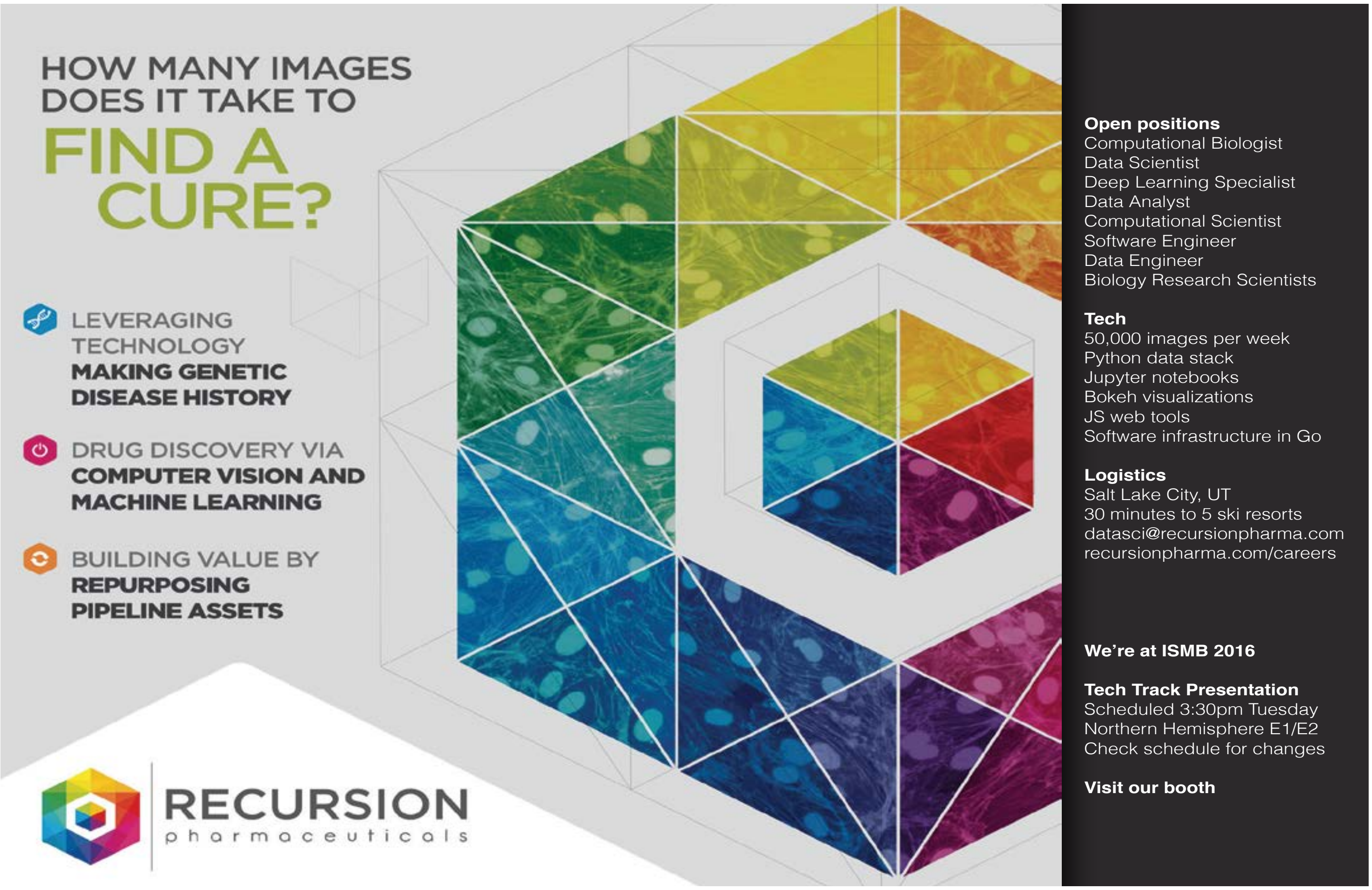
NDEx, the Network Data Exchange, is a collaborative software infrastructure for storing, sharing and publishing biological network knowledge. The NDEx Project maintains a free, public website and is developed in close collaboration with the Cytoscape team and the Ideker laboratory at UC San Diego.

Booth 17

Cambridge University Press

http://www.cambridge.org/lifesciences

Cambridge University Press is a not-for-profit organization that advances learning, knowledge and research worldwide. It is an integral part of the University of Cambridge and for centuries has extended its research and teaching activities through a remarkable range of academic and educational books and journals.



Exhibitors

Booth 18

PLOS

http://www.plos.org

PLOS (Public Library of Science) is a nonprofit Open Access publisher, innovator and advocacy organization dedicated to accelerating progress in science and medicine by leading a transformation in research communication. The PLOS suite of influential journals contain rigorously peer-reviewed Open Access research articles from all areas of science and medicine.

Booth 19

GOBLET: Global Organisation for Bioinformatics Learning Education & Training

http://www.mygoblet.org

GOBLET's mission is to provide a global, sustainable support and networking structure for bioinformatics educators/trainers and students/trainees. This includes a training portal for sharing materials, tools and techniques; guidelines and best practice documents; opportunities to train the trainers; and a community of individuals actively engaged in bioinformatics training and learning).

Booth 20

CRC Press

http://www.crcpress.com

CRC Press, part of the Taylor and Francis Group, is the premier publisher of textbooks, reference books, and ebooks on computational biology. Stop by our booth to view our latest titles on computational biology and systems biology and take advantage of our conference discount and be sure to enter our raffle for your chance to win. If you are interested in writing a book please stop by the booth to speak with Sunil Nair about your idea.

Booth 23

European Conference on Computational Biology (ECCB 2016)

http://www.eccb2016.org/ ECCB 2016

European Conference on Computational Biology (The Hague, The Netherlands, 3-7 September 2016) warmly welcomes scientists working in a variety of disciplines, including bioinformatics, (computational/systems) biology, and medicine. Participating in ECCB 2016 will be the perfect opportunity to network and keep abreast of cutting edge research. Early bird registration deadline: July 29.

Exhibitors

Booth 25

Oxford University Press

http://www.oup.com

Oxford University Press publishes some of most respected and prestigious computational biology journals in the world. They include Bioinformatics, an official journal of ISCB, Database: The Journal of Biological Databases and Curation, and Nucleic Acids Research, among many others. Visit our stand to browse books and to pick up sample copies of journals.

Booth 27

ELIXIR Denmark

http://www.elixir-denmark.org

ELIXIR Denmark, which is established in partnership between Danish Universities, leads the community-driven development of the ELIXIR Tools and Data Services Registry. This provides essential scientific and technical information about analytical tools and data services for bioinformatics; It is freely accessible, via the bio.tools portal, and available for registering resources.

Booth 28

Elsevier

http://www.elsevier.com

Elsevier is a world-leading provider of information solutions that enhance the performance of science, health, and technology professionals, empowering them to make better decisions, and deliver better care.

Booth 30

Recursion Pharmaceuticals

http://www.recursionpharma.com

Recursion is a 2-year-old startup with fewer than 20 people, but we generate rich biological data at a pace comparable to some of the biggest institutions doing biology and disease research. We combine high-throughput cellular imaging experiments with intelligent computational methods, rapidly testing thousands of drugs against hundreds of diseases.

Booth 31

QIAGEN Bioinformatics

https://www.qiagenbioinformatics.com

QIAGEN Bioinformatics is powered by CLC bio, Ingenuity, and BIOBASE. We offer bioinformatics software tools for next generation sequencing (NGS) data analysis and interpretation. Our solutions are designed to be universal, so you can mix and match the technologies best suited to your needs.

RT01-RT05

Career/Recruiters Tables

https://www.iscb.org/ismb2016-career

- **RT01 THE JACKSON LABORATORY**
- **RT02 UNIVERSITY OF NEBRASKA AT OMAHA**
- **RT03 DUKE UNIVERSITY**
- **RT04 BIOINFORMATICS AND COMPUTATIONAL BIOLOGY @ ISU**
- **RT05 SYLVESTER COMPREHENSIVE CANCER CENTER AT UNIVERSITY OF MIAMI, MILLER SCHOOL OF MEDICINE**

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sbv™ IMPROVER

SYSTEMS BIOLOGY VERIFICATION

sbv IMPROVER Systems Toxicology Computational Challenge Results

The aim of this Challenge was to verify that robust and sparse human-specific or species-independent gene signatures predictive of exposure status can be extracted from whole blood gene expression data.

Technology Track Agenda:

Dr Bob Terbrueggen, DxTerity:
- How signatures could be used in a clinical setting

sbv IMPROVER Scientists & Best Performers:
- Challenge Introduction
- Scoring approach and lessons learned
- Presentation of best performing methods

Monday July 11th 2016
10:10am - 12:40pm
America's Seminar Room, Dolphin Hotel, 5th Floor

www.sbvimprover.com/comp-start

Technology Track Presentations

Sunday, July 10

6:00 PM - 7:00 PM	TT01	**Transparent toxicology via enhanced peer review platform** • *Stephanie Boue, Philip Morris International R&D*	**AMERICA'S SEMINAR**

Monday, July 11

10:10 AM - 12:40 PM	TT02	**Chemical Exposure Response Markers Identification in Blood and Genomic-based Diagnostics — Lessons Learned from the sbv IMPROVER Systems Toxicology Computational Challenge** • *Carine Poussin, Philip Morris International R&D*	**AMERICA'S SEMINAR**
2:00 PM - 3:00 PM	TT03	**Repeatable Science at Scale: Using Common Workflow Language and Docker for science on AWS** • *Angel Pizarro, Amazon Web Services*	**AMERICA'S SEMINAR**
3:30 PM - 4:30 PM	TT04	**Biological interpretation of 'omics data: The power of causal analysis** • *Andreas Kraemer, QIAGEN Bioinformatics*	**AMERICA'S SEMINAR**
6:00 PM - 6:20 PM	TT05	**Bisulfite sequence analysis on CyVerse Discovery Environment** • *Jawon Song, Texas Advanced Computing Center*	**NORTHERN HEMISPHERE A1/A2**
6:00 PM - 6:20 PM	TT06	**GenePattern Notebook: An integrated analytical environment for genomic research** • *Michael Reich, UC San Diego*	**NORTHERN HEMISPHERE A3/A4**
6:00 PM - 6:20 PM	TT07	**BioSchemas: schema.org development for the Life Sciences** • *Niall Beard, University of Manchester*	**AMERICA'S SEMINAR**
6:20 PM - 6:40 PM	TT08	**The bioBakery: a platform for comprehensive analysis of microbial community shotgun sequencing data** • *Eric Franzosa, Harvard T. H. Chan School of Public Health*	**NORTHERN HEMISPHERE A1/A2**
6:20 PM - 6:40 PM	TT09	**Introducing N-of-1-pathways transcriptome analytic tools: Enabling precision medicine through single-subject studies** • *Yves Lussier, University of Arizona*	**NORTHERN HEMISPHERE A3/A4**
6:20 PM - 6:40 PM	TT10	**FAIRDOM: Publishing FAIR Data and Models in Interdisciplinary Life Sciences** • *Natalie Stanford, University of Manchester*	**AMERICA'S SEMINAR**
6:40 PM - 7:00 PM	TT11	**PISKa: a HPC tool for stochastic agent and rule-based modeling of spatially explicit complex biological systems** • *Tomas Perez-Acle, Fundacion Ciencia & Vida*	**NORTHERN HEMISPHERE A1/A2**

Tuesday, July 12

10:10 AM - 10:30 AM	TT12	**Big data technology for designing high-quality oligonucleotides via exhaustive homology tests** • *Min-Soo Kim, DGIST*	**AMERICA'S SEMINAR**
10:30 AM - 10:50 AM	TT13	**MyGene.info and MyVariant.info: high-performance web services for querying gene and variant annotation** • *Chunlei Wu, The Scripps Research Institute*	**AMERICA'S SEMINAR**
10:50 AM - 11:10 AM	TT14	**Exploring Open-Access Genetic Variants & Clinical Associations: The European Variation Archive at EMBL-EBI** • *Cristina Gonzalez Garcia, EMBL-EBI*	**AMERICA'S SEMINAR**
11:40 AM - 12:00 PM	TT15	**GenomeSpace: An environment for frictionless bioinformatics** • *Sara Garamszegi, The Broad Institute of MIT and Harvard*	**AMERICA'S SEMINAR**
12:00 PM - 12:20 PM	TT16	**Recent Developments in the Pathway Tools Software and BioCyc Databases** • *Peter Karp, SRI International*	**AMERICA'S SEMINAR**
12:20 PM - 12:40 PM	TT17	**Open PHACTS now offers patent information and interactions from pathways** • *Chris Evelo, Maastricht University*	**AMERICA'S SEMINAR**
2:00 PM - 2:20 PM	TT18	**Integrating 3D Structure with Protein, Gene, and Validation Information at the RCSB PDB** • *Peter Rose, UC San Diego*	**AMERICA'S SEMINAR**
2:00 PM - 2:20 PM	TT19	**Accelerated NGS Interpretation via the GeneCards Suite** • *Marilyn Safran, Weizmann Institute of Science*	**NORTHERN HEMISPHERE E3/E4**
2:20 PM - 2:40 PM	TT20	**Phyre2: Protein modeling and analysis made easy** • *Mark Wass, University of Kent, United Kingdom*	**AMERICA'S SEMINAR**
2:20 PM - 2:40 PM	TT21	**Read-Based Phasing Using WhatsHap** • *Marcel Martin, SciLifeLab*	**NORTHERN HEMISPHERE E3/E4**
2:40 PM - 3:00 PM	TT22	**Using CATH-Gene3D to predict the structure and function of novel protein sequences** • *Christine Orengo, University College London*	**AMERICA'S SEMINAR**
2:40 PM - 3:00 PM	TT23	**Large Scale Analyses with Galaxy** • *John Chilton, Galaxy Project*	**NORTHERN HEMISPHERE E3/E4**
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3:30 PM - 3:50 PM	TT25	**bio.tools - life science software registry** • *Jon Ison, ELIXIR Denmark*	**AMERICA'S SEMINAR**
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3:50 PM - 4:10 PM	TT27	**Visualizing and analyzing protein data with UniProt** • *Sangya Pundir, EMBL-EBI*	**AMERICA'S SEMINAR**
3:50 PM - 4:10 PM	TT28	**BACNET: An interactive platform for analysis and publication of multi-omics study** • *Christophe Bécavin, Institut Pasteur*	**NORTHERN HEMISPHERE E3/E4**
4:10 PM - 4:30 PM	TT29	**Linking literature and data through text mining in Europe PMC: SciLite - An annotation platform for biocuration** • *Senay Kafkas, EMBL-EBI*	**AMERICA'S SEMINAR**
4:10 PM - 4:30 PM	TT30	**GeneWeaver.org: A system for cross-species heterogeneous functional genomic data integration** • *Elissa Chesler, The Jackson Laboratory*	**NORTHERN HEMISPHERE E3/E4**

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MEET THE 2016 ISCB FELLOWS, CONT.

Aviv Regev Winner of the 2008 Overton Prize. Core Member and Chair of the Faculty, Broad Institute, Professor, Department of Biology, Massachusetts Institute of Technology, USA, and Investigator, Howard Hughes Medical Institute. Regev has made significant contributions to the field through research in systems biology, particularly for her work on molecular circuitry that drives the function of mammalian cells, gene regulation, and single cell genomics.

Lincoln Stein Professor, Department of Molecular Genetics, University of Toronto, and Interim Scientific Director of the Ontario Institute for Cancer Research, Canada. Stein has made many fundamental contributions to the emergence of computational biology as a field through his roles in the formative consortia of computational biology, including the Human Genome Project, HapMap, Reactome, Wormbase, BioPerl and ModEncode. He has written the widely-used Perl CGI module, contributed to major portions of BioPerl, GBrowse and JBrowse, software used across the bioinformatics community, and mentored many scientists who have gone on to become successful independent researchers.

Sarah Teichmann Head of Cellular Genetics, Wellcome Trust Sanger Institute, UK. Teichmann has made numerous significant contributions to the field that include elucidating the domain characteristics of prokaryotic proteins, introducing graph theory to represent protein domain combinations as networks, developing predictive models for transcription factor-DNA interactions in gene regulation, and statistical methods for single-cell transcriptomics. Teichmann has mentored numerous trainees who have become scientific leaders, and she has served on numerous editorial boards and organized multiple conferences.

Anna Tramontano Chair Professor, Department of Physics, University of Rome "La Sapienza", Italy. Tramontano is a leader in the field of computational biology through her research to analyse and model the structure of proteins of biomedical relevance, and her work to organise the community assessment of protein structure prediction (CASP) project. Tramontano has been a major force in bringing attention to computational biology and bioinformatics to leaders of European science and policy makers and has served the community through her roles in the ISCB leadership.

Shoshana J. Wodak Professor, Visiting Group Leader, Vlaamse Institute of Biotechnology, Structural Biology Research Center, Free University of Brussels, Brussels, Belgium. Wodak's seminal research contributions include docking algorithms for the prediction of protein-protein interactions, protein structure prediction, molecular simulations, and automated protein design. Wodak is also well known for her work on the representation and analysis of genome-scale protein interaction networks. Wodak has been playing an active role in the management of CAPRI (Criticial Assessment of Predicted Interactions), a community-wide initiative on evaluating methods for the prediction of protein interactions and has mentored numerous students and trainees who have gone on to establish independent research programs.

Haim Wolfson Professor, Department of Computer Science, Tel Aviv University, Israel. Wolfson pioneered the introduction of Computer Vision motivated 3D pattern discovery algorithms into computational structural biology, co-developing the geometric hashing methodology, and developing highly efficient algorithms for protein structure alignment, protein-protein docking, binding site comparison, and integrative modeling of large multi-molecular assemblies. Wolfson has held several key leadership positions at Tel Aviv University and has served on numerous program committees for major computational biology conferences including ISMB, ECCB, and RECOMB.

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ISCB COMMUNITY JOURNAL UPDATE

2015 seen the official release of the ISCB Community Journal (ICJ). We were very excited to launch in July at ISMB 2015 in Dublin, and since then, the journal has created 17 channels to host research content from ISCB Conferences and the ISCB Communities of Special Interest. Each channel is a dedicated space that enables the ISCB communities to disseminate not just articles, but all of the conference research (posters and slides) in one centralized venue.

The ICJ shift towards wholly open science publishing and provides the ISCB communities with a place to rapidly publish any results they think are worth sharing. It uses a model of immediate publication followed by transparent invited peer review and necessitates the inclusion of all supporting data, enabling easy reanalysis, replication attempts and data reuse. All published articles receive a recognisable ISCB citation, and once articles pass peer review, all are indexed in PubMed, Scopus and other major bibliographic databases, together with all versions; associated data sets and referee reports are deposited in PubMed Central.

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As well as traditional research articles the ICJ also accepts articles of different sizes (single figure papers up to full length research articles), method papers, software tools, data notes and any other piece of research that is written up for peer review. By publishing in this way the intension is to help the ISCB Communities communicate and discuss their work in a truly open and collaborative way.

ISCB COMMUNITY JOURNAL UPDATE, CONT.

To see the open peer review process in practice, here are some examples of the types of articles that have been published in the ICJ:

Research article from the ISCB Africa channel: Transcription factor motif quality assessment requires systematic comparative analysis [version 2; referees: 2 approved]: http://f1000research.com/articles/4-1429/v2.

Software tool article from the Regulatory and Systems Genomics channel: CausalTrail: Testing hypothesis using causal Bayesian networks [version 1; referees: 2 approved]: http://f1000research.com/articles/4-1520/v1.

The "Messages from the ISCB" channel features all the latest ISCB news, and one that really stood out this year was the ISCB reaction to New England Journal of Medicine editorial on data sharing (http://f1000research.com/articles/5-157/v1). The message explains how the sharing of data is vital in order to speed up knowledge discovery and foster new collaborations across disciplines. This message is aligned with the ICJ which has a robust data sharing policy where all primary research articles include the submission of the data underlying the results, together with details of any software used to process results.

Over the next few months the ICJ will look forward to hosting published papers and conference presentations from the COSIS and the upcoming ISCB meetings in 2016. As this is a community journal we value your ideas and comments, so please do not hesitate to come and visit us at our Booth at ISMB 2016 where we will host a meet the editor session or email us anytime at research@f1000.com.

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2016 ISCB ACCOMPLISHMENT BY A SENIOR SCIENTIST

Award Given to Søren Brunak The International Society for Computational Biology (ISCB) recognizes an established scientist each year with the Accomplishment by a Senior Scientist Award for the significant contributions he or she has made to the field. This award is bestowed to scientists who have contributed to the advancement of computational biology and bioinformatics through their research, service, and education work. Professor Søren Brunak of the Novo Nordisk Foundation Center for Protein Research in Copenhagen, Denmark has been selected as the winner of the 2016 Accomplishment by a Senior Scientist Award.

The ISCB awards committee, chaired by Dr. Bonnie Berger of the Massachusetts Institute of Technology in the United States, selected Brunak as the 2016 winner. Brunak will receive this award and deliver a keynote address at the 2016 Intelligent Systems for Molecular Biology meeting (ISMB 2016) being held in Orlando, Florida on July 8 - 12, 2016. ISMB is ISCB's world class annual meeting that brings together computational biologists and interdisciplinary scientists from around the globe.

Brunak's early interest in physics began with a childhood friendship with Jakob Bohr, grandson of Nobel Laureate physicist Niels Bohr. He considers this early informal exposure to physics instrumental in developing his interest in the field but acknowledges that his physics teacher in primary school also nurtured his interest. Brunak said, "I was primed by the fact that one of my childhood friends was Jakob Bohr. I grew up close to this family. Maybe I was therefore listening a little more to what the physics teacher would come up with. He was good at turning deep questions into something that could be understood by kids our age."

Brunak went on to study physics formally as a graduate student but first took a detour in astronomy. He recalled, "First I went into astronomy, but I found it increasingly difficult to explain at dinner parties the importance of astronomy." He then completed his Master of Science in physics in 1987 at the Niels Bohr Institute, University of Copenhagen. "I had been fascinated by computers. My masters thesis was titled *The Physics of Computation*[1], and I studied what happens in the computer when it computes. I was inspired by the work of Rolf Landauer and Charles Bennett at IBM. They worked on determining if you could compute without dissipating heat in reversible physical processes where no information would be discarded." It was Brunak's interest in the work of Bennett that stimulated his interest in biology. "Bennett used DNA transcription as an example of how a computation (a copy operation) can be done without dissipating a lot of energy. My thesis was also about computation processes in the brain, which are related to machine learning. It's also about throwing information away so what you are after is distilled out of the data. In the big data context, there is a huge information reduction need so my experience with the physics of computation has inspired me when designing machine learning algorithms that use a lot of information and end up with a yes or no, for example answering the question of whether a protein structure is helical or not at a given position in the 1 In Danish "Computerens Fysik" amino acid sequence. A lot of bioinformatics is about throwing information away in a smart way so what you are really after is retained."

Brunak completed his Ph.D. in computational biology in 1991 in the Department of Structural Properties of Materials at the Technical University of Denmark. He then went on in 1993 to become founder and director of the Center for Biological Sequence Analysis at the Technical University of Denmark, a large center that still exists. His early work in bioinformatics focused on protein structure. He recalled, "I worked with protein structure with machine learning approaches. Meetings were small, data sets were small. We tried to get a lot out of little. We were raised in the data-poor era. The machine learning approach is not only good for boiling down but also for extracting." Even during this era of limited data, Brunak considered computer power an important priority. "During my early studies in the late 1970s I started with punch cards and huge magnetic tapes. During my PhD I obtained a grant for a fast four processor Apollo 10000 machine, and I later always spent a lot of money on supercomputers so computer speed was not a problem. Now it is a real problem because we have millions of instances of a genome. We are in a situation where computer science matters in a new way. I have been around computers so long so I've seen a lot of special purpose hardware developed. But people always go back again and again to the general purpose computer that can take any algorithm, or do things like align sequences with any setting."

Brunak's early bioinformatics studies looked at both structure and function and were not limited to sequence properties. Machine learning was integral to these studies, and he went on to write an authoritative text on the subject with Pierre Baldi in 1998, titled *Bioinformatics: A Machine Learning Approach*. Brunak developed several widely used algorithms rooted in machine learning including NetGene, which predicted introns and exons and splice sites, and SignalP, a signal peptide predictor. He recounted, "This was the time of the genome project, so we started doing exon and intron and splice site prediction using this method called NetGene. Both SignalP and NetGene were interesting in that they integrated several different predictors and exploited the same data from different angles. With NetGene, we had a splice site predictor and an exon predictor and we put them together and we got a much better algorithm out of it than staying just in just the splice site or coding/non-coding domain. In SignalP we also used the same data in two different ways."

Brunak recalls some of the surprises of his early research. "My first *Nature* paper was a small paper in 1990. It was a paper where we predicted splice sites using machine learning with neural networks. We noticed a group of splice sites that the network really didn't want to learn. We just kept training it and it still would not learn them. We started looking at them and it turned out that half of them were database errors, and the other half were more interesting, they were errors made by experimentalists when they interpreted their [sequence] gels. They had put the splice site in the wrong place. The would learn the rare, but true GC donor sites very late, but still learn them. It was an interesting paper that showed the power of machine learning--that it could be a little more clever than the quality of the data. Nature was getting tough on GenBank for removing errors, and here was a computational approach for cleaning up datasets. We used the same technique with SignalP to identify likely errors. [We thought] either it's an error or super unusual and therefore interesting. We could see in some databases, with signal peptides, that 10-15% of the data was wrong." Brunak saw this tedious work as an important contribution to cleaning up data sets and spent several years on this effort.

During the Human Genome Project era, Brunak recognized with many others in the field the limits of gene prediction from sequence information alone. But his research using neural networks alluded to some of our present day understanding of the complexities of genomes. Brunak said, "It's not surprising now that gene prediction was not 100% successful. Now we know that there's transcription everywhere and that what constitutes a gene is highly complex. In 1992 we had a paper in *The Journal of Molecular Biology* (JMB) examining the ways how a neural network looks for gene features in order to produce a prediction. It turned out when we predicted introns and exons, it looked for a specific GC-rich signal. It was not easy to get a paper

2016 ISCB ACCOMPLISHMENT BY A SENIOR SCIENTIST, cont.

accepted into JMB, especially when you were trying to deconvolute theoretically neural network parameters into some biological signal. The pattern it looked for was perhaps known to a referee as an early example of an enhancer. Part of the reason of the success of the machine learning approach is that we didn't need to know upfront the features that were behind biological mechanisms."

Brunak's research focus has shifted direction in recent years during this era of large scale genome projects. In 2007, he was a co-founder of the Novo Nordisk Foundation Center for Protein Research at the University of Copenhagen. The Center's main goal is to look for proteins of therapeutic value, and they are developing approaches that fit into a healthcare context. Brunak leads the translational disease systems biology group, which looks at genome, proteome and health data, where some cover the entire Danish population. Brunak explained, "I am interested in disease trajectories, the order in which you get diseases, comorbidities and follow-on diseases. If you get type 2 diabetes, you won't get the same complications as your neighbor. There are certain trajectories that are more probable than others." For the entire Danish population, almost all personal information, including education, job status and health records, are tied to a Dane's personal identification number. As such, researchers including Brunak have an abundance of unique data to work with, and much of his work has focused on boiling down this data into meaningful observations. "My contribution is to put patients into progression groups and interpret proteomics data. We for example group diabetics and will see how their trajectories differ. Having the ability to work from the molecular side and having health data is presumably going to be powerful. We have data from 11 million people living and dead. We also essentially have the family tree from the entire country because it's encoded in the personal identification number."

Brunak's enduring contributions to computational biology and bioinformatics have spanned his career, and given the scope of his recent work, he is certain to make a lasting and valuable contribution to the field.

[1] In Danish ”Computerens Fysik”

PLOS COMPUTATIONAL BIOLOGY OVERVIEW JULY 2016

PLOS Computational Biology celebrated its 10th anniversary last year and has continued to prosper over 2015-2016, with an average of nearly 143 articles submitted per month. As well as publishing high quality research, PLOS Computational Biology enables members of the community to contribute to scientific communication through the creation of resources for current and future generations of computational biologists.

The journal's Topic Pages Collection has gone from strength to strength throughout 2015 and 2016. These articles increase the coverage of computational biology topics in Wikipedia while rewarding authors for their efforts. All Topic Pages undergo a fully open peer-review process on the Topic Pages wiki, with the reviews and responses posted to both the static article and Wikipedia talk page on publication. Recent examples include 'Horizontal Gene Transfer'[1,2] by Ravenhall et al. and 'Hypercycle'[3,4] by Szostak et al. Christopher Dessimov discusses his Topic Page 'Horizontal Gene Transfer' in his lab blog[5]. All of these articles can be located on their own collection site[6] or on a Wikipedia playlist[7].

During the past year, *PLOS Computational Biology* was also given the opportunity to look into the labs of Alice McHardy[8], Florian Markowetz[9], and Christine Vogel[10] with three new 'About My Lab' perspectives. These authors took the time to share valuable insights from their experiences of running a lab, from the lab's early days and the best ways to delegate and manage time, to advice on establishing yourself as a successful leader.

As always, our Ten Simple Rules Collection[11] continues to be popular as it passeswisdom on to younger researchers as they progress through their career. Over the last year many authors have used the Ten Simple Rules Collection to share their experiences, including:

- Santiago Schnell who discussed how to successfully keep a useful notebook in a dry lab in Ten Simple Rules for a Computational Biologists' Laboratory Notebook[11].
- William Michener[12] who looked at how to create a data management plan that can be easily understood by other groups (i.e. funders) but would also be easy to implement by your research team, ultimately ensuring your data are safe, sharable and maximise the return on investment.
- Andrew Lonsdale *et al.*[13] discussed theirexperiences with establishing a Bioinformatics Journal Club, including the idea that the best time to have it may be in a local café before work and recommend 8 AM!

We would like to express our thanks to Scott Markel and Fran Lewitter for their work in curating and editing this collection. PLOS Computational Biology could not function without the assistance and support of the community and we would like to thank everyone who has helped to make the last year such a success. In addition, we would like to welcome onto the board; Kim Blackwell and Wolfgang Einhäuser as Deputy Editors, as well as over 25 new Associate Editors.

PLOS Computational Biology is a Community Journal; we value your ideas and comments so please don't hesitate to visit us at Booth 18 at ISMB or via ploscompbiol@plos.org.

Popular papers of 2015

Lobo D, Levin M (2015) Inferring Regulatory Networks from ExperimentalMorphological Phenotypes: A Computational Method Reverse-Engineers Planarian Regeneration. PLoS Comput Biol 11(6): e1004295. doi:10.1371/journal.pcbi.1004295

Griffith M, Walker JR, Spies NC, Ainscough BJ, Griffith OL (2015) Informatics for RNA Sequencing: A Web Resource for Analysis on the Cloud. PLoS Comput Biol 11(8): e1004393. doi:10.1371/journal.pcbi.1004393

Liu S, Smith AS, Gu Y, Tan J, Liu CK, Turk G (2015) Computer Simulations Imply Forelimb-Dominated Underwater Flight in Plesiosaurs. PLoS Comput Biol 11(12): e1004605. doi:10.1371/journal.pcbi.1004605

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The PLOS Computational Biology 'Topic Page' collection image. CC-0

[file: Turk_D_15-00902R2_Image]
Computer Simulations Imply Forelimb-Dominated Underwater Flight in Plesiosaurs. Image credit: Shiqiu Liu

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***15th European Conference on Computational Biology**
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http://www.eccb2016.org/

***15th International Conference on Bioinformatics (InCoB2016)**
Sep 21, 2016 through Sep 23, 2016
https://incob16.apbionet.org/

NOVEMBER

RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges
Nov 06, 2016 through Nov 10, 2016
http://www.iscb.org/recomb-regsysgen2016

ISCB-Latin America
Nov 21, 2016 through Nov 23, 2016
http://www.iscb.org/iscb-latinamerica2016

DECEMBER

Rocky 2016
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http://www.iscb.org/rocky2016

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http://psb.stanford.edu/

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http://www.biostec.org/

APRIL

NGS 2017
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http://www.iscb.org/ngs2017

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