ISCB Newsletter

SUMMER 2017 ISSUE 02


iSCB

ISMB

CELEBRATING 25 YEARS OF ISMB

ECCB

2017 • PRAGUE

JULY 21–25

CONFERENCE PROGRAM

CONTENTS

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
www.iscb.org

Featuring the ISMB/ECCB 2017 Conference Program

LETTER FROM THE PRESIDENT

Dear Members and Colleagues,

This year marks the 25th Anniversary of the Intelligent Systems for Molecular Biology (ISMB) conference. Over the year's we have watched ISMB grow from a small meeting to one of the largest and most respected computational biology and bioinformatics meetings in the world. ISCB also celebrates a milestone as well as we enter into our 20th year of operation. Since its founding in 1997, ISCB has grew significantly with nearly 3,200 members worldwide, a robust student council, and growing communities of special interest (COSIs). 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.

You will see some changes this year at the ISMB/ECCB 2017. In an effort to streamline the science presented during the conference, ISCB in collaboration with the organizers of the ISCB Communities of Special Interest (COSIs), formally SIGs, worked diligently over the course of the last 12 months to reorganize the scientific program. In essence the meeting will encompass all of the familiar themes and tracks, such as proceedings, highlight, or late breaking topics, that made ISMB/ECCB a pillar of the community in previous years, but will now offer an improved quality in the experience for you, the delegate. You now have the opportunity to listen to talks on the same theme, opportunities to engage in discussions and networking with other like-minded researchers, in a much more themed-focused program. We welcome your feedback from your experience of this newly designed format so that we can continue to make your conference experience great!

Over the course of the last nine months, the ISCB Board of Directors has been deep in strategic conversation about the organization. Results of these conversations lead to the development of the ISCB Strategic Map, which is expected to be finalized by the end of this year. This strategic map will help guide the Society over the next three-five years. Keystones to the strategic map are the focused core competencies and goals of ISCB.

1. MEMBERSHIP

Strengthen ISCB's role as the natural home and the professional society for all individuals with an interest in the spectrum of computational biology research and its applications.

2. EDUCATION

Deliver high-quality computational biology education and training to interested communities across the world, and help drive the assimilation of computation into all life science-related educational programs.

3. MEETINGS

Provide a forum to foster fresh dialogues and perspectives, to learn about and shape the future of the discipline.

4. PROFESSION

Advance computational biology as a profession, its ability to accelerate research, advocate and provide resources and policies to extend the frontiers of computational science for the benefit of society at large.

5. COMMUNITIES

Stimulate, cultivate and promote interactions and collaborations within the diverse scientific and technical fields that collectively embody the discipline of computational biology and bioinformatics.

These core competencies reflect the greatest need service to our members and the community at large. We look forward to the finalization of the strategic map and the milestones associated with it, which will enhance the value of membership at ISCB and the promotion of our science.

March of this year brought great sadness when we learned of the passing of long-time board member and renown Italian computational biologist, Anna Tramontano. Enclosed in this issue is a In Memoriam article which celebrates Anna's life and accomplishments. ISCB also dedicated ISMB/ECCB 2017 to the memory of Anna. ISCB is working on establishing a memorial fund in Anna's name to continue her efforts in supporting students from under-developed countries.

This issue of the ISCB newsletter is filled with great information including the celebration of the ISCB Fellows, ISCB Award Recipients, the ISMB/ECCB 2017 Conference Program, updates from our official journals, 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

IN MEMORIAM
ANNA TRAMONTANO 1957–2017

Janet M Thornton, Alfonso Valencia and Torsten Schwede

Anna Tramontano, who died unexpectedly in March 2017, was an Italian computational biologist of renown. Anna's work focused on protein structure and modelling studies, and she was a dedicated leader in the bioinformatics community, in her own country and worldwide. Anna was devoted to training in this emerging field, which lies at the interface of biology, chemistry, physics and computational sciences. She was not only a good scientist, but also a great organizer, coordinator, and colleague, and she mentored and inspired the next generation of scientists.

Anna trained as a physicist in her home town of Naples, before being attracted by the exciting new developments in structural molecular biology. In a postdoc at the University of California San Francisco, she authored a powerful graphics program to display protein structures, at a time when using computers to visualize 3D structure was still in its infancy. Uniquely at the time, the program allowed comparison of protein structures, an approach which has become the cornerstone of studies in protein evolution and function. The tool was later commercialized and became widely used by structural biologists.

In 1988, Anna moved on to join Arthur Lesk at EMBL in the Biocomputing Programme in Heidelberg, where she started her best-known work - analysing and predicting the structure of antibodies. Arthur had worked with Cyrus Chothia in Cambridge to interpret how the newly determined immunoglobulin fold was able to recognize a plethora of antigens, by subtle changes in specific loops. Anna and Arthur went on to use this knowledge to predict structures of antibodies from sequence, using novel molecular modelling approaches. They developed a bespoke Ig-modelling approach, based on a careful analysis of the available structures and understanding the constraints imposed by the b-sandwich framework. Their work showed that it was possible to predict the structure of the antibody binding site with high accuracy, based on the principle that the loops responsible for antigen binding can only assume a limited number of conformations, depending on their length and the identity of residues at key positions both within and outside the loop. To quote Anna, this work "opened the road to the rational redesign of antibodies, especially for therapeutically important purposes."

At that time, EMBL was home to some of the most outstanding computational bioinformatics groups in the world. Those students and postdocs went on to lead many of the scientific developments in our field, both in Europe and beyond. One of these was the establishment of the International Society of Computational Biology (ISCB), of which Anna later became a Fellow and Vice-President, and which today hosts the largest bioinformatics meeting (ISMB) in the world. Anna was also passionate about the European Conference on Computational Biology (ECCB) - as an organizer and the chair of the steering committee, including her commitment to helping young scientists to participate.

Retaining her life-long interest in the applications of molecular modelling for therapeutic targets, Anna returned to Rome as a group leader at IRBM, a newly established research institute that was later acquired by Merck & Co, and became head of department. She continued to work on many potential drug targets, including the hepatitis C proteases and interleukin-6 in complex with its receptors. She was involved in developing many methods for inhibitor design, protein design and docking. In 2001, driven by her interests in the newly available genomic data, she returned to academia as a full professor at the Sapienza University in Rome. She continued to focus on structural bioinformatics, especially for proteins involved in biomedical problems and also branching out to consider RNA molecules and their structures.

Determining the structure of a protein from its sequence has been a long-standing challenge, with implications for drug discovery and environmental interventions. Progress was initially slow and one limitation of the early days of protein structure prediction was that many papers claimed significant progress, yet it remained difficult to judge whether real progress was actually achieved. To address this problem, John Moult and colleagues established a bi-annual challenge, CASP – the Critical Assessment of Structure Prediction – in which protein models built from sequence data are compared with the corresponding but not yet public experimental structures – thus fully blinded methods testing. This series of experiments and associated conferences has had a profound impact on the practice and assessment of structure prediction and modelling. Anna was always a major force in CASP, first as an influential participant, then as an assessor, and later as a long-standing member of the organizing committee. Anna acted as chief editor for CASP special issues of the journal Proteins, introduced rigorous statistics into model evaluation, pioneered new areas of evaluation, and organized many Europe-based planning workshops and international meetings. In all this, she was always passionately concerned with two things: maintaining the highest standards of scientific rigor and the mentoring, training, and recognition of young scientists. She also added her critical approach to the assessment of the results of a newer initiative – CAFA (the Critical Assessment of protein Function Annotation experiment).

Anna was a builder of bridges. She was deeply involved in many early European research projects aimed at integrating biological information and tools to describe protein structures and to predict structure, function and potential therapeutics by modelling.

IN MEMORIAM
ANNA TRAMONTANO 1957–2017, CONT'D

In particular, she was part of the small steering committee for “BioSapiens”, the EU FP6 project that for the first time brought together many nascent bioinformatics research groups across Europe to use computational approaches to ‘understand life’. In that role Anna coordinated training, organizing many workshops and popular training sessions. With great Italian flair, she hosted the first all-hands meeting, setting the tone for the rest of the project and working tirelessly to ensure that the project not only delivered its objectives but, most importantly, that we all worked together to achieve our common goals.

As the size and complexity of biological data increased, the need for a pan-European infrastructure for biodata and tools became apparent. Driven by the European Strategic Forum for Research Infrastructures (ESFRI) and building on previous European framework projects, the concept of ELIXIR was developed. ELIXIR unites Europe’s leading life science organisations in managing and safeguarding the increasing volume of data generated by publicly funded research; it also sustains bioinformatics resources and enables users in academia and industry to access services. In the early days, it was challenging to establish a vision for ELIXIR and to engage the funders and politicians, but Anna brought her wide experience, endless enthusiasm and dogged determination; she first led the efforts that ultimately resulted in Italy joining ELIXIR.

Anna was proud to be an Italian scientist and embraced her substantial teaching responsibilities, including lectures to undergraduates. She taught with great passion: from biochemistry to bioinformatics, both for biomedicine and physics students. She created and directed a program for Masters in Bioinformatics at Sapienza, which has enabled many biologists, biotechnologists, physicists and chemists to enter the field. Her unique and catchy way of explaining difficult concepts, often with jokes, captured the students’ attention. Her door was always open to students who often turned to Anna for advice, support and as a reference.

Anna’s long-standing participation and giving back to the community, as an alumna, collaborator, scientific advisor, councilor and friend, are well documented. She served on innumerable scientific bodies, including ERC, EMBL’s Scientific Advisory Council, EMBO’s Fellowship and Courses Committees and on countless scientific reviews across the world. In those review roles, Anna was clear sighted, often critical and challenging, but always in a constructive way. Recently, Anna was a member of the National Board of Trustees Research (CNGR), an Italian ministerial body that sets out general criteria for the selection and evaluation of research activities, chooses the scientists participating at selection committees and coordinates the activities of these committees.

Throughout her career, Anna extended her dedication to training young scientists with farther-reaching operations. Within ELIXIR, she led the training efforts and campaigned hard for a bioinformatics training framework that could serve everyone in Europe. Anna’s model for the original BioSapiens summer schools deeply influenced the format of EMBL-EBI’s own programme. Cath Brooksbank, head of training at EMBL-EBI, said that Anna had “the perfect combination of leadership and listening skills” – and was “so committed to her calling that nothing was too much work - and she fostered that commitment in those she worked with.” Importantly, she also threw herself into training programs for under-represented scientists in challenging environments – work that took her to Cuba, Africa, and most recently Saudi Arabia. Her influence is captured by Nelson Ndegwa, former president of the Regional student group of Eastern Africa interested in bioinformatics and computational biology: “I first got in contact with Anna in 2007. We were interested in having (…) courses but we didn’t have resources to fund such activities. Anna at the first request to give us a workshop, was very delighted to travel all the way from Italy to Nairobi and in addition was happy to sponsor some students from the neighboring countries in the East African region to travel and attend the event as travel scholarships are quite hard to come by. She gave a 3-day Proteomics course in Nairobi in 2009 (picture). She also generously sourced for vast majority of the funding that went into supporting 52 students from Africa to attend the ISCB-ASBCB 2009 conference in Bamako, Mali. She connected many students to labs in Europe and beyond for various opportunities (study/internships). She was an academic mother to many of us in Africa and our lives will forever be a testimony of her generosity and commitment.”

Anna was loved by her close family, including her brother and his children, and all her scientific colleagues and friends around the world. But Anna’s training of the next generation of scientists will be a great and reminding legacy. She was an exceptional mentor and promoter of young scientists, and she knew how to bring out the best in everyone. She will be sorely missed.

We thank many of those who shared their thoughts and memories with us here, especially Manuela Helmer Citterich, John Moult and Nelson Ndegwa, as well as many other colleagues in Rome and worldwide.

2017 ISCB INNOVATOR AWARD
AVIV REGEV

2017 marks the second year of the ISCB Innovator Award, which recognizes an ISCB scientist who is within two decades of having completed his or her graduate degree and has consistently made outstanding contributions to the field. The 2017 winner is Dr. Aviv Regev, Professor of Biology at the Massachusetts Institute of Technology (MIT), a Core Member and Chair of the Faculty of the Broad Institute of MIT and Harvard, and an HHMI Investigator. Regev will receive her award and deliver a keynote address during ISMB/ECCB 2017 in Prague, Czech Republic (July 21 - July 25, 2017).

AVIV REGEV: SEEING CELLS AS LIFE'S SMALLEST CIRCUITS

Aviv Regev first pursued her studies in a unique interdisciplinary program at Tel Aviv University, where she planned to focus on math and computer science[1]. But she discovered her interest in biology in the classroom of evolutionary biologist Eva Jablonka. Regev said, "I found biology because of her – in my first year as an undergrad, I took a genetics course with her in what is now called the 'flipped classroom' style. It was all abstract and inferential, and I was hooked."

Before starting her PhD thesis at Tel Aviv University, Regev began to really think about cells as computers, particularly how they are comprised of circuits. Regev's deep interest in this concept started at a conference where new approaches for modeling concurrent computation were featured, and she immediately considered this as a way to model cell circuitry. She was able to develop her ideas into a PhD project under the mentorship of Udi Shapiro and Eva Jablonka, and she recalled, "No one was working on this type of project. I did, however, have the great fortune to find Udi, who listened to my idea. He thought it was important. He didn't want to work on it himself – but he wanted me to be able to work on it."

Regev completed her PhD in 2002 and was selected to be a Bauer Fellow at the Center for Genomics Research at Harvard University, which gave her an intellectual community, as well as freedom and funding to build a small independent research group. She continued to pursue her interest in modeling cell circuits using gene expression and genomic data, and she developed with her colleagues several widely used algorithms and computational tools, including Module Networks and Synergy. She received early support from Andrew Murray at Harvard University, who shared Regev's view that it was critical to deeply understand both theory and experiments.

In 2006, Regev was given a joint faculty appointment at MIT and the Broad Institute, and she started applying her cell circuit modeling algorithms to understanding different cell types, particularly cells of the immune system. Once again, Regev struck out on an independent line of research. She recalled, "Many people were not focused on circuits. But that was OK. I wanted to build and be part of a community that would open a new direction." Eric Lander at Broad – a longtime supporter of female and young scientists with leadership potential -- stood behind and supported Regev's independent scientific vision at this critical point in her career.

Regev's independent research program has blossomed since she founded her lab, and she has applied her interest in how cellular circuits function and rewire to a wide range of biological questions, including how immune cells rapidly respond and differentiate, how hematopoietic stem cells develop into different blood cells, and how evolutionary changes occur over millions of years. She is both a computational biologist with keen instincts about how to extract insight from data, and an experimental biologist with the ability to create new methods and deploy cutting edge technology to address fundamental questions.

Regev continues to be drawn to seemingly intractable problems, such as biological scenarios with a massive number of hypothetical combinations or interactions, and making them into manageable problems by using sampling approaches. Her work on cells of the immune system reflects this focus, and she recalls one of her most unexpected findings emerged in 2012 while working with collaborators on applying single-cell RNA-seq to the analysis of dendritic cells. In contrast to present day technology, which enables the profiling of thousands of cells quickly and cheaply, this study only looked at 18 cells and required a tremendous effort. Regev recalled, "What we found was surprising in two ways. First, we were examining just one cell type which we thought was well-defined, so we did not expect to find major differences in gene expression between the cells – yet we saw 1,000-fold differences, from which we could recover regulatory molecules that accounted for this variation. Second, we discovered surprising patterns in alternative splicing – some cells preferentially used one isoform, others used another. We had been expecting the cells to use both. This added up to a bigger surprise: we weren't really looking at one group of cells. We were looking at two subgroups, which we now know represent different developmental programs. A great deal of my work now focuses on understanding heterogeneity of this type – defining and understanding cells at a much higher resolution than we could before."

Regev has passed along her love of science through her mentorship of postdocs, graduate students, and undergraduates, and outside of the lab she has maintained an intense teaching load and worked to overhaul the undergraduate genetics course to include quantitative content. She is grateful to her mentors who gave her freedom to pursue her own scientific interests and this has guided her style of mentorship. She said, "Today, when I see a person with an idea, I don't care about career stage -- maybe they're a grad student or an undergrad; maybe they are a seasoned staff scientist. I care about who they are. Do they show the seeds of independence, vision, and leadership? And what is their idea? If it's challenging in entirely new ways, and can transform the world, it should be grown. As I mentor my students and postdocs, I try to let them spread their own wings – to be their colleague and collaborator."

At Broad, Regev was recently appointed Chair of the Faculty, and in this role she has been focusing on initiatives to strengthen and build communities around computational biology and advance software engineering approaches to biological data analysis. She has served the greater computational biology community in many ways through work on numerous advisory boards, journal editorial boards, and program committees for conferences. Regev has been a reviewing editor for eLife since its inception, and more recently a senior editor with a major responsibility for computational biology, genomics and theory papers.

Regev is gratified by her selection for the 2017 ISCB Innovator Award, and she said, "Biology is such a data science now, and ISCB is the community that made that happen – so it is especially exciting and gratifying to be receiving such an honor from peers in this community."

---

[1] https://www.hhmi.org/scientists/aviv-regev

2017 ISCB ACCOMPLISHMENT BY A SENIOR SCIENTIST AWARD
PAVEL PEVZNER

The International Society for Computational Biology (ISCB) recognizes an established scientist each year with the Accomplishment by a Senior Scientist Award for significant contributions he or she has made to the field. This award honors scientists who have contributed to the advancement of computational biology and bioinformatics through their research, service, and education work. Pavel Pevzner, PhD, Ronald R. Taylor Professor of Computer Science and Director of the NIH Center for Computational Mass Spectrometry at University of California, San Diego, has been selected as the winner of the 2017 Accomplishment by a Senior Scientist Award.

The ISCB awards committee, chaired by Dr. Bonnie Berger of the Massachusetts Institute of Technology, selected Pevzner as the 2017 winner.

PAVEL PEVZNER: IN SEARCH OF LIFE'S PERFECT PUZZLES

Pevzner was born in Kursk, Russia, and spent his childhood in the city of Murom, which was a hub of the Soviet electronics industry. His father was an electrical engineer and his mother was a teacher, but he admits that his early education got off to a rocky start. He described himself as a poor student who was more interested in having fun, but around age 10, he grew more interested in books.1 Pevzner's interest and abilities in mathematics were soon recognized, and at age 14 he was sent to the Boarding High School at Moscow State University, founded by world-renowned mathematician Andrey Kolmogorov, for children gifted in math and physics. In spite of Pevzner's rigorous high school math studies, he had difficulty getting into Moscow State University because of the anti-semitic admission policies aimed at ethnic Jews.2

As an undergraduate, Pevzner studied at the Russian Institute of Railway Engineers, which was known for its applied mathematics program. He did well throughout his course of study and published a number of papers on discrete mathematics as an undergraduate. In 1985, he joined a bioinformatics lab at Institute of Genetics of Microorganisms VNIIGENETIKA, and received his Ph.D. in Mathematics and Physics in 1988 from the Moscow Institute of Physics and Technology.

Pevzner was completing his graduate work during the era of "Perestroika" and "Glastnost," and for the first time in decades, scientists were being granted permission to travel abroad and were even told that the government would pay for their travels. Pevzner jumped on this opportunity and notified the Russian government that he wanted to work with Mike Waterman at the University of Southern California (USC), a pioneer in the field of bioinformatics and 2006 ISCB Accomplishments by a Senior Scientist Award winner. In 1989, Pevzner reached out to Waterman personally, not quite trusting that his request to the government would be enough to facilitate his travels (it was never granted). During their correspondence, Waterman sent him an open problem, which Pevzner ended up solving. Waterman was surprised that someone had solved this problem and eventually invited him to pursue postdoctoral work in his lab. Pevzner spent two years as a postdoc with Waterman at USC.

In 1992, Pevzner established himself as an independent researcher and started his lab in the Department of Computer Science at Pennsylvania State University. Three years later he returned to USC as a professor in the Department of Mathematics. In 2000, he moved to San Diego and was named Ronald R. Taylor Chair Professor of Computer Science at the University of California, San Diego (UCSD). In 2006, he was named a Howard Hughes Medical Institute Professor.

Pevzner's research interests span the field of bioinformatics and his work has been guided by applying algorithmic ideas to bioinformatics problems. Pevzner has made significant contributions to a wide array of subfields, including genome assembly, understanding how genome rearrangements influence evolution, and developing new algorithms for sequencing antibodies and antibiotics using mass spectrometry. He continues to be fascinated and amazed by scientific discovery, and he explained, "The most surprising thing for me was a realization that dominant biological theory often falls apart when new data and new methods to analyze them become available. Three times in my career I had to refute the biological theories that I worked on: the Master Alu theory of repeat evolution, the NME theory that connects the N-terminal Methionine Excision and protein half-lives, and the Random Breakage Theory of chromosome evolution."

In this era of abundant genome data, Pevzner is currently interested in reconstructing the detailed evolution of the human genome, down to each new repeat and rearrangement that affected the genome, by using hundreds of primate genomes that will be sequenced in the near future. In a more practical domain, Pevzner's other goal is to develop a computational approach to antibiotics discovery, a problem of great importance due to emerging antibiotics resistance. He describes antibiotics discovery as one of the last bastions of modern biology that remains barely touched by bioinformatics.

Beyond Pevzner's academic contributions, he has served the computational biology community in many ways. Seventeen years ago, he helped launch RECOMB (Conference in Research in Computational Molecular Biology) together with Waterman and Sorin Istrail. He has served as a member of numerous editorial boards in the fields of computational biology and computer science.

Throughout his career, Pevzner has mentored many students; 22 of his former graduate and postdoctoral trainees are now professors at various universities. He has seen significant changes to the way he teaches his undergraduate courses along the way. He explained, "The way I teach my undergraduates has completely changed: I haven't given a traditional classroom lecture in three year now. I feel that traditional 1000-year old educational technology (classroom lecture) is coming to its end and will soon be substituted by more efficient "Intelligent Tutoring Systems." My goal in recent years was to develop the first such system for bioinformatics that will be launched in Spring 2017 on edX."

Pevzner is humbled by his selection as the winner of the 2017 ISCB Accomplishment by a Senior Scientist Award – he acknowledges that he did not earn this recognition alone. He said, "This award really goes to my teachers and my students and postdocs over the last quarter of a century."

---

1 https://www.scientific-computing.com/feature/life-puzzle-solver
2 http://www.npr.org/2014/03/28/295789948/the-real-problem

2017 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD
FRAN LEWITTER

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. Fran Lewitter is the 2017 winner of the Outstanding Contributions to ISCB Award and will be recognized at the 2017 Intelligent Systems for Molecular Biology (ISMB)/European Conference on Computational Biology meeting in Prague, Czech Republic being held from July 21-25, 2017.

Fran Lewitter completed her PhD in Human Genetics and Statistical Genetics at the University of Colorado Boulder. After completing postdoctoral work in Genetic Epidemiology at Harvard Medical School, she worked on the first five years of the GenBank project. Lewitter then worked in the Biology Department at Brandeis University in a number of capacities, including supporting molecular biology computing and being involved with their Genetic Counseling program. In 1994, she joined the Whitehead Institute for Biomedical Research in Cambridge MA. to run a bioinformatics core facility. For twenty years, she worked with and trained basic biomedical researchers who were doing sequencing or were using bioinformatics to gain a deeper understanding of different biological questions. She was later named the Founding Director of Bioinformatics and Research Computing and was given a larger staff as the demand for bioinformatics information grew in the late 1990s and early 2000s.

Lewitter’s first encounter with ISCB occurred when she attended ISMB 2001 in Copenhagen, Denmark, followed by a one-day satellite meeting, Workshop on Education in Bioinformatics (WEB). At the time, Whitehead did not have a large bioinformatics community, and she was in search of peers who were running bioinformatics core facilities and teaching bioinformatics to biologists. “One thing that attracted me to go [to ISMB] was the one day workshop on education and bioinformatics, since I was so heavily involved in educating people. I went to every meeting since then.” At ISMB 2002 in Edmonton, Lewitter helped organize an informal gathering of bioinformatics core facility managers, and this unique gathering spurred the organization of a mailing list, which became an invaluable resource for Lewitter and her peers as they faced challenges and questions unique to running a core facility.

Since her early encounters with ISCB, Lewitter has become a tireless advocate for bioinformatics education and training on behalf of ISCB. As a core facility director, she has offered her unique academic perspective and voice through her service on the ISCB Education Committee and as a member of the Board from 2008-2017. Lewitter recognized the growing demand for bioinformatics training early in her involvement with ISCB, and she worked to strengthen ISCB’s role in supporting bioinformatics education and training by promoting the inclusion of bioinformatics education content in the main conference programs. To this end, she has organized Workshops on Education in Bioinformatics (WEB) at ISMB meetings since 2009, and she has helped build ISCB community activities including the CoBE COSI (Computational Biology Education Community of Special Interest). Lewitter’s leadership of the ISCB Education Committee helped unite the global bioinformatics education community through shared objectives and brought greater awareness of the committee’s work through tutorials and training opportunities offered at ISCB conferences. Lewitter recognizes that one of the most critical aspects of training is “to introduce biologists to bioinformatics vocabulary whether or not they would be using the primary bioinformatics tools.” This fosters better collaborations between bioinformatics experts and bench scientists and is necessary to facilitate the ongoing integration of bioinformatics into all aspects of biology.

Lewitter has been instrumental in bringing together ISCB and GOBLET (the Global Organization for Bioinformatics Learning, Education and Training) and coordinating activities by which these two organizations work together to further bioinformatics training on a global scale. She has advocated for the development and maintenance of bioinformatics education resources on ISCB webpages, and these electronic resources are valuable tools used by the global bioinformatics education community.

Lewitter has valued her membership in ISCB for providing her opportunities to “get to know innovative people.” She has especially appreciated meeting other core facility directors and managers. Lewitter said, “ It’s gratifying to hear I am doing the right thing, or other people have ideas that can help me or I can help them. It is good to talk to other people about issues of running a core facility, what courses to teach or what tools are the best to teach?” Despite having retired from Whitehead Institute three years ago, she enjoys her continued involvement in ISCB activities. She is also heartened by the rising generation of ISCB members who are involved with the ISCB Student Council. Lewitter hopes ISCB will continue to grow and thrive and is grateful for being recognized for her steadfast efforts to promote and further bioinformatics education.

2017 ISCB OVERTON PRIZE
CHRISTOPH BOCK

The International Society for Computational Biology (ISCB) each year recognizes the achievements of an early to mid-career scientist with the Overton Prize. This prize honors the untimely death of Dr. G. Christian Overton, an admired computational biologist and founding ISCB Board member. Winners of the Overton Prize are independent investigators who are in the early to middle phases of their careers and are selected because of their significant contributions to computational biology through research, teaching, and service.

ISCB is pleased to recognize Dr. Christoph Bock, Principal Investigator at the CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences in Vienna, Austria as the 2017 winner of the Overton Prize. Bock will be presenting a keynote presentation at the 2017 International Conference on Intelligent Systems for Molecular Biology/ European Conference on Computational Biology (ISMB/ECCB) in Prague, Czech Republic being held during July 21-25, 2017.

CHRISTOPH BOCK: AT HOME IN THE EPIGENOME

Christoph Bock's scientific curiosity was nurtured from a young age. His parents were math and science teachers, and while they did not push him to pursue these areas of study, he sees how this intellectually stimulating environment cultivated his natural curiosity and provided a critical foundation to his career as a scientist. Bock started exploring computer programming from the age of twelve, and he realizes in retrospect how learning to code was a valuable tool for practicing problem solving and scientific thinking.

During high school, Bock specialized in physics and math. His undergraduate studies at the University of Mannheim focused on computer science and business information systems, emphasizing machine learning and artificial intelligence. Toward the end of his studies, Bock yearned to tackle questions with broader relevance than the "toy problems" he encountered in his course work. Bock recalled, "Human biology seemed the biggest challenge and also most societally relevant. I was lucky that Jürgen Hesser offered a bioinformatics lecture and agreed to supervise my Master's thesis at the University of Mannheim". His Master's research work focused on protein structure prediction and homology modeling.

Bock pursued his PhD studies in bioinformatics under the supervision of Thomas Lengauer at the Max Planck Institute for Informatics, studying epigenetic regulation of the genome. "Moving into bioinformatics and epigenetics, I had to catch up on a lot of important biological knowledge", Bock recalled. "Reading papers and collaborating was key, but it also helped that my research focused on a field that was quite young, with ample opportunity to try out something new."

He attributes much of his bioinformatics training to the time spent in the research group of Thomas Lengauer, and he has been grateful for his mentor's continued support and collaboration throughout his early career. Bock also acknowledges the important guidance and feedback on his research provided by Jörn Walter, who co-supervised his PhD dissertation and introduced Bock to the international epigenetics community.

Bock's first encounter with epigenetics data transformed his scientific career path, and he has been one of the first bioinformaticians that dedicated their work to epigenetic data. "When I started my PhD studies in 2004, the largest epigenetic dataset consisted of just over 100 data points, and one of my first papers established epigenome prediction as a means of inferring what was still very difficult and costly to measure experimentally."

In the following years, next generation sequencing transformed the field, and it became possible to collect several billion data points in a single epigenome mapping experiment. This development created a strong demand for bioinformatic methods. "Working at the forefront of the epigenome revolution has been the highlight of my scientific research so far. But the most exciting times may still be ahead as epigenome research is starting to become broadly relevant for medicine, and I am looking forward to contributing to this development."

Bock developed several software tools as part of his PhD, including BiQ Analyzer for processing DNA methylation data and EpiGRAPH for analyzing and predicting epigenome profiles in their genomic context. Bock went on to pursue postdoctoral studies under Alexander Meissner at the Broad Institute. There, Bock was exposed to the world of wet-lab biology, and he discovered the thrill and power of jointly developing new laboratory techniques and computational methods, which he used to study the epigenome of pluripotent and hematopoietic stem cells.

In 2012, Bock started his own research group at CeMM, an institute dedicated to advancing precision medicine through basic and translational research. He was hired by Giulio Superti-Furga, Scientific Director of CeMM, who, as Bock said, "Provided ample encouragement and let me try things that were initially quite far outside of my comfort zone, such as starting a wet lab and leading a next generation sequencing technology platform." Bock has thrived at CeMM, where he has been able to work with many passionate researchers within the institute and at the neighboring Medical University of Vienna.

At CeMM, Bock has also developed his personal style of being a PI and mentor, acting as a catalyst of ideas and projects for an interdisciplinary team. He explained, "Our lab combines computational and wet-lab biology on roughly equal terms, with a good dose of technology development – including single-cell sequencing, CRISPR, epigenome editing, machine learning, and more. There is also an extensive network of collaborations, ranging from fundamental biology to immediate clinical applications in the area of personalized and precision medicine. It is a great privilege to work with such an interdisciplinary and creative group of smart people."

Bock considers the success of his students and postdocs as a key measure of his achievement as a PI. He explained, "I work hard to maintain an environment in which every group member can build a great CV and learns what he or she needs to advance in their scientific career. So far, we have a 100% success rate of postdocs moving on to attractive PI jobs, which is great for young lab. But it is clear that helping others succeed in their career is not an easy task, and you need to create room for success and failure, and a safety net that encourages risk taking."

Bock is still excited about epigenetics and what it can teach us about a cell's past, present and future. He hopes that epigenomic data can be used to understand the regulatory logic of cells and to determine what goes awry in diseases like cancer. Bock said, "We are pursuing an engineering-inspired "build it to understand it" approach to cancer biology, where we combine CRISPR epigenome editing and computationally designed drug combinations to rationally reprogram normal cells into cancer cells and vice versa. Building upon a breakthrough technology for pooled CRISPR screening with single-cell sequencing, We seek to decipher complex biological pathways and gene regulatory networks in high throughput, in order to overcome the classical "one gene, one postdoc" paradigm of functional (epi-) genomics."

Bock is deeply gratified to be honored with the Overton Prize, especially since he will receive his award this year in Prague. He said, "Ten years ago, I attended ISMB 2007 in Vienna – one of the first conferences where I presented my PhD project on epigenome prediction. That year, Eran Segal won the Overton Prize, and his keynote lecture about DNA's regulatory code reinforced my interest in understanding the role of epigenome regulation in biology and medicine. ISMB 2007 was also my first time in Vienna, and the great impressions from that visit surely contributed to the fact that a job ad from Vienna caught my attention a few years later. This year, it will be my pleasure to give the Overton Prize lecture at ISMB 2017 in Prague, ten years and just a few hundred kilometers away from a truly career-defining ISMB 2007."

IN MEMORIAM

GUIDO CAPITANI 1970–2017

Guido Capitani passed away on May 2, 2017. Guido was 46, and is much missed by his friends and colleagues. He was a prolific crystallographer, with 70 protein structures in the Protein Data Bank (PDB) over the past two decades. He also made significant contributions to computational structural biology, particularly in the analysis of protein-protein interfaces. He was a devoted scientist, with 69 peer-reviewed publications over his life, and a mentor to a number of masters, PhD, and post-doctoral scientists.

Guido was a long-time ISCB member and regularly presented his work at ISMB and 3DSIG conferences. He was a respected and liked member of our community and a past keynote speaker and session chair at 3DSIG.

Guido grew up in Bologna, Italy. His education was marked by accolades, with perfect scores on high school and university final exams. He studied chemistry for two years at the University of Bologna and then at the University of Padua, where he graduated cum laude. He moved to Switzerland for his doctorate, where he would reside for the remainder of his career. His doctoral thesis, "X-ray crystallographic studies of chloroplastic thioredoxins and of vitamin B6-dependent enzymes," earned him a doctorate in biophysics summa cum laude from Basel Biozentrum in 1998.

From there, he worked with Markus Grütter at the University of Zurich, elucidating the structures of numerous proteins. Notable structures include thioredoxin structures, glutamate decarboxylase, and bacterial type 1 pili. The type 1 pilus enables E. coli to infect humans by attaching to sugar moieties that reside on the urethral epithelium. Work highly relevant to our well-being. He also began teaching courses on crystallography and bioinformatics during this period. He enjoyed teaching and continued lecturing at the University of Zurich and ETH Zurich throughout his career.

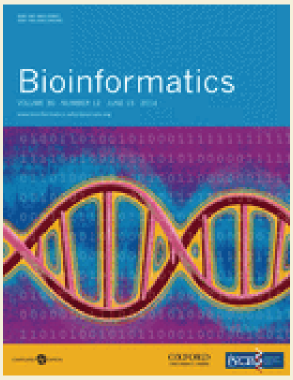
In 2008, Guido started a successful research group at Paul Scherrer Institute. He continued to solve protein structures at the Swiss Light Source, and also put forward a program of large-scale bioinformatic analysis of structures. This includes the Evolutionary Protein-Protein Interface Classifier (EPPIC) for assessing the biological relevance of protein-protein interfaces. His expertise in protein interfaces was widely appreciated in the community, and Guido was appointed as an assessor for the Critical Assessment of protein Structure Prediction (CASP) this year.

Guido was a remarkable person. He was soft-spoken and considerate, and always had an open ear available for anyone. He was a successful grantsman (including a recent large grant on Big Data in Structural Biology that he will unfortunately not be able to supervise), but always behaved with humility and treated his group members with respect. He was a fiery defender of open access publication, open source software, and open science. Although he is gone, the projects he started will live on through the community of users and contributors that continue to work with them.

BIOINFORMATICS UPDATE

Bioinformatics has had a very busy and successful 2016. We continue to serve ISCB members and the wider computational biology community and we thank our authors, reviewers, and readers for the continued support.

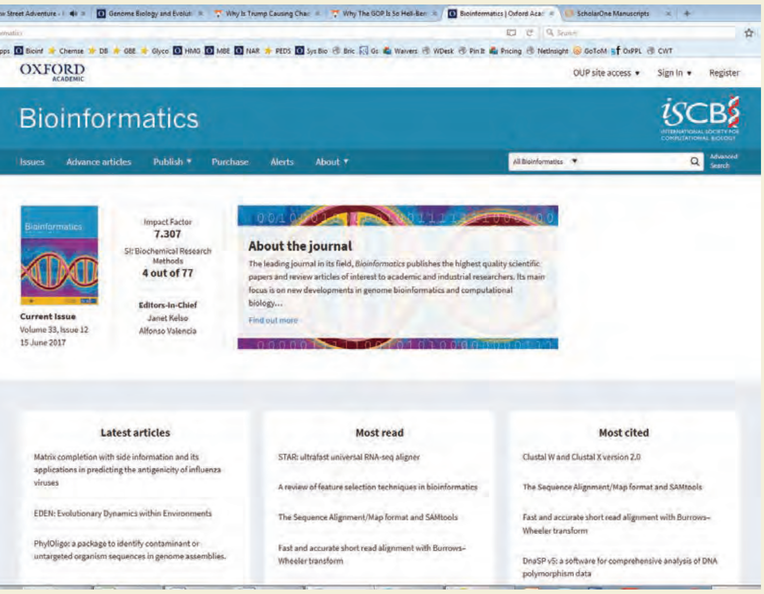
Bioinformatics has a new impact factor of 7.307 for 2016, taking the journal to second place in the Mathematical and Computational Biology category.



At the start of 2017 *Bioinformatics* launched on the new Oxford Academic platform (https://academic.oup.com/bioinformatics). The new site showcases journal content on the homepage, and allows easier navigation to virtual issues, ISCB articles, and information about the Society. In the future we are excited to explore the opportunities for semantic enrichment that our new platform enables.

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:

iEnhancer-2L: a two-layer predictor for identifying enhancers and their strength by pseudo k-tuple nucleotide composition, by Liu, Bin; Fang, Longyun; Long, Ren; et al. https://doi.org/10.1093/bioinformatics/btv604



Impact Factor
7.307
SI: Biochemical Research Methods
4 out of 77

Current Issue
Volume 33, Issue 12
15 June 2017

Editors-In-Chief
Janet Kelso
Alfonso Valencia

About the journal

The leading journal in its field, *Bioinformatics* publishes the highest quality scientific papers and review articles of interest to academic and industrial researchers. Its main focus is on new developments in genome bioinformatics and computational biology...

Latest articles

Matrix completion with side information and its applications in predicting the antigenicity of influenza viruses

EDEN: Evolutionary Dynamics within Environments

PhylOligo: a package to identify contaminant or untargeted organism sequences in genome assemblies.

Most read

STAR: ultrafast universal RNA-seq aligner

A review of feature selection techniques in bioinformatics

The Sequence Alignment/Map format and SAMtools

Fast and accurate short read alignment with Burrows-Wheeler transform

Most cited

Clustal W and Clustal X version 2.0

The Sequence Alignment/Map format and SAMtools

Fast and accurate short read alignment with Burrows-Wheeler transform

DnaSP v5: a software for comprehensive analysis of DNA polymorphism data

Gapped sequence alignment using artificial neural networks: application to the MHC class I system, by Andreatta, Massimo; Nielsen, Morten https://doi.org/10.1093/bioinformatics/btv639

Cytoscape.js: a graph theory library for visualisation and analysis, by Franz, Max; Lopes, Christian T.; Huck, Gerardo; et al. https://doi.org/10.1093/bioinformatics/btv557

iPTM-mLys: identifying multiple lysine PTM sites and their different types, by Qiu, Wang-Ren; Sun, Bi-Qian; Xiao, Xuan; et al. https://doi.org/10.1093/bioinformatics/btw380

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

NanoOK: multi-reference alignment analysis of nanopore sequencing data, quality and error profiles, by Richard M. Leggett, Darren Heavens, Mario Caccamo, Matthew D. Clark and Robert P. Davey

https://doi.org/10.1093/bioinformatics/btv540

Probing the binding affinity of amyloids to reduce toxicity of oligomers in diabetes, by Mohamed Raef Smaoui, Henri Orland and Jérôme Waldispühl

https://doi.org/10.1093/bioinformatics/btv143

BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS, by Katharina J. Hoff, Simone Lange, Alexandre Lomsadze, Mark Borodovsky and Mario Stanke

https://doi.org/10.1093/bioinformatics/btv661

Our submission rate for 2016 was over 2000 papers, of which in the region of 38% were accepted. Of our published papers, around 30% were published open access, with authors choosing between CC-BY-NC and CC-BY licences.

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 (https://academic.oup.com/bioinformatics/pages/ISCB_articles).

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 ISMBECCB 2017 in the wonderful city of Prague – see you there!

With best wishes,
The Bioinformatics Editorial team

iSCB

ISMB

CELEBRATING 25 YEARS OF ISMB

ECCB

2017 • PRAGUE

JULY 21–25

CONFERENCE PROGRAM

Welcome to ISMB/ECCB in Prague!

On behalf of the organizing committee of ISMB/ECCB 2017, the Board of Directors of the International Society for Computational Biology (ISCB) and Steering Committee of European Conference on Computational Biology (ECCB), we wish you a very warm welcome. ISMB joins forces with ECCB and takes place in Europe this year in the beautiful city of Prague. This large gathering promises to be the key meeting for computational biologists in 2017.

This year sees a radical restructuring of the conference, which has been designed to let you connect more easily to researchers sharing common interests and to come together and listen to exciting new developments in your field. At the heart of the meeting are events by fifteen of our established communities (COSIs – Communities of Special Interest) reflecting most of the major research themes and training in computational biology. These communities will each run their respective sessions (COSI tracks or workshops) as part of the conference, rather than before or after as in previous years. You will have the opportunity to attend any of these sessions, choosing the presentations of most interest to you and taking the opportunity to network with other participants. Our five distinguished keynote speakers, including the 2017 ISCB award winners, will cover topics as diverse as reconstructing cellular circuits, limb development, the epigenome, elucidating regulation and computational mass spectrometry. In addition, the meeting will encompass all of the familiar themes and tracks, such as proceedings, highlight, or late breaking topics – as well as the Special Sessions, Technology Tracks, Workshops and two Special Tracks (BD2K, ELIXIR), which are so important for transferring knowledge and expertise.

The newly organized COSI tracks include talks from Proceedings submissions, which will be published in a special issue of the journal Bioinformatics, together with other scientific talks on previously published research (Highlights) and exciting Late-Breaking unpublished research.

Scientifically, the multi-track program presents cutting-edge research in a wide-ranging set of topics, from protein and RNA sequence, structure and function to networks, regulation and systems modeling and new clinical data for translation to medicine. More technical sessions focus on core bioinformatics competencies, bio-ontologies, new ways to handle and visualize and combine data, as well as improved sequence algorithms. We hope you like the new structure and that the diversity of options and depth of presented research affords you a stimulating and productive time in Prague.

The program includes

- 5 Keynote addresses, including our 2017 ISCB Award Winners
- 15 community-led COSI tracks and workshops
- Special Sessions on Machine Learning in Systems Biology, Metagenomes, Immune Oncology, and Competency-Based Approaches to Education
- Special Tracks by ELIXIR (EU Life Science Data Infrastructure) and BD2K (NIH Big Data to Knowledge Program)
- The Technology Track
- The pre-conference Student Council Symposium organized by and for students
- Pre-conference Tutorials
- Equally as important, there are more than 900 posters on display throughout the conference and presented by their authors in four sessions. Discussions directly with authors can be so much more revealing than just hearing a presentation, so do go along.

We acknowledge all the chairs of the Proceedings, COSIs, Poster, Technology Track, Travel Fellowship, Tutorials, Art in Science, and Student Council Symposium committees. 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/ECCB 2017.

As Conference Chairs we also appreciate the support of the very many volunteers who 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: Bruno Gaeta, 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 Diane Kovats, ISCB Executive Director, and Steven Leard, the ISMB Conference Director, there would be no ISMB/ECCB meeting! We are immensely grateful to Diane, Steven and their teams 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 computational biologists.

Finally, we thank the city of Prague for its welcoming hospitality and wish you all a great conference!

Yours sincerely,

Moreau   Janet Thornton

Yves Moreau   Janet Thornton
Conference Co-Chairs

ISMB/ECCB 2017 Scientific Organizing Committee

CONFERENCE CHAIRS

Yves Moreau, KU Leuven, Belgium

Janet Thornton, European Bioinformatics Institute, European Molecular Biology Laboratory, United Kingdom

ISMB/ECCB 2017 STEERING COMMITTEE

Alfonso Valencia, *President, ISCB,* Barcelona Supercomputing Center, Spain

Bruno Gaeta, *Treasurer,* University of New South Wales, Australia

Janet Kelso, *Conference Advisory Council Co-chair,* Max Planck Institute for Evolutionary Anthropology, Germany

Diane E. Kovats, *ISCB Executive Director,* United States

Steven Leard, *ISMB Conference Director,* Canada

Christine Orengo, *Conference Advisory Council Co-chair,* University College London, United Kingdom

Proceedings Chairs

Niko Beerenwinkel, ETH Zurich, Switzerland

Yana Bromberg, Rutgers University, United States

Posters Chairs

Casey Greene, University of Pennsylvania, United States

Arjun Krishnan, Michigan State University, United States

Technology Track Chair

Dominic Clark, European Bioinformatics Institute, Cambridge, United Kingdom

Travel Fellowship Chair

Lucia Peixoto, Washington State University, United States

Tutorial Chairs

Michelle D. Brazas, Ontario Institute for Cancer Research, Canada

Fran Lewitter, Whitehead Institute for Biomedical Research, United States

Patricia M. Palagi, SIB Swiss Institute of Bioinformatics, Switzerland

Art in Science Chair

Milana Frenkel-Morgenstern, Bar-Ilan University, Israel

Student Council Symposium Chairs

Julien Fumey, French National Centre for Scientific Research – I2BC, France

Mehedi Hassan, University of South Wales, United Kingdom

For a complete list of committees go to https://www.iscb.org/ismbeccb2017-committee/committeelisting

Posters on Display

CONGRESS HALL FOYER, LEVEL 2

SESSION A

SATURDAY JULY 22

Posters set up 7:30 AM – 10:00 AM

Poster Help Desk located in Congress Foyer, Level 2

SESSION A Posters with Authors
ODD Numbered 6:00 PM - 7:00 PM

SUNDAY JULY 23

SESSION A Posters with Authors
EVEN Numbered 6:00 PM – 7:00 PM

Poster Removal 7:00 PM

SESSION B

MONDAY JULY 24

Posters set up 7:30 AM – 10:00 AM

Poster Help Desk located in Congress Foyer, Level 2

SESSION B Posters with Authors
ODD Numbered 6:00 PM – 7:00 PM

TUESDAY JULY 25

SESSION B Posters with Authors
EVEN Numbered 1:00 PM – 2:00 PM

Poster Removal 4:30 PM

Poster not removed at outlined times will be taken down and placed on side tables. ISCB will not be responsible for damaged or missing posters.

Prague Congress Centre

GROUND FLOOR

FIRST FLOOR

SECOND FLOOR

Distinguished Keynote Presentations

ROOM: FORUM HALL

FRIDAY, JULY 21 • 6:15 PM – 7:15 PM

ISCB 2017 Innovator Award Keynote
Aviv Regev, Broad Institute of MIT and Harvard, Cambridge, United States

Reconstructing Cellular Circuits: From Cells to Tissues

Introduction by: Bonnie Berger, ISCB Vice President

SATURDAY, JULY 22 • 8:30 AM – 9:30 AM

James Sharpe, EMBL-CRG Systems Biology Unit, Centre for Genomic Regulation (CRG), Barcelona, Spain

Dynamic computer modeling to span the scales: from molecular circuits to organogensis

Introduction by: Janet Thornton, ISMB/ECCB 2017 Conference Co-chair

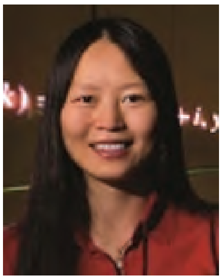
SUNDAY, JULY 23 • 8:30 AM – 9:30 AM

ISCB 2017 Overton Prize Award Keynote
Christoph Bock, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria

Bioinformatics for Personalized Medicine: Looking Beyond the Ge-nome

Introduction by: Thomas Lengauer, ISCB President Elect

MONDAY, JULY 24 • 8:30 AM – 9:30 AM



Zhiping Weng, Director, Program in Bioinformatics and Integrative Biology;
Professor, Biochemistry and Molecular Pharmacology; University of Massachusetts Medical School, Worcester, United States

ENCODE Encyclopedia: Featuring a Registry of Candidate Regulatory Elements and the Visualization Tool SCREEN for Searching Them

Introduction by: Yves Moreau, ISMB/ECCB 2017 Conference Co-chair

TUESDAY, JULY 25 • 4:45 PM – 5:45 PM

ISCB 2017 Accomplishments by a Senior Scientist Award Keynote
Pavel Pevzner, Department of Computer Science and Engineering, University of California, San Diego, La Jolla, United States

Bioinformatics: A Servant or the Queen of Molecular Biology?

Introduction by: Alfonso Valencia, ISCB President

Details available on the conference app – see page 27 for details.

Schedule-at-a-Glance • Friday

PRAGUE CONGRESS CENTRE

*schedule as of June 27 and subject to change

FRIDAY, JULY 21

	NORTH HALL	TERRACE 1	MEETING HALL V	MEETING HALL IV
	3:00 PM – 7:30 PM Conference Registration			CONGRESS HALL FOYER 1
8:30 AM				**Student Council Symposium**
10:00 AM	**Tutorial AM1**: Single cell transcriptomics	**Tutorial AM2**: Ontologies in Computational Biology	**Tutorial AM3**: 3D Genome Data Processing, Analysis, and Visualization	
11:30 AM	COFFEE BREAK – TUTORIALS			
11:45 AM	AM1 continued	AM2 continued	AM3 continued	
1:30 PM	LUNCH BREAK			
2:30 PM	**Tutorial PM6**: Making Galaxy Work for You	**Tutorial PM5**: Prediction of Regulatory Networks from Expression and Chromatin Data	**Tutorial PM4**: Network Analysis in Cytoscape: Advanced Topics	
4:00 PM	COFFEE BREAK – TUTORIALS			
2:30 PM	PM6 continued	PM5 continued	PM4 continued	
6:00 PM	TUTORIALS AND STUDENT COUNCIL SYMPOSIUM END			
6:15 PM	Welcome and **ISCB 2017 Innovator Award** **Keynote KN01: Aviv Regev,** Broad Institute of MIT and Harvard *Reconstructing Cellular Circuits: From Cells to Tissues*			ROOM: FORUM HALL
7:15 PM	OPENING RECEPTION WITH EXHIBITORS			CONGRESS HALL FOYER 2

Free WIFI: ISMBECCB Password: PRAGUE17

Details available on the conference app – see page 27 for details.

Schedule-at-a-Glance • Saturday

PRAGUE CONGRESS CENTRE

*schedule as of June 27 and subject to change

SATURDAY, JULY 22

	FORUM HALL	MEETING HALL IA	MEETING HALL IB	MEETING HALL IV	MEETING HALL V	PANORAMA	TERRACE 1	NORTH HALL
	7:30 AM – 7:30 PM Conference Registration							CONGRESS HALL FOYER 1
8:15 AM	Morning Welcome and conference updates **Outstanding Contributions to ISCB Award Presentation**							ROOM: FORUM HALL
8:30 AM	**Keynote KN02: James Sharpe**, EMBL-CRG Systems Biology Unit, Centre for Genomic Regulation (CRG) *Dynamic computer modeling to span the scales: from molecular circuits to organogensis*							
9:30 AM	COFFEE BREAK WITH EXHIBITORS							CONGRESS FOYER 2
10:00 AM	**3Dsig COSI**	**RegGen COSI**	**RNA COSI**	**BOSC COSI**	**Workshop 01**: Workshop on Education in Bioinformatics (WEB)	**SysMod COSI**		**CAMDA COSI**
12:30 PM	LUNCH: EXHIBITION / POSTER AREA							CONGRESS FOYER 2
12:45 PM – 1:45 PM BIRDS OF A FEATHER		**BoF A1**: The Computational Biology Education (CoBE) COSI BOF	**BoF A2**: JPI Career Development: "On Leadership and Management"	BOSC COSI continued	**BoF A6**: Future of phospho-proteomics	**BoF A5**: Diagnostic relevance of transcriptome sequencing for rare Mendelian diseases	**BoF A4**: Promoting gender diversity in Bioinformatics	**BoF A3**: ERC funding schemes
2:00 PM	3Dsig COSI continued	RegGen COSI continued	RNA COSI continued	BOSC COSI continued	**Special Session 01**: Competency-based approaches to education and training in computational biology: bring your own educational challenge	SysMod COSI continued	**Technology Track**	CAMDA COSI continued
4:00 PM	COFFEE BREAK WITH EXHIBITORS							CONGRESS FOYER 2
4:30 PM	3Dsig COSI continued	RegGen COSI continued	RNA COSI continued	BOSC COSI continued	Special Session 01 continued	SysMod COSI continued	**Technology Track**	CAMDA COSI continued
6:00 PM – 7:00 PM	POSTER PRESENTATIONS (SESSION A ODD NUMBERED)							CONGRESS FOYER 2

Free WIFI: ISMBECCB Password: PRAGUE17

Schedule-at-a-Glance • Sunday

PRAGUE CONGRESS CENTRE

*schedule as of June 27 and subject to change

SUNDAY, JULY 23

	FORUM HALL	MEETING HALL IA	MEETING HALL IB	MEETING HALL IV	MEETING HALL V	PANORAMA	TERRACE 1	NORTH HALL
	7:30 AM – 7:30 PM Conference Registration							CONGRESS HALL FOYER 1
	10:00 AM – 9:00 PM ISMB/ECCB 2017 Wikipedia Editathon							ROOM 2.1
8:15 AM	Morning Welcome and conference updates							ROOM: FORUM HALL
8:30 AM	**ISCB 2017 Overton Prize Award** **Keynote KN03: Christoph Bock**, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences *Bioinformatics for Personalized Medicine: Looking Beyond the Ge-nome*							
9:30 AM	COFFEE BREAK WITH EXHIBITORS							CONGRESS FOYER 2
10:00 AM	**3Dsig COSI**	**RegGen COSI**	**BD2K Special Track 01:** Celebrating BD2K – Machine Learning – Centres of Excellence	**BOSC COSI**	**Special Session 02**: Critical Assessment of Metagenome Interpretation (CAMI)	**NetBio COSI**	**Technology Track**	**CAMDA COSI**
12:30 PM	LUNCH: EXHIBITION / POSTER AREA							CONGRESS FOYER 2
				BOSC COSI continued	12:45 PM Join Us for the ISCB Town Hall 			ROOM: TERRACE 1
2:00 PM	3Dsig COSI continued	RegGen COSI continued	**BD2K Special Track 02:** Celebrating BD2K – Metadata and Indexing – CEDAR Center at Stanford and	BOSC COSI continued	Special Session 02 continued	NetBio COSI continued	**Technology Track**	CAMDA COSI continued
4:00 PM	COFFEE BREAK WITH EXHIBITORS							CONGRESS FOYER 2
4:30 PM	3Dsig COSI continued	RegGen COSI continued	**BD2K Special Track 03**: Celebrating BD2K – NIH Commons	BOSC COSI continued		NetBio COSI continued	**Technology Track**	CAMDA COSI continued
6:00 PM – 7:00 PM	POSTER PRESENTATIONS (SESSION A EVEN NUMBERED)							CONGRESS FOYER 2

Free WIFI: ISMBECCB Password: PRAGUE17

Details available on the conference app – see page 27 for details.

Schedule-at-a-Glance • Monday

PRAGUE CONGRESS CENTRE

*schedule as of June 27 and subject to change

MONDAY, JULY 24

	FORUM HALL	MEETING HALL IA	MEETING HALL IB	MEETING HALL IV	MEETING HALL V	PANORAMA	TERRACE 1
	7:30 AM – 7:30 PM Conference Registration CONGRESS HALL FOYER 1						
8:15 AM	Morning Welcome and **Introduction of ISCB 2017 Distinguished Fellows** ROOM: FORUM HALL						
8:30 AM	**Keynote KN04: Zhiping Weng,** University of Massachusetts Medical School *ENCODE Encyclopedia: Featuring a Registry of Candidate Regulatory Elements and the Visualization Tool SCREEN for Searching Them*						
9:30 AM	COFFEE BREAK WITH EXHIBITORS CONGRESS HALL FOYER 2						
10:00 AM	**HiTSeq COSI**	**VarI COSI**	**Workshop 02**: Bioinformatics Core Workshop	**BioVis COSI**	**Bio-Ontologies COSI**	**Function COSI**	**Technology Track**
12:30 PM	LUNCH: EXHIBITION/POSTER AREA CONGRESS HALL FOYER 2						
12:45 PM – 1:45 PM BIRDS OF A FEATHER		**BoF B5**: Equity, Diversity, and Inclusion in ISCB and in Bioinformatics	**BoF B1**: JPI Career Development: "Becoming a Leader in the Open Data Movement"	**BoF B2**: How to build your scientific network as an early career researcher	**BoF B4**: What can the Galaxy Project do for you?	**BoF B6:** Future of Hi-C Data?	**BoF B3**: Cytoscape Community Meeting: Latest updates and Roadmap
2:00 PM	HiTSeq COSI continued	VarI COSI continued	**Special Session 03**: Computational Immune Oncology	BioVis COSI continued	Bio-Ontologies COSI continued	Function COSI continued	**Technology Track**
4:00 PM	COFFEE BREAK WITH EXHIBITORS CONGRESS HALL FOYER 2						
4:30 PM	HiTSeq COSI continued	VarI COSI continued		BioVis COSI continued	Bio-Ontologies COSI continued	Function COSI continued	
6:00 PM – 7:00 PM	POSTER PRESENTATIONS (SESSION B ODD NUMBERED) CONGRESS HALL FOYER 2						
7:30 PM	ISCB CONFERENCE DINNER (*TICKETED EVENT IN SUPPORT OF TRAVEL FELLOWSHIP FUND — SOLD-OUT) U FLEKÜ RESTAURANT						

Free WIFI: ISMBECCB Password: PRAGUE17

Schedule-at-a-Glance • Tuesday

PRAGUE CONGRESS CENTRE

*schedule as of June 27 and subject to change

ISCB
ISMB
CELEBRATING 25 YEARS OF ISMB
ECCB
2017 • PRAGUE

TUESDAY, JULY 25

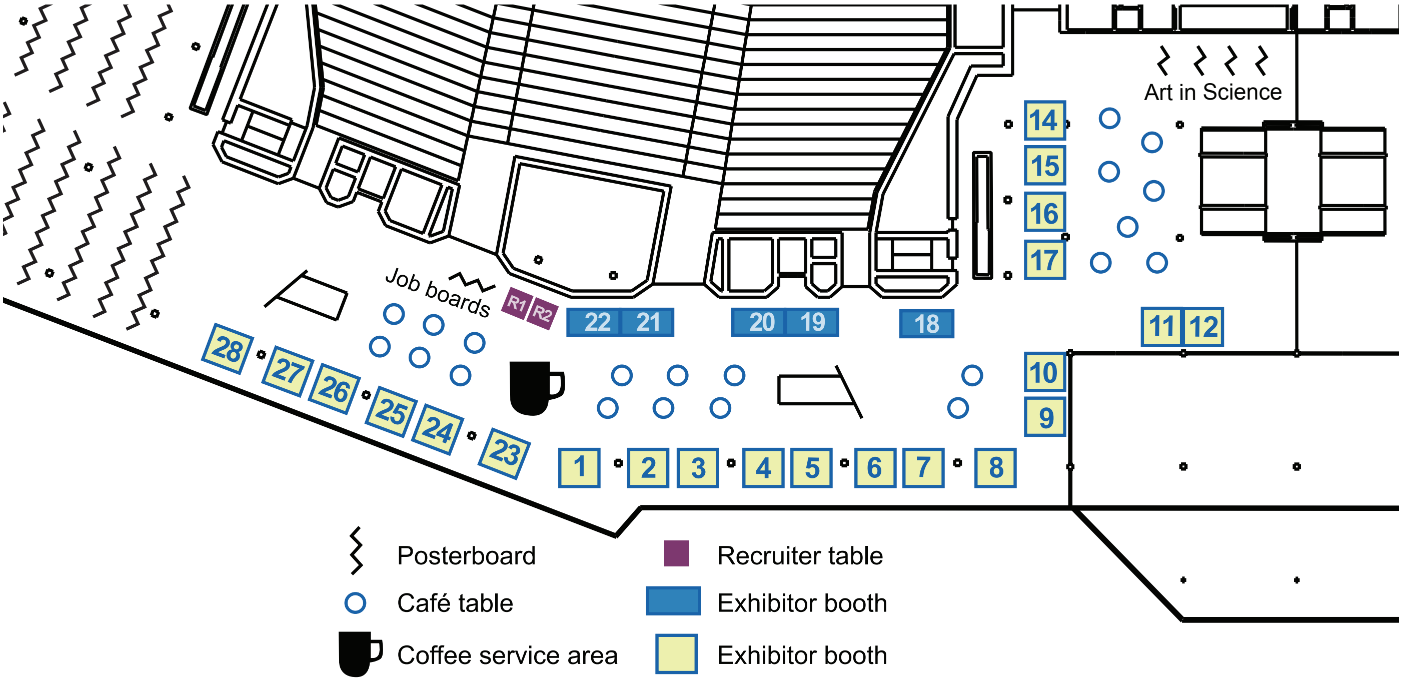
	FORUM HALL	MEETING HALL IA	MEETING HALL IB	MEETING HALL IV	MEETING HALL V	PANORAMA	TERRACE 1	NORTH HALL
	7:30 AM – 6:00 PM Conference Registration							CONGRESS HALL FOYER 1
8:30 AM	**HiTSeq COSI**		**Abstracts: Non-COSI Areas**	**TransMed COSI**	**Bio-Ontologies COSI**	**Function COSI**		**Special Session 04**: Machine Learning in Systems Biology (MLSB)
9:30 AM	COFFEE BREAK WITH EXHIBITORS							CONGRESS HALL FOYER 2
10:00 AM	HiTSeq COSI	**ELIXIR Special Track**	Abstracts continued	TransMed COSI continued	Bio-Ontologies COSI continued	Function COSI continued	**Technology Track**	Special Session 04 continued
12:30 PM	LUNCH POSTER PRESENTATIONS (SESSION B EVEN NUMBERED)							CONGRESS HALL FOYER 2
2:00PM	HiTSeq COSI	ELIXIR Special Track continued	Abstracts continued	TransMed COSI continued	Bio-Ontologies COSI continued	Function COSI continued		Special Session 04 continued
4:30 PM	GRAB AND GO REFRESHMENT BREAK							CONGRESS HALL FOYER 2
4:45 PM	**ISCB 2017 Senior Scientist Award** **Keynote KN05: Pavel Pevzner,** University of California, San Diego *Bioinformatics: a Servant or the Queen of Molecular Biology?*							ROOM: FORUM HALL
5:45 PM	**Awards Presentations**							

Free WIFI: ISMBECCB Password: PRAGUE17

Details available on the conference app – see page 27 for details.

Exhibitors

CONGRESS HALL FOYER 2



Exhibitor Booth

1	CRC Press/Taylor & Francis Group
2	European Bioinformatics Institute
3	BioExcel
4	Oxford University Press
5	Genomics, Proteomics & Bioinformatics
6	Springer-Verlag London Ltd
7	The Royal Society
8	BD2K
9	Overleaf
10	sbv IMPROVER
11	DNAStack
12	European Research Council
14	Cambridge University Press
15	GOBLET
16	PLOS: Public Library of Science
17	NDEx
18	Jalview
19	University of California, San Diego
20	the hyve
21	Elsevier
22	ENPICOM
23	F1000Research
24	ELIXIR
25	ELIXIR
26	International Society for Computational Biology
27	ISCB-Student Council
28	European Comference on Computation Biology (ECCB)

Recruiter Tables

R1	St. Jude Children’s Research Hospital
R2	The Jackson Laboratory

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Technology Track Presentations

SATURDAY, JULY 22 TO TUESDAY, JULY 25

ROOM: TERRACE 1

SATURDAY, JULY 22

CHAIR: HENNING HERMJAKOB, EMBL-EBI

2:00–2:55 PM **Stephanie Boue**, sbv IMPROVER - Philip Morris International
TT01: Systems biology verification project: crowdsourcing computational method benchmarking, results verification, and in depth peer review – Past, present, and future.

3:00–3:55 PM **Marc Fiume,** Global Alliance for Genomics & Health
TT02: Dockstore: reproducible bioinformatics workflows in the cloud

CHAIR: DOMINIC CLARK, EMBL-EBI

4:30–4:50 PM **James Taylor,** Johns Hopkins University
TT03: Supporting highly scalable scientific data analysis with Galaxy

4:50–5:10 PM **Michael Sternberg,** Imperial College London
TT04: Phyre2: Protein modeling and analysis made easy

5:15–5:35 PM **Peter Karp,** SRI International
TT05: Recent Developments in the Pathway Tools Software and BioCyc Databases

5:35–5:55 PM **Simon Fishilevich,** Weizmann Institute of Science
TT06: GeneHancer-enriched VarElect: non-coding variant interpretation tool for genome sequencing

SUNDAY, JULY 23

CHAIR: DOMINIC CLARK, EMBL-EBI

10:00–10:20 AM **Ted Liefeld,** The University of California San Diego
TT07: GenomeSpace: Open source interoperability platform with crowd-sourced analysis recipes

10:20–10:40 AM **Michael Reich,** UCSD
TT08: The GenePattern Notebook Environment

10:40–11:00 AM **Niema Moshiri,** University of California, San Diego
TT09: Using Online Classes to Flip Bioinformatics Classrooms

11:10–11:30 AM **Konrad Krawczyk,** Oxford University
TT10: Computational Antibody Design Software and Database

11:30–11:50 AM **Andrew Nightingale,** EMBL-EBI
TT11: Combine Your Data with Functional Annotations from UniProt Using Protein Services

11:50–12:10 PM **Christine Orengo,** University College London
TT12: Using CATH-Gene3D to predict the structure and function of novel protein sequences and examine the impacts of genetic variations

CHAIR: KEES VAN BOCHOVE, THE HYVE

2:00–2:55 PM **Kees van Bochove,** The Hyve
TT13: Reference open source infrastructure for FAIR Research Data Management in academic hospitals

3:00–3:55 PM **Yuxia Jiao,** Genomics, Proteomics & Bioinformatics
TT14: Genomics, Proteomics & Bioinformatics (GPB) –- a rising journal in the field

CHAIR: DOMINIC CLARK, EMBL-EBI

4:30–5:25 PM **Allen Clark,** Google Inc.
TT28: Deep learning in medicine: An introduction and applications to next-generation sequencing and disease diagnostics

MONDAY, JULY 24

CHAIR: ROB FINN, EMBL-EBI

10:00–10:55 AM **Chris Cheadle,** Elsevier Inc
TT15: Pathway Studio Use Case: A disease-centric analysis of Pre-Eclampsia

11:00–11:55 AM **John Lees-Miller,** Overleaf
TT16: Lay out your manuscripts, theses and reports like a pro with LaTeX for Biologists

12:00–12:20 PM **Geoffrey Barton,** University of Dundee
TT17: Jalview and the Dundee Resource for Sequence Analysis and Structure Prediction

CHAIR: DOMINIC CLARK, EMBL-EBI

2:00–2:20 PM **Luca Cherubin,** European Bioinformatics Institute
TT18: BioSamples – a solution for sample meta data storage and query

2:20–2:40 PM **Damian Roqueiro,** ETH Zurich
TT19: easyGWAS: A cloud-based platform for comparing the results of genome-wide association studies

2:40–3:00 PM **Alfonso Munoz-Pomer Fuentes,** European Bioinformatics Institute
TT20: Expression Atlas: A platform for integrating and displaying expression data

3:00–3:20 PM **Kevin Brennan,** Stanford University
TT21: Pancancer analysis using MethylMix 2.0.

TUESDAY, JULY 25

CHAIR: EDGARDO FERRAN, EMBL-EBI

10:00–10:20 AM **Marco Roos,** Leiden University Medical Center
TT23: Overview of a suite of tools and training material for implementing FAIR data principles

10:20–10:40 AM **Anton Nekrutenko,** The Pennsylvania State University
TT24: Galaxy Interactive Environments: Combining the computational power of Galaxy with the analytical flexibility of Jupyter

10:40–11:00 AM **Subho Banereje,** University of Illinois at Urbana Champaign
TT25: Bringing Innovations in Systems and Analytics to the Bedside: Design of the CompGen Machine

11:10–11:30 AM **Sean O'Donoghue,** Garvan Institute Of Medical Research
TT26: Aquaria - Simplifying discovery and insight from protein structures

11:30–11:50 AM **David Sehnal,** Central European Institute of Technology
TT27: The LiteMol suite – interactive web-based visualization of large-scale macromolecular structure data

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE
Details available on the conference app – see page 27 for details.

Special Sessions

SATURDAY, JULY 22 TO TUESDAY, JULY 25

SATURDAY, JULY 22

2:00 – 6:00 PM • ROOM: MEETING HALL V

SST01: Competency-based approaches to education and training in computational biology: bring your own educational challenge

Organizer(s): Michelle Brazas, Ontario Institute for Cancer Research; Catherine Brooksbank, EMBL-EBI; Bruno Gaeta, University of New South Wales; Nicola Mulder; H3ABioNet; Russell Schwartz, Carnegie Mellon University; Lonnie Welch, Ohio University

2:00 PM	**Cath Brooksbank,** EMBL-EBI & **Lonnie Welch,** Ohio University *Status of the ISCB competency profile*
2:15 PM	**Russell Schwartz,** Carnegie Mellon University *Keynote: Rethinking computational biology skills for molecular biology students*
2:30 PM	**Bruno Gaeta,** University of New South Wales *Keynote: Developing the new generation of bioinformatics engineers*
2:45 PM	**Nicola Mulder,** H3ABioNet *Applying competency-based approaches to a pan-African bioinformatics education initiative*
3:00 PM	**Bruno Gaeta,** University of New South Wales *Course and curriculum development breakout groups*
5:30 PM	**Michelle Brazas,** Ontario Institute for Cancer Research *How to apply and improve curriculum and competency guidelines feedback*

SUNDAY, JULY 23

10:00 AM – 4:00 PM • ROOM: MEETING HALL V

SST02: Critical Assessment of Metagenome Interpretation (CAMI)

Organizer(s): Thomas Rattei, University of Vienna; Alexander Sczyrba, University of Bielefeld, CeBiTec; Alice McHardy, Helmholtz-Center Braunschweig

10:00 AM	**Shinichi Sunagawa,** ETH Zurich *Keynote: Metagenomics – from basics to applications in the human gut and ocean microbiome*
10:30 AM	**Alice McHardy,** HZI Braunschweig *Overview on CAMI, the initiative for Critical Assessment of Metagenome Interpretation*
11:15 AM	**Nils Willassen,** UiT Tromso *The ELIXIR Marine Metagenomics Use Case*
11:40 AM	**Rob Finn,** *EBI Hinxton* *EBI metagenomics*
12:05 PM	**Christian Sieber,** JGI *Advanced strategies for genome resolved metagenomics*
2:00 PM	**Alex Sczyrba and colleagues** *Practical demonstration of docker and bioboxes*
3:00 PM	*Discussion on CAMI2*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Special Sessions

SATURDAY, JULY 22 TO TUESDAY, JULY 25

MONDAY, JULY 24

2:00 – 4:00 PM • ROOM: MEETING HALL IB

SST03: Computational Immune Oncology

Organizer(s): Jadwiga Bienkowska, Pfizer Oncology Research and Drug Development

Jadwiga Bienkowska, Pfizer Oncology Research and Drug Development
Part A: Computational Challenges in Development of Cancer Immune Therapies

Wenyan Zhong, Pfizer Oncology Research and Drug Development
Part B: Integrative analysis of molecular and cellular properties of murine syngeneic models to aid model selection and biomarker discovery for immune-oncology programs

Bjoern Peters, La Jolla Institute for Immunology
Part C: Optimizing the identification of immunogenic neoepitopes

Aaron M. Newman, Stanford University
Part D: Genomic Dissection of Tumor Composition with CIBERSORT

TUESDAY, JULY 25

8:30 AM – 4:30 PM • ROOM: NORTH HALL

SST04: International Workshop on Machine Learning in Systems Biology (MLSB)

Organizer(s): Chloe-Agathe Azencott, MINES ParisTech; Magnus Rattray, University of Manchester

8:40 AM	**Fabian Theis,** Helmholtz Center Munich *Lineage estimation from single-cell RNAseq time-series*
10:00 AM	**Yuanhua Huang,** University of Edinburgh *Transcriptome-wide splicing quantification in single cells*
10:25 AM	**Alexis Boukouvalas,** University of Manchester *Gaussian processes for identifying branching dynamics in single cell data*
10:50 AM	**Anna Goldenberg,** The Hospital for Sick Children, Toronto *Data Integration in Computational Biology and Medicine: Current Progress and Future Directions*
11:40 AM	**Ladislav Rampášek,** University of Toronto *Modeling Post-treatment Gene Expression Change with a Deep Generative Model*
2:15 PM	**Anthony Coutant,** Laboratoire d'Informatique de Paris Nord (LIPN - UMR 7030) *Generative Learning of Dynamic Structures using Spanning Arborescence Sets*
2:40 PM	**Julio Saez-Rodriguez,** RWTH Aachen University *Understanding and predicting drug efficacy in cancer: from machine learning to biochemical models*
3:30 PM	**Xiao He,** ETH Zurich *Kernelized Rank Learning for Personalized Drug Recommendation*
3:55 PM	**Iiris Sundin,** Aalto University *Ask the doctor — Improving drug sensitivity predictions through active expert knowledge elicitation*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE
Details available on the conference app – see page 27 for details.

Birds of a Feather

SATURDAY, JULY 22 & MONDAY, JULY 24

12:45 PM – 1:45 PM

SATURDAY, JULY 22

BoF A1: The Computational Biology Education (CoBE) COSI BOF

ROOM: MEETING HALL IA

Organizers: **Fran Lewitter**, Whitehead Institute, **Teresa Attwood**, University of Manchester; **Lonnie Welch**, Ohio University

BoF A2: JPI Career Development: "On Leadership and Management"

ROOM: MEETING HALL IB

Organizer: **Lucia Peixoto**, Washington State University

Panelists: **Larry Hunter**, University of Colorado; **Janet Kelso**, Max Planck Institute for Evolutionary Anthropology; **Nils Gehlenborg**, Harvard Medical School

BoF A3: ERC funding schemes

ROOM: NORTH HALL

Organizer: **Konstantina Topouridou**, European Research Council Executive Agency

BoF A4: Promoting gender diversity in Bioinformatics

ROOM: TERRACE 1

Organizer: **Malvika Sharan**, European Molecular Biology Laboratory

BoF A5: Diagnostic relevance of transcriptome sequencing for rare Mendelian diseases

ROOM: PANORAMA

Organizer: **Numrah Fadra**, University of Minnesota, Mayo Clinic

BoF A6: Future of phosphoproteomics

ROOM: MEETING HALL V

Organizer: **Jenny Vuong, Sandeep Kaur,** CSIRO, Garvan, UNSW

MONDAY, JULY 24

BoF B1: JPI Career Development: "Becoming a Leader in the Open Data Movement"

ROOM: MEETING HALL IB

Organizer: **Lucia Peixoto**, Washington State University

Panelists: **Philip E. Bourne**, University of Virginia; **Casey Greene**, University of Pennsylvania; **Michael Markie**, F100 Research

BoF B2: How to build your scientific network as an early career researcher

ROOM: MEETING HALL IV

Organizer: **Farzana Rahman**, ISCB Student Council; **Dan DeBlasio**, ISCB Student Council; **Diane E Kovats**, ISCB

BoF B3: Cytoscape Community Meeting: Latest updates and Roadmap

ROOM: TERRACE 1

Organizer: **Barry Demchak**, University of California at San Diego

BoF B4: What can the Galaxy Project do for you?

ROOM: MEETING HALL V

Organizer: **Martin Cech**, Penn State University

BoF B5: Equity, Diversity, and Inclusion in ISCB and in Bioinformatics ?

ROOM: MEETING HALL IA

Organizer: **Kieran O'Neill**, Aurora Blucher, **Monica Munoz-Torres**, Malvika Sharan

BoF B6: Future of Hi-C Data?

ROOM: PANORAMA

Organizer: **Benedetta Frida Baldi, Sean O'Donoghue,** The Garvan Institute of Medical Research UNSW, CSIRO

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Workshops

SATURDAY, JULY 22 & MONDAY, JULY 24

10:00 AM – 12:30 PM

SATURDAY, JULY 22

ROOM: MEETING HALL V

WK01: Workshop on Education in Bioinformatics (WEB): Open Science platforms for bioinformatics education

Organizer(s): Mainá Bitar, QIMR Berghofer; Michelle Brazas, OICR; Fran Lewitter, Whitehead Institute; Patricia Palagi, SIB Swiss Institute of Bioinformatics

10:05 AM	**Francis Ouellette,** Génome Québec *Part A: The Benefits of Open Access Data, Tools, Platforms and Publications in Bioinformatics Education*
10:30 AM	**Lonnie Welch,** Ohio University *Part B: Wikipedia as a bioinformatics teaching tool*
11:00 AM	**Ann Meyer,** Ontario Institute for Cancer Research *Part C: GitHub: Not just a code repository*
11:30 AM	**Niall Beard,** University of Manchester, ELIXIR-UK *Part D: TeSS: A bioinformatics education workflow platform*
12:00 PM	*Part E: Open Discussion: Use cases for repurposing open source tools for bioinformatics training*

MONDAY, JULY 24

ROOM: MEETING HALL IB

WK02: Bioinformatics Core Workshop: Standing on Two Legs: Managing Operations in a Core and Ensuring Scientific Reproducibility

Organizer(s): Madelaine Gogol, Stowers Institute; Hans-Rudolf Hotz, Friedrich Miescher Institute for Biomedical Research; Hemant Kelkar, University of North Carolina; Alastair Kerr, University of Edinburgh; Brent Richter, Partners HealthCare of Massachusetts General and Brigham and Women's Hospitals; Alberto Riva, University of Florida

Brent Richter, Partners HealthCare of Massachusetts General and Brigham and Women's Hospitals
Introduction

Russell Hamilton, University of Cambridge
Part A: Setting up a new bioinformatics core facility: a first year review

Annette McGrath, CSIRO The University of Queensland
Part B: Managing people in a core facility

Phil Ewels, SciLifeLab
Part D: Developing Reliable QC at the Swedish National Genomics Infrastructure

Lennart Opitz, University of Zurich
Part E: Reproducible and fully documented data analyses at the Functional Genomics Center Zurich

Plan Your Perfect Conference Experience

Download the ISCB Multi-Conferences Mobile APP Today!

Updated information

Create your own schedule

Catch up with your friends

BOSC COSI TRACK SCHEDULE (BIOINFORMATICS OPEN SOURCE CONFERENCE)

SATURDAY, JULY 22 & SUNDAY, JULY 23 • ROOM: MEETING HALL IV

https://www.open-bio.org/wiki/BOSC_2017

SATURDAY, JULY 22

10:00 AM **Nomi Harris,** Berkeley
Introduction and welcome

10:10 AM **Hilmar Lapp,** Duke
The Open Bioinformatics Foundation

10:20 AM **Kai Blin,** Technical University of Denmark
OBF in the Google Summer of Code. Wrapping up 2016 and presenting the 2017 projects

10:30 AM **Brad Chapman,** Harvard
Codefest 2017 summary

10:45 AM **Janko Simonovic,** Seven Bridges
Rabix Executor: an open-source executor supporting recomputability and interoperability of workflow descriptions

10:56 AM **Ivan Batic,** Seven Bridges
Rabix Composer: an open-source integrated development environment for the Common Workflow Language

11:05 AM **Maja Nedeljkovic,** Seven Bridges
CWL-svg: an open-source workflow visualization library for the Common Workflow Language

11:07 AM **Maja Nedeljkovic,** Seven Bridges
CWL-ts: an open-source TypeScript library for building developer tools for the Common Workflow Language

11:15 AM **Denis Yuen,** OICR
The GA4GH Tool Registry Service (TRS) and Dockstore — Year One

11:22 AM **Brian O'Connor,** University of California, Santa Cruz
The GA4GH Task Execution System (TES) and Funnel Server

11:28 AM **Peter Amstutz,** Curoverse
The GA4GH Workflow Execution Schema (WES)

11:34 AM **Brian O'Connor,** UCSC
The GA4GH/DREAM Infrastructure Challenges

11:45 AM **Kevin Sayers,** Center for Genomic Regulation (CRG)
Workflows interoperability with Nextflow and Common WL

11:50 AM **Stian Soiland-Reyes,** The University of Manchester
CWL Viewer: The Common Workflow Language Viewer

11:55 AM **Kieran O'Neill,** BC Cancer Agency
Screw: tools for building reproducible single-cell epigenomics workflows

12:03 PM **Jiwen Xin,** The Scripps Research Institute
BioThings Explorer: Utilizing JSON-LD for Linking Biological APIs to Facilitate Knowledge Discovery

12:08 PM **Anil Thanki,** Earlham Institute
Discovery and visualisation of homologous genes and gene families using Galaxy

12:13 PM **Alessia Visconti,** King's College London
YAMP : Yet Another Metagenomic Pipeline

2:00 PM **Philip Ewels,** Science for Life Laboratory
MultiQC: Visualising results from common bioinformatics tools

2:18 PM **Alexander Rose,** RCSB Protein Data Bank, San Diego Supercomputer Center, UC San Diego Rutgers
NGL - a molecular graphics library for the web

2:23 PM **Aditya Bharadwaj,** Virginia Tech
GRAPHSPACE: Stimulating interdisciplinary collaborations in network biology

2:28 PM **Timothy Booth,** Edinburgh Genomics
Efficient detection of well-hopping duplicate reads on Illumina patterned flowcells

2:36 PM **Monther Alhamdoosh,** CSL Limited
An ensemble approach for gene set testing analysis with reporting capabilities

2:41 PM **Timo Sachsenberg,** University of Tuebingen
OpenMS 2.0: a flexible open-source software platform for mass spectrometry data analysis

2:46 PM **Brad Chapman,** Harvard Chan School, Bioinformatics Core
Interoperable, collaborative multi-platform variant calling with bcbio

2:51 PM **Kees Bochove,** The Hyve
Gene Set Variation Analysis in cBioPortal

3:00 PM **Bjoern Gruening,** Uni-Freiburg
The backbone of research reproducibility: sustainable and flexible tool deployment

3:18 PM **Pjotr Prins,** University Medical Center Utrecht
Reproducible bioinformatics software with GNU Guix

3:23 PM **Ricardo Wurmus,** Max Delbrueck Center for Molecular Medicine
Reproducible and user-controlled software management in HPC with GNU Guix

3:28 PM **John Chilton,** Galaxy Project
A Ubiquitous Approach to Reproducible Bioinformatics across Computational Platforms

3:36 PM **Keiichiro Ono,** University of California, San Diego Trey Ideker Lab
Revitalizing a classic bioinformatics tool using modern technologies: the case of the Cytoscape Project

3:41 PM **Olga Vrousgou,** EMBL-EBI
The SPOT ontology toolkit : semantics as a service

3:46 PM **Sourav Singh,** Vishwakarma Institute of Information Technology
Biopython Project Update 2017

4:30 PM **Dawn Field,** Goeteborg University
Keynote: Understanding the Biocode: Global Sharing of Data

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

BOSC COSI TRACK SCHEDULE (BIOINFORMATICS OPEN SOURCE CONFERENCE)

SATURDAY, JULY 22 & SUNDAY, JULY 23 • ROOM: MEETING HALL IV

https://www.open-bio.org/wiki/BOSC_2017

SUNDAY, JULY 23

10:05 AM **Jonathan Sobel,** Hackuarium, UNIL
BeerDeCoded: exploring the beer metagenome

10:23 AM **Monica Munoz-Torres,** Lawrence Berkeley National Laboratory
Supporting curation communities & collecting technical dividends

10:41 AM **Pjotr Prins,** UMC Utrecht
Journal of Open Source Software (JOSS)

10:59 AM **Berenice Batut,** University of Freiburg
Building an open, collaborative, online infrastructure for bioinformatics training

11:17 AM **Dexter Pratt,** UCSD
Software and social strategies for community sourced biological networks and ontologies

11:22 AM **Nicola Mulder,** University of Cape Town
Distance-based, online bioinformatics training in Africa: the H3ABioNet experience

11:30 AM **Martin Cech,** Galaxy Team, Penn State
Recent object formation in the core of Galaxy

11:35 AM **Brett Beaulieu-Jones,** University of Pennsylvania
Reproducibility of computational workflows is automated using continuous analysis

11:40 AM **Kate Voss,** Broad Institute
Full-stack genomics pipelining with GATK4 + WDL + Cromwell

11:45 AM **Kenzo-Hugo Hillion,** Bioinformatics and Biostatistics HUB, C3BI, Institut Pasteur
ToolDog — generating tool descriptors from the ELIXIR tool registry

11:50 AM **Chunlei Wu,** The Scripps Research Institute
BioThings SDK: a toolkit for building high-performance data APIs in biology

12:00 PM **Ted Liefeld,** University of California San Diego
Integrating cloud storage providers for genomic analyses

12:05 PM **Madeleine Ball,** Open Humans Foundation
Open Humans: Opening human health data

12:10 PM **Kai Blin,** Technical University of Denmark
Fighting Superbugs with Open Source Software

12:15 PM **Seth Carbon,** Lawrence Berkeley National Laboratory
Users, Communication, and a Light Application-Level API: A Request for Comments

2:00 PM **Nivethika Mahasivam,** The Hyve
RADAR-CNS — Research Infrastructure for processing wearable data to improve health

2:18 PM **Andrew Su,** The Scripps Research Institute
Using Wikidata as an open, community-maintained database of biomedical knowledge

2:36 PM **Stephen Lincoln,** Invitae
Emerging public databases of clinical genetic test results: Implications for large scale deployment of precision medicine

2:41 PM **Philippe Rocca-Serra,** Oxford
Discovering datasets with DATS in DataMed

2:46 PM **Carole Goble,** The University of Manchester / ELIXIR-UK
Bioschemas for life science data

2:51 PM **Annemarie Eckes,** Earlham Institute, Norwich Research Park, Norwich
Introducing the Brassica Information Portal: Towards integrating genotypic and phenotypic Brassica crop data

3:00 PM **Andrew Su,** The Scripps Research Institute; **Carole Goble,** The University of Manchester; **Madeleine Ball,** Open Humans Foundation; **Monica Munoz-Torres,** Lawrence Berkeley National Laboratory; **Nick Loman,** University of Birmingham
Panel: Open Data — Standards, Opportunities and Challenges

4:30 PM **Nick Loman,** University of Birmingham
Keynote: Open data meets ubiquitous sequencing: challenges and opportunities

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE
Details available on the conference app – see page 27 for details.

CAMDA COSI TRACK SCHEDULE

SATURDAY, JULY 22 & SUNDAY, JULY 23 • ROOM: NORTH HALL

www.camda.info

SATURDAY, JULY 22

10:00 AM	**Joaquin Dopazo,** University Hospital Virgen del Rocío *Welcome and opening remarks*
10:05 AM	**Lodewyk Wessels,** Netherlands Cancer Institute *Molecular networks as determinants of response and outcome*
11:00 AM	**David P. Kreil,** Boku University Vienna *The CAMDA Challenges*
11:10 AM	**Léon-Charles Tranchevent,** Luxembourg Institute of Health *Predicting clinical outcome of neuroblastoma patients using an integrative network-based approach*
11:30 AM	**Hilal Kazan,** Antalya International University *Predicting clinical outcomes in neuroblastoma with genomic data integration*
11:50 AM	**Chen Suo,** Fudan University *Accumulation of Potential Driver Genes with Genomic Alterations Predicts Survival in High-Risk Neuroblastoma*
2:00 PM	**Margherita Francescatto,** Fondazione Bruno Kessler *Multi-omics integration for neuroblastoma clinical endpoint prediction*
2:30 PM	**Yatong Han,** Harbin Engineering University *Integration of Molecular Features with Clinical Information for Predicting Outcome for Neuroblastoma Patients*
2:50 PM	**Kun Huang,** The Ohio State University *Integration analysis based on survial associated co-expression gene modules for predicing neuroblastom patients survival times*
3:10 PM	**Maciej Kandula,** Boku University Vienna *A multi-layer network approach to data integration for patient stratification*
3:30 PM	**Marta Hidalgo,** Hospital Virgen del Rocio *Models of cell signalling uncover molecular mechanisms of high-risk neuroblastoma and predict outcome*
4:30 PM	**Tyler Grime,** University of Florida *Predicting survival times for neuroblastoma patients using RNA-Seq expression profiles*
4:50 PM	**Tieliu Shi,** East China Normal University *Integration of CNV and RNA-seq data can increase the predictive power of Neuroblastoma endpoint*
4:59 PM	**Vladimir Uzun,** University of Sheffield *Computational Approaches to Assessing Clinical Relevance of Pre-clinical Cancer Models*
5:08 PM	**Michał Okoniewski,** ETH Zurich *Analysis of CAMDA RNA-seq data with the knowlegde of protein domains in genes*
5:17 PM	**Chandrima Bhattacharya,** Indian Institute of Engineering Science and Technology, Shibpur *Microbiome Diversity on Materials*
5:26 PM	**Haruo Suzuki,** Keio University *Codon usage diversity in city microbiomes*
5:35 PM	**Susmita Datta,** University of Florida *Unraveling bacterial fingerprints of city subways from microbiome 16S gene profiles*
5:44 PM	**Alina Frolova,** The Institute of Molecular Biology and Genetics of NASU *Assessing reproducibility of metagenomics studies and diversity of public transport systems microbiome profiles of New York, Boston and Sacramento cities*
5:53 PM	**Josef Moser,** Austrian Centre of Industrial Biotechnology (ACIB) *Identification of mobile elements in metagenomic data.*

SUNDAY, JULY 23

10:00 AM	**Pawel Labaj,** Boku University Vienna *Welcome and opening remarks*
10:10 AM	**Moreno Zolfo,** CIBIO, University of Trento *Strain-level bacterial and viral diversity in the MetaSUB dataset*
10:40 AM	**Serghei Mangul,** UCLA *Viral and eukaryotic communities of urban ecosystems across US metropolitan areas*
11:10 AM	**Samuel Gerner,** FH Campus Wien *Assessment of urban microbiome assemblies with the help of targeted mock communities*
11:30 AM	**Yuyang Qiao,** Shanghai Jiao Tong University *MetaBinG2: a fast and accurate metagenomics sequence classification method for samples with many unknown organisms*
12:00 PM	**Caner Bagci,** University of Tuebingen *LAST + MEGAN-LR Approach to the Oxford Nanopore Wiggle Space Challenge*
2:00 PM	**Cesare Furlanello,** FBK *Towards a scientific blockchain framework for reproducible data analysis*
2:55 PM	**Djork-Arné Clevert,** Bayer AG *Rectified Factor Networks for Biclustering of Omics Data*
3:25 PM	**Dat Duong,** UCLA *Applying meta-analysis to Genotype-Tissue Expression data from multiple tissues to identify eQTLs and increase the number of eGenes*
3:55 PM	**Joaquin Dopazo,** University Hospital Virgen del Rocío *Best presentation award voting*
4:30 PM	**Wenzhong Xiao,** Harvard Medical School; Stanford Genome Technology Center *Future challenges in Big Data: Precision Medicine, Human Exposome, …*
5:00 PM	**Pawel Labaj,** Boku University Vienna *Panel discussion: key insights & future challenges*
5:40 PM	**David P. Kreil,** Boku University Vienna *Award announcements and closing remarks*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

3DSIG COSI TRACK SCHEDULE

SATURDAY, JULY 22 & SUNDAY, JULY 23 • ROOM: FORUM HALL

https://www.fourwav.es/3dsig17

SATURDAY, JULY 22

10:00 AM	**Rafael Najmanovich,** University of Montreal *Opening remarks*
10:20 AM	**Abdullah Kahraman,** University of Zurich; Sabanci University *Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability*
10:40 AM	**Mary Jo Ondrechen,** Northeastern University *How nature builds electrostatic interactions in natural enzymes: What can we learn for enzyme design?*
11:00 AM	**Kam Zhang,** RIKEN *Computational design of a symmetrical beta-trefoil lectin with cancer cell binding activity*
11:20 AM	**Mark Hallen,** Toyota Technological Institute at Chicago *CATS (Coordinates of Atoms by Taylor Series): Protein design with backbone flexibility in all locally feasible directions*
11:40 AM	**Ilan Samish,** Amai Proteins *Computational Protein Design: Judge the protein by the cover, story and taste (Keynote)*
2:00 PM	**Mirco Michel,** Stockholm University *Large-scale structure prediction by improved contact predictions and model quality assessment*
2:20 PM	**Wim Vranken,** ULB/VUB *Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins*
2:40 PM	**Roland Dunbrack,** Fox Chase Cancer Center; Temple University *Density-based clustering in structural bioinformatics: application to beta turns and antibody CDRs*
3:00 PM	**Andrei Lupas,** Max Planck Institute for Developmental Biology *Proteins from Peptides*
3:20 PM	**Charlotte Deane,** University of Oxford *Improving fragment assembly protein structure prediction*
3:40 PM	**Chen Keasar,** Ben-Gurion University *MESHI-score a method for estimation of protein model accuracy*
4:30 PM	**Daisuke Kihara,** Purdue University *Protein bioinformatics of low resolution structural data (Keynote)*
5:20 PM	**Edoardo Sarti,** National Institutes of Health *EncoMPASS: An Encyclopedia of Membrane Proteins Analyzed by Structure and Symmetry*
5:40 PM	**Jinbo Xu,** Toyota Technological Institute *Folding membrane proteins by deep transfer learning*

SUNDAY, JULY 23

10:00 AM	**Min Xu,** Carnegie Mellon University *Deep learning based subdivision approach for large scale macromolecules structure recovery from electron cryo tomograms*
10:20 AM	**Juan Rodriguez-Rivas,** Spanish National Cancer Research Centre *Conservation of coevolving protein interfaces bridges prokaryote–eukaryote homologies in the twilight zone*
10:40 AM	**Jose Duarte,** University of California, San Diego *Automated evaluation of quaternary structures from protein crystal structures*
11:00 AM	**Varsha Badal,** The University of Kansas *Deep Learning in text mining for protein docking using full-text articles*
11:20 AM	**Michael Estrin,** Tel Aviv University *SnapDock — Template Based Docking by Geometric Hashing*
11:40 AM	**Michael Schroeder,** TU Dresden *Improving cancer chemotherapy with structure-based drug repositioning (Keynote)*
2:00 PM	**Anna Vangone,** Utrecht University *PRODIGY: a structure-based method for the prediction of binding affinity in biomolecular complexes*
2:20 PM	**Ravinder Abrol,** California State University Northridge *Identifying Multiple Active Conformations of G Protein-Coupled Receptors Using Focused Conformational Sampling*
2:40 PM	**Louis-Philippe Morency,** University of Montreal *The Impact of Conformational Entropy on the Accuracy of the Molecular Docking Software FlexAID in Binding Mode Prediction*
3:00 PM	**Gaurav Chopra,** Purdue University *Interactome based drug design based on disease-disease relationships*
3:20 PM	**Phillip Bourne,** University of Virginia *Will data sciences approaches impact our science? (Discussion)*
4:30 PM	**Dariusz Plewczynski,** University of Warsaw *Three-dimensional organisation of human genome*
4:50 PM	**Amarda Shehu,** National Cancer Institute *From Mutations to Mechanisms and Dysfunction via Computation and Mining of Protein Energy Landscapes*
5:10 PM	**Stuart MacGowan,** University of Dundee *What can human variation tell us about proteins?*
5:30 PM	**Rafael Najmanovich,** University of Montreal *Closing remarks*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

RegGen COSI TRACK SCHEDULE

SATURDAY, JULY 22 & SUNDAY, JULY 23 • ROOM: MEETING HALL IA

http://tare.medisin.ntnu.no/reggen/2017/

SATURDAY, JULY 22

10:00 AM	**Alexander Stark** *Decoding transcriptional regulation in Drosophila*
10:50 AM	**Jan Grau,** Martin Luther University Halle-Wittenberg *Accurate prediction of in-vivo transcription factor binding across cell types*
11:10 AM	**Lin Zhu,** Tongji University *Direct AUC Optimization of Regulatory Motifs*
11:30 AM	**Leelavati Narlikar,** Duke University *On the importance of modeling diversity in regulation when working with cross-linking-based high-throughput experiments*
11:50 AM	**Shaun Mahony,** Pennsylvania State University *Deconvolving sequence features associated with transcription factor binding dynamics during direct motor neuron programming*
12:10 PM	**Maureen Sartor,** University of Michigan *Advancing the functional interpretation of high-throughput gene regulatory data*
2:00 PM	**Boris Lenhard,** *TADs are ancient features that coincide with Metazoan clusters of extreme noncoding conservation*
2:40 PM	**Pang Wei Koh,** Stanford University *Denoising Genome-wide Histone ChIP-seq with Convolutional Neural Networks*
3:00 PM	**Yang Yang,** Carnegie Mellon University *Exploiting sequence-based features for predicting enhancer-promoter interactions*
3:20 PM	**Shrutii Sarda,** University of Maryland *Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal-promoters*
3:40 PM	**Lisa Barros de Andrade E Sousa,** Max Planck Institute for Molecular Genetics *Predicting gene silencing dynamics during X chromosome inactivation with Random Forests*
4:30 PM	**Sai Zhang,** Tsinghua University *TITER: predicting translation initiation sites by deep learning*
4:50 PM	**Albert Pla,** University of Oslo *A Deep Learning Approach to Predict miRNA Targets by Analyzing Whole miRNA & isomiR Transcripts*
5:10 PM	**Michael R. Brent,** WUSTL *Model-based transcriptome engineering promotes a fermentative transcriptional state in yeast*
5:30 PM	**Poster Presenters** *One minute flash talks by poster presenters*

SUNDAY, JULY 23

10:00 AM	**Cole Trapnell** *Powering quantitative models of gene regulation in development with single-cell genomics*
10:50 AM	**R. Gonzalo Parra,** Max Planck Institute for Biophysical Chemistry *scTree: reconstructing complex cellular lineage trees from single-cell RNA-seq data*
11:10 AM	**Zahra Karimaddini,** ETH Zürich *Unraveling Cortical Development Using Population and Single-cell RNA-Seq Data*
11:30 AM	**Sara Aibar,** VIB-KU Leuven Center for Brain and Disease Research *Gene regulatory network analysis in single cells*
11:50 AM	**Fatemeh Behjati Ardakani,** Max Planck Institute for Informatics *Integrative analysis of single-cell expression data reveals distinct regulatory states in bidirectional promoters*
12:10 PM	**Kieran O'Neill,** BC Cancer Agency *Determining the Mechanism of 5-Azacytidine Resistance in Myeloid Malignancies Using Single-cell DNA Methylation Sequencing Paired With Flow Cytometry*
2:00 PM	**Lila Rieber,** Pennsylvania State University *miniMDS: 3D structural inference from high- resolution Hi-C data*
2:20 PM	**Christopher Cameron,** McGill University *Reducing Noise in Hi-C Interaction Matrices at Restriction Fragment Resolution*
2:40 PM	**Ruslan Sadreyev,** Massachusetts General Hospital/Harvard Medical School *High-resolution analysis of short-range chromatin interactions reveals small topologically associating domains*
3:00 PM	**Monica Nicolau,** University of California, Davis *Comparative Chromosomal Folding Analysis*
3:20 PM	**Christoph J. Thieme,** Max-Delbrück Centre for Molecular Medicine *Genome Architecture Mapping: an orthogonal approach to 3C technologies*
3:40 PM	**Carmen Bravo González-Blas,** VIB-KU Leuven *Regulatory topic modelling on single-cell ATAC-seq data*
4:30 PM	**Judith Zaugg** *Genetic and epigenetic variation in regulatory elements across individuals*
5:10 PM	**Greg Carter,** The Jackson Laboratory *Genetic Variation Mediates the Epigenetic Response to Corticosteroids in Mice*
5:30 PM	**Lukas Chavez,** German Cancer Research Center *Therapeutic Targeting of Tumors as Informed by Oncogenic Enhancer Profiling*
5:50 PM	**Poster Presenters** *One minute flash talks by poster presenters*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

RNA COSI TRACK SCHEDULE

SATURDAY, JULY 22 • ROOM: MEETING HALL IB

http://irbgroup.org/rna-sig-17/

9:55 AM	**Introductions**
10:00 AM	**Fran Supek,** Centre for Genomic Regulation *The rules and impact of nonsense-mediated mRNA decay in human cancers*
10:15 AM	**Guan Ning Lin,** Shanghai Jiao Tong University *Splicing isoform expression provides insights into neurodevelopmental disorders*
10:30 AM	**Pavel Sumazin,** Baylor College of Medicine *lncRNA dysregulation alters the activity of driver genes in cancer*
10:45 AM	**Eduardo Eyras,** Pompeu Fabra University *Alternative splicing remodels the proetin interaction network of cancer gene drivers*
11:00 AM	**Hosna Jabbari,** University of Alberta *Computational framework to design effective oligonucleotides for exon skipping of Duchenne Muscular Dystrophy*
11:15 AM	**Ernesto Picardi,** University of Bari & IBIOM-CNR *Single cell transcriptomics reveals specific RNA editing signatures in the human brain*
11:30 AM	**Martin Mikl,** Weizmann Institute of Science *Dissecting the complexity and cell-to-cell variability of alternative splicing regulation*
11:45 AM	**Bart Cuypers,** Univeristy Of Antwerp *Advancing parasite transcriptomics with spliced-leader sequencing experimental and computational workflows*
11:52 AM	**Alina Selega,** University of Edinburgh *Transcriptome-wide modelling of RNA life cycle*
12:00 PM	**Sabrina Krakau,** Max Planck Institute for Molecular Genetics *Capturing target-specific protein-RNA interaction footprints from iCLIP-seq data*
12:15 PM	**Alina Munteanu,** Max Delbruck Center *SSMART: Sequence-structure motif identification for RNA-binding proteins*
2:00 PM	**Yiliang Ding,** John Innes Centre *From the genome-wide in vivo RNA structure probing data to the RNA secondary structure prediction*
2:35 PM	**Michelle Wu,** Stanford University School of Medicine *Recurrent neural network models to quantitatively predict RNA-RNA interactions*
2:50 PM	**Juraj Michalik,** Inria Saclay *Efficient approximations of RNA kinetics landscape using non-redundant sampling*
3:10 PM	**Alexey Uvarovskii,** University Hospital Heidelberg, German Center for Cardiovascular Research *pulseR: Versatile computational analysis of RNA turnover from metabolic labeling experiments*
3:17 PM	**Hilal Kazan,** Antalya International University *Genome-wide analysis for identification of lncRNAs that sponge RNA-binding proteins*
3:25 PM	**David Staněk,** Czech Academy of Sciences *Polypyrimidine tract determines splicing efficiency of lincRNAs*
4:30 PM	**Mingfu Shao,** Carnegie Mellon University *DeepBound: Accurate identification of transcript boundaries via deep convolutional neural fields*
4:50 PM	**Angela Garibaldi,** University of California, Irvine *Global analysis of pre-mRNA splicing uncovers the slow splicing kinetics of alternative splicing*
5:05 PM	**Reut Shalgi,** Technion *Widespread regulation of transcriptional readthrough is a hallmark of the mammalian proteotoxic stress response*
5:20 PM	**Dmitri Pervouchine,** Skolkovo Institute of Science and Technology *Deciphering the regulation of alternative pre-mRNA splicing by coupling RBP binding profiles with long-range RNA structure*
5:35 PM	**Anupama Jha,** University of Pennsylvania *Integrative Deep Models for Alternative Splicing*
7:00 PM	**RNA Society Poster Prize Winners**

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

SysMod COSI TRACK SCHEDULE

SATURDAY, JULY 22 • ROOM: PANORAMA

http://sysmod.info/SysMod_ISMB_2017

10:00 AM	**Rainer Breitling,** University of Manchester *Modeling in uncertain times*
10:50 AM	**Jan Hasenauer,** Helmholtz-Zentrum München *A scalable moment-closure approximation for large-scale biochemical reaction networks*
11:10 AM	**Dennis Pischel,** Otto-von-Guericke University Magdeburg *Efficient Simulation of Intrinsic, Extrinsic and External Noise in Biochemical Systems*
11:30 AM	**Eugenio Cinquemani,** INRIA Grenoble – Rhone-Alpes *Estimation of time-varying growth, uptake and excretion rates from dynamic metabolomics data*
11:50 AM	**Claudine Chaouiya,** Instituto Gulbenkian de Ciência *Reversed dynamics to uncover basins of attraction of asynchronous logical models*
2:00 PM	**Jana Wolf,** Max Delbrück Center for Molecular Medicine *Computational modeling of promoter occupancies in MYC-dependent gene regulation*
2:50 PM	**Ina Koch,** Johann Wolfgang Goethe-University *Manatee invariants for functional analysis of signaling pathways in complex networks*
3:10 PM	**Fabian Fröhlich,** Helmholtz-Zentrum München *Large Scale Mechanistic Modeling Enables Robust Prediction of Cancer Cell Drug Response*
3:30 PM	**Pauline Traynard,** Institut Curie *Incorporating patient-specific molecular data into a logic model of prostate cancer*
4:30 PM	**Chiara Damiani,** University Milano-Bicocca *popFBA: tackling intratumour heterogeneity with Flux Balance Analysis*
4:50 PM	**Matteo Barberis,** Universiteit van Amsterdam *Who's driving? Cell cycle robustness investigated by a multi-scale framework integrating cell cycle and metabolism in budding yeast*
5:10 PM	**John A. Bachman,** Harvard Medical School *Explanation of drug effects using a mechanistic model automatically assembled from natural language, databases, and literature*
5:30 PM	**Tamir Tuller,** Tel Aviv University *Tracking and Engineering the Evolution of Organismal Fitness via Multi-Organism mRNA Translation Whole Cell Simulations*

Learn more about ISCB

ISCB TOWN HALL SUNDAY JULY 23

12:45 PM – 1:45 PM

ROOM: TERRACE 1

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

BD2K Special Track

SUNDAY, JULY 23 • ROOM: MEETING HALL IB

https://bd2kccc.org/

Introduction and Keynote

10:00 AM **Susan Gregurick,** NIH NIGMS
Introduction and Overview of BD2K

10:30 AM **Warren Kibbe,** NIH NCI
Keynote:"Data Commons in the age of Precision Medicine"

Session 1: Machine Learning

CHAIRS: JIAWEI HAN AND HARRY CAUFIELD

11:00 AM **Mark Craven,** U Wisconsin - Madison
Learning to Uncover Host-Virus Interactions

11:15 AM **Krishna Kalari,** Mayo Clinic
Genome-guided Framework for Personalized Cancer Treatment

11:30 AM **Jiawei Han,** UIUC
Construction of Biological Networks from Massive Text Data: A Data-Driven Approach

11:45 AM **Jian Ma**, Carnegie Mellon U
Decoding genome structure

12:00 PM **Wei Wang**, UCLA
Aztec: A machine learning empowered platform for FAIR biomedical software

12:15 PM **Saurabh Sinha**, UIUC
KnowEnG: Knowledge Network-guided analysis of genomics data on the Cloud

Session 2: Metadata and Indexing

CHAIR: MARK MUSEN

2:00 PM **Mark Musen,** *Stanford*
*CEDAR: Technology for using metadata standards to ease sharing, integration,
and reuse of biomedical data*

2:20 PM **Henning Hermjakob,** EMBL-EBI
OmicsDI – Discovery and Connectivity Analysis of Omics Datasets

2:40 PM **Susanna-Assunta Sansone,** Oxford
Going FAIR: where are we?

3:00 PM **Nils Gehlenborg,** Harvard
To be FAIR, we should give Ontologies and Data Visualization a try.

3:20 PM **Roberto Toro,** Institut Pasteur
Open Neuroimaging Laboratory and BrainBox

3:40 PM **Kristina Hettne,** Leiden University Medical Ctr
Inferring and explaining gene-disease associations through implicit knowledge

Session 3: Data Science, Open Science, and the Commons

CHAIR: PEIPEI PING

4:30 PM **Maria Giovanni,** NIH NIAID
Opportunities for Data Intensive Research in Infectious Diseases

4:45 PM **Anthony Kerlavage,** NIH NCI
The NCI Cancer Research Data Commons

5:00 PM **Shannon McWeeney,** OHSU
TBD

5:15 PM **Angel Pizarro,** Amazon Web Services
Accelerating Research on the Cloud

5:30 PM **Panel Discussion**

ISMB/ECCB 2017 Wikipedia Editathon

SUNDAY JULY 23 • ROOM 2.1

10:00 AM – 9:00 PM

Wikiproject Computational Biology, together with ISCB, is hosting a Wikipedia and Wikidata editathon at ISMB/ECCB 2017. ISCB is committed to furthering knowledge of computational biology to all. Wikipedia has been an important avenue for both scientists and the public alike to find out about our science. This editathon aims to bring Wikipedia to the bioinformaticians attending ISMB, to give them the tools to improve the coverage of computational biology-related articles.

The editathon will follow a drop-in format. Throughout the day, the room will be open, with computers available, for conference attendees to come and contribute to Wikipedia articles in their field of expertise. To help attendees get familiar with Wikipedia and guide them through this process, there will be printed resources as well as experienced volunteers on hand. To ensure that attendees' minds are well fed, there will also be free snacks available!

NetBio COSI TRACK SCHEDULE

SUNDAY, JULY 23 • ROOM: PANORAMA

http://connect.iscb.org/communities/netbio

10:00 AM	**Alexander Pico,** Gladstone Institutes *Welcome*
10:15 AM	**Vipin Vijayan,** University of Notre Dame *Alignment of dynamic networks*
10:30 AM	**Robert F. Murphy,** Carnegie Mellon University *Image-based Spatiotemporal Causality Inference for Protein Signaling Networks*
10:45 AM	**Marinka Zitnik,** Stanford University *Predicting multicellular function through multi-layer tissue networks*
11:00 AM	**Sean Robinson,** Université Grenoble Alpes/University of Turku *Incorporating Interaction Networks into the Determination of Functionally Related Hit Genes in Genomic Experiments with Markov Random Fields*
11:15 AM	**Michael Kramer,** University of California, San Diego *Active Interaction Mapping reveals the hierarchical organization of autophagy*
11:30 AM	**Sokratis Kariotis,** University of Sheffield *PathSys: Integrating pathway curation, profiling methods, and public repositories: An infrastructure for functional molecular data sharing*
11:45 AM	**Christoph Ogris,** Stockholm University *A novel method for network crosstalk analysis that improves accuracy of pathway annotation*
11:50 AM	**Zachary Stanfield,** Case Western Reserve University *Drug Response Prediction as a Link Prediction Problem*
11:55 AM	**Michael R. Brent,** WUSTL *NetProphet 2.0: Mapping Transcription Factor Networks by Exploiting Scalable Data Resources*
12:00 PM	**Poster Authors** *Poster Highlights*
2:00 PM	**Frank Kramer,** University Medical Center Goettingen *Flash Journal Club*
2:15 PM	**Stefan Avey,** Yale School of Medicine *Multiple network-constrained regressions expand insights into influenza vaccination responses*
2:30 PM	**Francesca Petralia,** Icahn School of Medicine at Mount Sinai *A New Method to Study the Change of miRNA-mRNA Interactions Due to Environmental Exposures*
2:45 PM	**Markus List,** Max Planck Institute for Informatics *Genome-wide competing endogenous RNA networks highlight biomarkers in cancer*
3:00 PM	**Katharina F Heil,** University of Edinburgh/KTH Stockholm *Using network analysis to identify a new key set of Parkinson's Disease associated gene*
3:15 PM	**Aurélien Naldi,** Université de Montpellier *Reconstruction and signal propagation analysis of the syk signaling network in breast cancer cells*
3:30 PM	**Maria Kondratova,** Institut Curie *Network based approach for analysis of cell heterogeneity and immune polarization in tumor microenvironment from single-cell data*
3:35 PM	**Lichy Han,** Stanford University *A PRObabilistic Pathway Score (PROPS) for Classification with Applications to Inflammatory Bowel Disease*
3:40 PM	**Jan Baumbach,** University of Southern Denmark *Comprehensive analysis of high-throughput screens with HiTSeekR – From RNAi, CRISPR/Cas9, miRNA and small compound screens to targeted signalling pathways*
3:45 PM	**Scott Ritchie,** The University of Melbourne *NetRep: a scalable permutation approach for assessing replication and preservation of network modules in large datasets*
3:50 PM	**Sergio Picart-Armada,** Universitat Politècnica de Catalunya *An R package for diffusion algorithms in biological networks*
4:30 PM	**Nadezhda T. Doncheva,** University of Copenhagen *The STRING app: bringing quality-controlled protein-protein and protein-chemical networks into Cytoscape*
4:35 PM	**Duc-Hau Le,** VINMEC Research Institute of Stem Cell and Gene Technology *HGPEC: a Cytoscape app for prediction of novel disease-gene and disease-disease associations and evidence collection based on a random walk on heterogeneous network*
4:40 PM	**T.M. Murali,** Virginia Tech *Pathways on demand: automated reconstruction of human signaling networks*
4:45 PM	**Karthik Raman,** Indian Institute of Technology Madras *Predicting Novel Metabolic Pathways through Subgraph Mining*
5:00 PM	**Gary Bader,** University of Toronto *Keynote: Pathway Genomics*
5:45 PM	*Closing*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

HiTSeq COSI TRACK SCHEDULE

MONDAY, JULY 24 & TUESDAY, JULY 25 • ROOM: FORUM HALL

http://hitseq.org

MONDAY, JULY 24

10:10 AM **Oliver Stegle,** EMBL-EBI
Keynote: Computational methods for dissecting the transcriptome and epigenome diversity between single cells

11:10 AM **Gryte Satas,** Brown University
Tumor Phylogeny Inference Using Tree-Constrained Importance Sampling

11:30 AM **Natalie Davidson,** MSKCC
Integrating Diverse Transcriptomic Alterations to Identify Cancer-Relevant Genes and Signatures

11:50 AM **Russell Schwartz,** Carnegie Mellon University
Deconvolution of heterogeneous bulk tumor genomic data via structured mixed membership models

12:10 PM **Denis Demircioğlu,** Genome Institute of Singapore
A Pan-cancer Analysis of Alternative Transcription Start Sites

2:00 PM **Jordan Eizenga,** University of California Santa Cruz
Modelling haplotypes with respect to reference cohort variation graphs

2:20 PM **Anas Rana,** University of Oxford
Quantitative assessment of genome integrity from whole genome sequencing data

2:40 PM **Birte Kehr,** Berlin Institute of Health
Diversity in non-repetitive human sequences not found in the reference genome

3:00 PM **Pınar Kavak,** Boğaziçi University
Discovery and genotyping of novel sequence insertions in many sequenced individuals.

3:20 PM **Xu Min,** Tsinghua University
Chromatin Accessibility Prediction via Convolutional Long Short-Term Memory Networks with k-mer Embedding

3:40 PM **Jie Zheng,** Nanyang Technological University
HopLand: Single-cell pseudotime recovery using continuous Hopfield network based modeling of Waddington's epigenetic landscape

4:30 PM **Rachid Ounit,** University of California, Riverside
Clarice – Fast, Accurate and Secure Metagenomic Profiler

4:50 PM **Adam M. Phillippy,** NIH
Keynote: What's old is new again: assembly and alignment algorithms for the long-read era.

TUESDAY, JULY 25

8:30 AM **Veli Mäkinen,** University of Helsinki
Keynote: Algorithmic aspects of sequence graph analysis

10:00 AM **Fabian Mueller,** Max Planck Institute for Informatics
DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation

10:20 AM **Serghei Mangul,** UCLA
Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing

10:40 AM **Lorena de La Fuente Lorente,** Centro de Investigación Príncipe Felipe (CIPF)
SQANTI: extensive characterization of long read transcript sequences to remove artifacts in transcriptome identification and quantification

11:00 AM **Yoseph Barash,** University of Pennsylvania
Outlier detection for improved differential splicing quantification from RNA-Seq experiments with replicates

11:20 AM **Rob Patro,** Stony Brook University
Improved Data-Driven Likelihood Factorizations for Transcript Abundance Estimation

11:40 AM **Shaun Jackman,** BC Cancer Agency Genome Sciences Centre
Tigmint: Correct Misassemblies Using Linked Reads From Large Molecules

12:00 PM **Kyle Kloster,** North Carolina State University
Computing Optimal Flow Decompositions for Assembly

2:00 PM **Prashant Pandey,** Stony Brook University
deBGR: An Efficient and Near-Exact Representation of the Weighted de Bruijn Graph

2:20 PM **Martina Fischer,** Robert Koch Institute
Abundance estimation and differential testing on strain level in metagenomics data

2:40 PM **Andre Kahles,** ETH Zurich
Metagenome representation with Scalable Reference Graphs

3:00 PM **Benjamin Linard,** LIRMM–CNRS
Rapid phylogenetic placement via ancestral reconstruction

3:20 PM **Jasmijn Baaijens,** Centrum Wiskunde & Informatica
De novo assembly of viral quasispecies using overlap graphs

3:40 PM **Xinan Liu,** University of Kentucky
SeqOthello: A Novel Indexing Structure to Support Accurate and Scalable Query over Large Scale Sequencing Reads

4:00 PM **Guillaume Marçais,** Carnegie Mellon University
Improving the performance of minimizers and winnowing schemes

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE
Details available on the conference app – see page 27 for details.

VarI-SIG COSI TRACK SCHEDULE

MONDAY, JULY 24 • ROOM: MEETING HALL IA

http://varisig.biofold.org/

10:00 AM	**Yana Bromberg, Emidio Capriotti, Hannah Carter** *Welcome from the committee*
10:10 AM	**Burkhard Rost,** TUM Munich/Columbia University *Common sequence variants affect molecular function more than rare variants?*
10:40 AM	**Maximilian Miller,** Rutgers University *Computational predictors fail to identify amino acid substitution effects at rheostat positions.*
11:00 AM	**Kymberleigh Pagel,** Indiana University *When loss-of-function is loss of function: assessing mutational signatures and impact of loss-of-function*
11:20 AM	**Martin Kircher,** Berlin Institute of Health *Assessing regulatory variant effect scores by massively parallel reporter assays*
11:40 AM	**Emidio Capriotti,** University of Bologna *PhD-SNPg: A webserver and lightweight tool for scoring single nucleotide variants*
12:00 PM	**Imane Boudellioua,** King Abdullah University of Science and Technology *Phenotype-driven discovery of digenic variants in personal genome sequences.*
12:20 PM	**Anika Joecker,** Qiagen *The importance of using a most comprehensive Knowledgebase for the identification of pathogenic variants in cancer and inherited diseases*
2:00 PM	**Sven Bergmann,** Université de Lausanne *Integration of molecular phenotypes into genome-wide association studies.*
2:30 PM	**Cue Hyunkyu Lee,** University of Ulsan College of Medicine; Asan Medical Center *Increasing the power of meta-analysis of genome-wide association studies to detect heterogeneous effects.*
2:50 PM	**Kyoko Watanabe,** VU University Amsterdam *FUMA: Functional mapping and annotation of genetic associations.*
3:10 PM	**Anastasia Gurinovich,** Boston University *PopCluster: A new algorithm to identify genetic variants with effects that change with ethnicity*
3:30 PM	**Magali Jaillard,** bioMerieux *Representing genetic determinants in bacterial GWAS with compacted De Bruijn graphs.*
3:50 PM	**Alexander Kaplun,** Variantyx *One test to rule them all: Clinical grade Whole Genome Sequencing as first-line genetic test.*
4:30 PM	**Niko Beerenwinkel,** ETH Zurich *Network-based integration of multi-omics data for prioritizing cancer genes.*
5:00 PM	**Matteo Manica,** ETH-IMSB//IBM Research *Inferring clonal composition from multiple tumor biopsies.*
5:20 PM	**Sarah Sandmann,** Institute of Medical Informatics *Evaluating Variant Calling Tools for Non-Matched Next Generation Sequencing Data.*
5:40 PM	**Yoichiro Nakatani,** Trinity College Dublin, University of Dublin *Genomes as documents of evolutionary history: a probabilistic macrosynteny model for the reconstruction of ancestral genomes.*
6:00 PM	*Closing remarks from the committee.*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

BioVis COSI TRACK SCHEDULE

MONDAY, JULY 24 • ROOM: MEETING HALL IV

http://biovis.net/2017/cfp_ismb/

10:00 AM	**Jan Aerts,** KU Leuven and **Marc Streit,** Johannes Kepler University Linz *Opening*
10:15 AM	NETWORKS AND SPATIAL DATA
10:15 AM	**Boudewijn P.F. Lelieveld,** Leiden University Medical Center *Invited Talk: Visual Analytics for spatial transcriptomics: from single cell to tissue and back*
11:00 AM	**Marwan Abdellah,** Blue Brain Project/EPFL *Reconstruction and visualization of large-scale volumetric models of neocortical circuits for physically-plausible in silico optical studies*
11:20 AM	**Sjoerd M.H. Huisman,** Delft University of Technology *BrainScope: interactive visual exploration of the spatial and temporal human brain transcriptome*
11:40 AM	**Jan Byška,** University of Bergen *AnimoAminoMiner: Exploration of Protein Tunnels and their Properties in Molecular Dynamics*
12:00 PM	**Henry Heberle,** University of São Paulo *CellNetVis: a web tool for visualization of biological networks using force-directed layout constrained by cellular components*
12:20 PM	**Benedetta Frida Baldi,** The Garvan Institute of Medical Research *Rondo: interactive visual exploration of genome spatial connectivity*
12:25 PM	**Andreas Dräger,** University of Tübingen *Visualization and creation of biochemical networks with Escher*
2:00 PM	MUTATIONS AND NEXT GENERATION SEQUENCING
2:00 PM	**Miriah Meyer,** University of Utah *Just a tool, or a science? The role of visualization in biology*
2:45 PM	**Alexandre Fassio,** UFMG *Vermont: multi perspective visual interactive platform for mutational analysis*
3:05 PM	**Ibrahim Tanyalcin,** Vrije Universiteit Brussel *MUTAFRAME - A Data Visualization Platform for Mutation Effect Prediction*
3:25 PM	**Chaochun Wei,** Shanghai Jiao Tong University *RPAN: Rice Pan-genome Browser for ~3,000 Rice Genomes*
3:45 PM	**Soumita Ghosh,** National University of Singapore *Systems-Level Interactive Data Exploration (SLIDE): user-driven visualization of large-scale omics data on a web browser with flexible customized graphics*
3:50 PM	**Ted Gibbons,** University of Tübingen *Interactive pangenome visualization using variant graphs*
4:30 PM	MACHINE LEARNING AND MEDICINE
4:30 PM	**Lan Huong Nguyen,** Stanford University *Bayesian unidimensional scaling for visualizing uncertainty in high dimensional datasets with latent ordering of observations*
4:50 PM	**Chen He,** University of Helsinki *MediSyn: uncertanty-aware visualization of multiple biomedical datasets to support drug treatment selection*
5:10 PM	**Divya Tej Sowpati,** Centre for Cellular and Molecular Biology *C-State: an interactive web app for simultaneous multi-gene visualization and comparative epigenetic pattern search*
5:30 PM	**John H Morris,** UCSF *Overcoming the visualization challenges of pE-MAP results*
5:35 PM	**Sarah O Fisher,** IBIMA *Extending R gplots Venn diagrams with polyominoes for 6 and 7 dimensions and an unconstrained graph representation*
5:40 PM	**Jan Aerts,** KU Leuven and **Marc Streit,** Johannes Kepler University Linz *Closing remarks*
6:00 PM	POSTER SESSION

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Bio-Ontologies COSI TRACK SCHEDULE

MONDAY, JULY 24 & TUESDAY, JULY 25 • ROOM: MEETING HALL V

http://www.bio-ontologies.org.uk

MONDAY, JULY 24

10:00 AM	**Michel Dumontier,** Maastricht University *Welcoming Remarks*
10:10 AM	**Robert Stevens,** Manchester University *Keynote: Ontologies: Necessary, but not sufficient*
11:10 AM	**Panel** *20 years of Bio-Ontologies at ISMB*
2:00 PM	**Maryam Habibi,** Humboldt-Universität zu Berlin *Deep Learning with Word Embeddings improves Biomedical Named Entity Recognition*
2:30 PM	**Lars Juhl Jensen,** University of Copenhagen *EXTRACT 2.0: text-mining-assisted interactive annotation of bio-medical named entities and ontology terms*
2:45 PM	**Milana Frenkel-Morgenstern,** Bar-Ilan University *A Text Mining Approach Characterizes Fusion Proteins and Their Interactions From PubMed Publications*
3:00 PM	**Catia Pesquita,** University of Lisbon *Keynote: Sense and similarity: making sense of similarity for ontologies*
4:45 PM	**Magdalena Zwierzyna,** BenevolentAI/University College London *Classification and analysis of a large collection of in vivo assay descriptions*
5:00 PM	**Eugenia Galeota,** Istituto Italiano di Tecnologia *Onassis: Ontology Annotation and Semantic Similarity Software*
5:15 PM	**Michel Dumontier,** Maastricht University *Break Out for Paper Writing: Challenges and Opportunities in Bio-Ontologies*

TUESDAY, JULY 25

8:30 AM	**Nigam Shah,** Stanford University *Keynote: Mining the Ultimate Phenome Repository*
10:30 AM	**Volodymyr Kuleshov,** Stanford University *A Machine-Compiled Database of Genome-Wide Association Studies*
11:00 AM	**Amrapali Zaveri,** Maastricht University *MetaCrowd: Crowdsourcing Biomedical Metadata Quality Assessment*
11:15 AM	**Bjoern Peters,** La Jolla Institute for Allergy and Immunology *Enabling community editing of assay terms in OBI while ensuring consistent use of design patterns with spreadsheet templates*
11:30 AM	**Kody Moodley,** Maastricht University *Assessing the quality of manually curated drug indication and usage information via ontology term mappings*
11:45 AM	**1 minute madness**
2:00 PM	**Gizem Soğancıoğlu,** Boğaziçi University *BIOSSES: A Semantic Sentence Similarity Estimation System for the Biomedical Domain*
2:30 PM	**Randi Vita,** La Jolla Institute for Allergy and Immunology *Using ontologies to find and correct errors in database content*
2:45 PM	**Sirarat Sarntivijai,** European Bioinformatics Institute *EFO 3: "Your" experimental factor ontology*
3:00 PM	**Bjoern Peters,** La Jolla Institute for Allergy and Immunology *Conventions to make ontology term labels predictable and unique*
3:15 PM	**Jo McEntyre,** EMBL-EBI *Enhancing evidence from literature in Open Targets – a platform for drug target validation*
3:45 PM	**Michel Dumontier,** Maastricht University *Closing Remarks*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Function COSI TRACK SCHEDULE

MONDAY, JULY 24 & TUESDAY, JULY 25 • ROOM: PANORAMA

http://biofunctionprediction.org

MONDAY, JULY 24

10:00 AM	**Function SIG organizers** • *Welcome, Day 1*
10:10 AM	**Maria Brbic,** IRB *The landscape of microbial phenotypic traits and associated genes*
10:30 AM	**Yannick Mahlich,** TUM Munich *fusionDB: assessing microbial diversity and environmental preference via functional similarity networks*
10:50 AM	**Da Chen Emily Koo,** New York University *Region-specific Function Prediction: automatically inferring function labels for protein regions*
11:10 AM	**Ahmet Süreyya Rifaioğlu,** Middle East Technical University *Investigation of Multi-task Deep Neural Networks in Automated Protein Function Prediction*
11:40 AM	**Dmitry Korkin,** Worcester Polytechnic Institute (WPI) *Determining Rewiring Functional Effects of Alternative Splicing Variants on Protein-Protein Interactions*
12:00 PM	**John Moult,** University of Maryland *Keynote: Community Driven Critical Assessment: how well does it work, what have we learned, and what next?*
2:00 PM	**Ilya Novikov,** Baylor College of Medicine *Reasoning on Gene Ontology Networks Predicts Novel Protein Annotations*
2:20 PM	**Cen Wan,** University College London *Predicting Protein Function Directly from STRING Network Topology using Deep Learning Techniques*
2:40 PM	**Christophe Dessimoz,** University of Lausanne *Proceedings Talk: Orthologous Matrix (OMA) algorithm 2.0: more robust to asymmetric evolutionary rates and more scalable hierarchical orthologous group inference*
3:10 PM	**Matthieu David,** University of Nantes *All-to-all spectra comparisons within minutes for peptides identification in tandem mass spectrometry*
3:30 PM	**Christina Marino-Buslje,** Fundación Instituto Leloir *Comparing residue-coevolution networks across protein families*
4:30 PM	**Seyed Ziaeddin Alborzi,** INRIA Nancy Grand-Est *Automatic Generation of Functional Annotation Rules Using Inferred GO-Domain Associations*
4:50 PM	**Peter Freddolino,** University of Michigan *Protein Function Prediction by COFACTOR in CAFA3*
5:10 PM	**Jonathan G. Lees,** UCL *A Domain-Based Machine Learning Approach for Function Prediction using CATH FunFams*
5:15 PM	**Itamar Borukhov,** Compugen Ltd. *Computational Functional Annotation: The Predictive Power of Different Data Sources*
5:20 PM	**Maxat Kulmanov,** King Abdullah University of Science and Technology *Predicting protein functions from sequence using a neuro-symbolic deep learning model*
5:25 PM	**Matt Jeffryes,** European Bioinformatics Institute *Crowdsourcing Protein Family Database Curation*
5:40 PM	**Jasmin Coulombe-Huntington,** Universite de Montreal *Proteome-wide chemical-genetic interaction map in human cells reveals drug mechanisms and novel gene functions*

TUESDAY, JULY 25

8:30 AM	**Function SIG organizers** *Welcome, Day 2*
8:40 AM	**Hagit Shatkay,** University of Delaware *Keynote: Tell Us where You are Going: Pondering Literature, Locations, Life and Proteins*
9:10 AM	**Daisuke Kihara,** Purdue University *Proceedings Talk: DextMP: Deep dive into Text for predicting Moonlighting Proteins*
10:00 AM	**Iddo Friedberg and Naihui Zhou,** Iowa State University *The third Critical Assessment of Function Annotation: Lessons Learned and Preliminary Results*
11:00 AM	*CAFA Predictor 1*
11:30 AM	*CAFA Predictor 2*
11:50 AM	**Huaiyu Mi,** University of Southern California *Phylogenetic- based gene function prediction in the Gene Ontology Consortium*
12:10 PM	**Rabie Saidie,** European Bioinformatics Insititute *A Self-training Approach for Functional Annotation of UniProtKB Proteins*
12:15 PM	**Giuseppe Profiti,** Università di Bologna *BAR 3.0: going beyond protein function annotation*
12:20 PM	**Liisa Holm,** University of Helsinki *PANNZER 2: Annotate a complete proteome in minutes!*
12:25 PM	**Mary Jo Ondrechen,** Northeastern University *Thinking outside the informatics box: Computed chemical properties for protein function annotation*
2:00 PM	**Petri Törönen,** University of Helsinki *Artificial Dilution Series: A General Framework for Benchmarking Classifier Evaluation Metrics*
2:20 PM	**Yuxiang Jiang,** Indiana University *Elucidating the Function Space of Proteins Defined by Ontologies*
2:40 PM	**Stavros Makrodimitris,** Delft University of Technology *Label-Space Dimensionality Reduction and a Similarity-Based Representation for Protein Function Prediction*
3:00 PM	**John Williams,** MRC Harwell Institute *Predicting Novel Abnormal Circadian Phenotypes in Mouse*
3:30 PM	**Ghazaleh Taherzadeh,** Griffith University *Structure-based prediction of protein-peptide binding regions using Random Forest*
3:50 PM	**Jeffrey Yunes,** UCSF *Automating Genomic Context Analysis with a Probabilistic Model of Protein Function and Relatedness*
4:00 PM	*Awards and Close*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

ELIXIR Special Track

TUESDAY, JULY 25 • ROOM: MEETING HALL IA

https://bd2kccc.org/

ELIXIR Platforms Update

Chair: Niklas Blomberg

10:00 AM	**Jo McEntyre,** ELIXIR – EBI *ELIXIR Data Platform: Sustaining Europe's life science data infrastructure*
10:30 AM	**Salvador Capella,** ELIXIR – ES *ELIXIR Tools Platform: Services and connectors to drive access and exploitation*
11:00 AM	**Norman Morrison,** ELIXIR Hub & **Chris Evelo,** ELIXIR – NL *ELIXIR Interoperability Platform: Integration of data and services*
11:30 AM	**Ludek Matyska,** ELIXIR – CZ *ELIXIR Compute Platform: Access, exchange and storage*
12:00 PM	**Patricia Palagi,** ELIXIR – CH *ELIXIR Training Platform: Professional skills for managing and exploiting data*

ELIXIR Use Cases and Capacity Building Update

Chair: Andrew Smith

2:00 PM	**Rob Finn,** ELIXIR – EBI & **Nils Peder Willssen,** ELIXIR – NO *ELIXIR Marine Metagenomics Use case: Marine metagenomic infrastructure as driver for research and industrial innovation*
2:30 PM	**Marco Roos,** ELIXIR – NL *ELIXIR Rare Disease Use case: ELIXIR infrastructure for Rare Disease research*
3:00 PM	**Susheel Varma,** ELIXIR Hub *ELIXIR Human Data Use case: Secure archiving, dissemination and analysis of human access-controlled data*
3:30 PM	**Jiri Vondrasek/Bengt Persson,** ELIXIR – CZ and NO *ELIXIR's Node Capacity Building programme*
4:00 PM	**Pablo Roman-Garcia,** ELIXIR Hub *Industry Engagement: ELIXIR and Open Innovation*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

TransMed COSI TRACK SCHEDULE

TUESDAY, JULY 25 • ROOM: MEETING HALL IV

http://transmedit.org

8:30 AM	**Reinhard Schneider,** University of Luxembourg *Welcome and Introduction*
8:40 AM	**Anguraj Sadanandam,** The Institute of Cancer Research *Metavariable based genome-phenome integrative analysis to facilitate personalized cancer medicine*
9:15 AM	**Michael Altenbuchinger,** University of Regensburg *Molecular signatures that can be transferred across different omics platforms*
10:00 AM	**Tim Hubbard,** King's College London *The 100,000 genomes project*
10:35 AM	**Omer Weissbrod,** Weizmann Institute of Science *Association testing of bisulfite sequencing methylation data via a Laplace approximation*
10:50 AM	**Xiaoke Hao,** Nanjing University of Aeronautics and Astronautics *Identification of Associations between Genotypes and Longitudinal Phenotypes via Temporally-constrained Group Sparse Canonical Correlation Analysis*
11:05 AM	**Lei Ding,** Indiana University Bloomington *Predicting phenotypes from microarrays using amplified, initially marginal, eigenvector regression*
11:20 AM	**Muhammad Ammad-Ud-Din,** University of Helsinki *Systematic identification of feature combinations for predicting drug response with Bayesian multi-view multi-task linear regression*
11:35 AM	**Johanna Klughammer,** CeMM *Epigenomic profiling of glioblastoma through treatment and progression*
11:45 AM	**Héctor Tejero,** Spanish National Research Cancer Centre, CNIO *Predicting cancer sequential treatments and drug repurposing with SATIE*
12:00 PM	**Elizabeth Coker,** The Institute of Cancer Research *canSAR: an integrated knowledgebase for cancer research and drug discovery*
12:15 PM	**Nikolaus Fortelny,** CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences *Integrative analysis of personalized, multidimensional datasets of glioblastoma patients*
2:00 PM	**Barend Mons,** Leiden University Medical Center *The Internet of FAIR data and Services*
2:35 PM	**Holger Fröhlich,** University of Bonn *Using Multi-Scale Genetic, Protein, Neuroimaging and Clinical Data for Predicting Alzheimer's Disease and Reconstruction of Relevant Biological Mechanisms*
2:50 PM	**Winston Haynes,** Stanford University *Understanding human disease relationships through integrated molecular and clinical analysis*
3:05 PM	**Emre Guney,** Institute for Research in Biomedicine (IRB Barcelona) *Integrating personalized gene expression profiles into predictive disease-associated gene pools*
3:20 PM	**Enrico Mossotto,** University of Southampton *Classification of Paediatric Inflammatory Bowel Disease using Machine Learning*
3:35 PM	**Kieran Campbell,** University of Oxford *Pseudotemporal disease trajectories from cross-sectional data*
3:50 PM	**Rachita Yadav,** Massachusetts General Hospital *Integrating genomics and transcriptomics to dissect the pathogenic mechanism of X-Linked Dystonia-Parkinsonism*
4:00 PM	**Anna Hake,** Max-Planck-Institut für Informatik *Prediction of HIV-1 sensitivity to broadly neutralizing antibodies shows a trend towards resistance over time*
4:10 PM	**Suganthi Balasubramanian,** Regeneron Pharmaceuticals *Understanding human knockouts*
4:20 PM	**Bissan Al-Lazikani,** *The Institute of Cancer Research (ICR)* *Concluding Remarks*

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

Abstracts NON-COSI AREAS SCHEDULE

TUESDAY, JULY 25 • ROOM: MEETING HALL IB

8:30 AM **Julián Candia,** National Institutes of Health
Nonlinear Mixed-Effects Modeling of Proteomics Antibody-Based Multiplex Assays: A Bioinformatics Post-Hoc Approach to Improve Signal-to-Noise Ratios

8:45 AM **Anne Wassermann,** Merck & Co Inc.
Chemical biology libraries: probing the proteome with small molecules

9:00 AM **Kyowon Jeong,** Seoul National University
Ultra-sensitive n-plexed protein quantification by a model-based reconstruction method

10:00 AM **Raul Rodriguez-Esteban,** F. Hoffmann-La Roche Ltd.
A Drug-Centric View of Drug Development: How Drugs Spread from Disease to Disease

10:15 AM **Nicolas De Neuter,** University of Antwerp
On the feasibility of mining CD8+ T-cell receptor patterns underlying immunogenic peptide recognition

10:30 AM **Seema Mishra,** University of Hyderabad
Immunoinformatics and Molecular Modeling exploration of T-cell Epitope-based Cancer Immunotherapy

10:45 AM **Nadia Atallah,** Purdue University
Single-cell RNA sequencing identifies novel roles and interacting partners of APE1 in Panceatic Ductal Adenocarcinoma Cells

11:00 AM **Ramon Diaz-Uriarte,** Universidad Autonoma de Madrid
Misleading arrows? Fitness landscapes and cancer progression models

11:15 AM **Katharina Jahn,** ETH Zurich
Reconstructing tumour evolution from single-cell sequencing data

11:30 AM **Robert Noble,** ETH Zurich
Impact of tissue architecture on the nature and predictability of tumour evolution

11:45 AM **Alexandra Vatsiou,** ICR
The spatio-temporal evolutionary dynamics of lymph node spread in early breast cancer

12:00 PM **Johannes G. Reiter,** Harvard University
Reconstructing metastatic seeding patterns of human cancers

12:15 PM **Francesco Vallania,** Stanford University
Leveraging heterogeneity in public data to reduce bias and increase accuracy of cell-mixture deconvolution

2:00 PM **Alberto Calderone,** University of Rome Tor Vergata
PubSqueezer: a Text-Mining Tool to Discover Connections in Scientific Literature

2:15 PM **Fabio Rinaldi,** IFI, University of Zurich
Digital assisted curation to the rescue of traditional literature curation for life-science databases

2:30 PM **Sophia Tsoka,** King's College London
Model tree by ensemble of piecewise linear models and its application to QSAR modeling

2:45 PM **Dianjing Guo,** The Chinese University of Hong Kong
A systematic identification of species-specific protein succinylation sites using joint element features information

3:00 PM **Kristina Heyn,** University of Regensburg
Using Ancestral Sequence Reconstruction to Characterize an Allosteric Bi-Enzyme Complex

3:15 PM **Maria Chikina,** University of Pittsburgh
Molecular biology of body-size variation: from evolution to human disease

3:30 PM **Yuki Yoshida,** Keio University
Comparative genomics of the tardigrades Hypsibius dujardini and Ramazzottius varieornatus

3:45 PM **Kazuharu Arakawa,** Keio University
Sequencing 1,000 spiders to elucidate the design mechanisms of spider silk proteins

4:00 PM **Dariusz Plewczynski,** University of Warsaw
How physical interactions between architectural proteins and DNA shape the three dimensional structure of Human genome

* ALL COFFEE AND LUNCH BREAKS AS PER MAIN SCHEDULE

Details available on the conference app – see page 27 for details.

ISMB/ECCB 2017 Appreciates the Support of the Following Sponsors

ISCB
ISMB
CELEBRATING 25 YEARS OF ISMB
ECCB
2017 • PRAGUE

GOLD SPONSORS

BD2K CCC

elixir

BRONZE SPONSORS

F1000Research
Open for Science

Overleaf

Google

OXFORD
UNIVERSITY PRESS

COPPER SPONSOR

intel®

GENERAL SPONSORS

VERTEX™

BioMed Central

PRA HA
PRA GUE
PRA GA
PRA G

elixir
CZECH REPUBLIC

Mary Ann Liebert, Inc. publishers

3DS BIOVIA

ÚOCHB AV ČR
IOCB PRAGUE

TRAVEL FELLOWSHIP SPONSORS

Akamai

Bio-Ontologies

HiTSeq

ECCB

SysMod

CAMDA2017

biovis

OBF

ISCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

PLOS COMPUTATIONAL BIOLOGY

OVERVIEW JULY 2017

PLOS Computational Biology continues to be a leading venue for high-quality research in all areas of computational biology, and also 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 Page' series has grown throughout 2016/17, with *PLOS Genetics* also announcing they are launching their own Topic Pages section[1] . These articles increase the coverage of computational biology (and now genetics) 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. A recent example of a Topic Page in *PLOS Computational Biology* is 'Transcriptomics Technologies'[2,3] by Lowe et al. Thomas Shafee, also an author of this article, is the new Topic Pages editor on *PLOS Genetics*. All of these articles can be located on their own collections page[4] or on a Wikipedia playlist[5].

As always, our 'Ten Simple Rules' collection[6] continues to be popular as it passes wisdom 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 insights and experiences, including:

Samuel Demharter et al. [7] who discussed how to make it through an interdisciplinary PhD in 'Ten simple rules for surviving an interdisciplinary PhD'

Philip E. Bourne et al. [8] who looked at preprints and what users should be aware of in 'Ten simple rules to consider regarding preprint submission'

Megan Yu et al.[9] spoke to undergraduates to ensure they were using their time wisely in 'Ten simple rules to make the most out of your undergraduate research career'

We would like to express our thanks to *PLOS Computational Biology* Editors Scott Markel and Fran Lewitter for their tireless work in curating and editing this collection.

To support the reproducibility of scientific research, PLOS has partnered with the open access repository protocols.io [10,11] to facilitate the communication of methodological details in laboratory protocols. Each protocol is assigned its own persistent identifier (DOI) with step-by-step instructions and reagent details. Authors can elect to supplement their Methods section with this level of detail and include a link in the Methods section of their manuscript. We believe this is a useful way to enhance the reproducibility of published results and foster collaboration.

In accordance with an Open Letter [12] that commits publishers to following best practices when collecting, processing, and displaying ORCiDs, as of December 7th 2016, *PLOS Computational Biology* and other PLOS journals now require the corresponding authors of new manuscripts to provide an ORCiD [13], which will be published with their article. ORCiD is a unique digital identifier used to disambiguate researchers from one another, ensuring that work is properly attributed, and that researchers receive credit for everything they do.

PLOS Computational Biology Methods [14] and Software [15] sections continue to thrive. Both Software and Methods papers can now be found via their respective collections [16,17].

PLOS Computational Biology could not publish quality research across multiple disciplines without the assistance and support of the community. The Editors and staff of the journal therefore thank everyone who has helped to make the last year such a success.

PLOS Computational Biology is a 'Community Journal'; we value your ideas and comments, so please don't hesitate to visit us at booth 16 at ISMB 2017 or email us at ploscompbiol@plos.org.

Popular papers of 2016/2017 based on most views:

Kass RE, Caffo BS, Davidian M, Meng X-L, Yu B, Reid N (2016) Ten Simple Rules for Effective Statistical Practice. PLoS Comput Biol 12(6): e1004961. https://doi.org/10.1371/journal.pcbi.1004961

Jonas E, Kording KP (2017) Could a Neuroscientist Understand a Microprocessor? PLoS Comput Biol 13(1): e1005268. https://doi.org/10.1371/journal.pcbi.1005268

Gauvrit N, Zenil H, Soler-Toscano F, Delahaye J-P, Brugger P (2017) Human behavioral complexity peaks at age 25. PLoS Comput Biol 13(4): e1005408. https://doi.org/10.1371/journal.pcbi.1005408

Aitchison L, Corradi N, Latham PE (2016) Zipf's Law Arises Naturally When There Are Underlying, Unobserved Variables. PLoS Comput Biol 12(12): e1005110. https://doi.org/10.1371/journal.pcbi.1005110

REFERENCES

http://blogs.plos.org/biologue/2017/04/12/continuing-to-bridge-the-journal-wikipedia-gap-introducing-topic-pages-for-plos-genetics/ accessed 14th June

Lowe R, Shirley N, Bleackley M, Dolan S, Shafee T (2017) Transcriptomics technologies. PLoS Comput Biol 13(5): e1005457. https://doi.org/10.1371/journal.pcbi.1005457

https://en.wikipedia.org/wiki/Transcriptomics_technologies

http://collections.plos.org/topic-pages

http://playlist.wiki/playlist/plos-computational-biology-topics

http://collections.plos.org/ten-simple-rules

Demharter S, Pearce N, Beattie K, Frost I, Leem J, Martin A, et al. (2017) Ten simple rules for surviving an interdisciplinary PhD. PLoS Comput Biol 13(5): e1005512. https://doi.org/10.1371/journal.pcbi.1005512

Bourne PE, Polka JK, Vale RD, Kiley R (2017) Ten simple rules to consider regarding preprint submission. PLoS Comput Biol 13(5): e1005473. https://doi.org/10.1371/journal.pcbi.1005473

Yu M, Kuo Y-M (2017) Ten simple rules to make the most out of your undergraduate research career. PLoS Comput Biol 13(5): e1005484. https://doi.org/10.1371/journal.pcbi.1005484

http://blogs.plos.org/plos/2017/04/protocols-io-tools-for-reproducibility/

https://www.protocols.io/

https://orcid.org/content/requiring-orcid-publication-workflows-open-letter

https://orcid.org/

http://journals.plos.org/ploscompbiol/s/submission-guidelines#loc-methods-submissions

http://journals.plos.org/ploscompbiol/s/submission-guidelines#loc-software-submissions

http://collections.plos.org/software

http://collections.plos.org/compbiol-methods

ISCB-Africa ASBCB Conference on Bioinformatics

OCTOBER 10 – 13, 2017 ▪ ENTEBBE, UGANDA

Official Conference

KEYNOTE SPEAKERS

MARY GALINSKI
Professor, Emory Vaccine Center
Emory University

DANIEL MASIGA
Head of Molecular Biology and Biotechnology
African Insect Science for Food and Health

B.F. FRANCIS OUELLETTE
CSO, VP Scientific Affairs
Génome Québec

NICOLE SORANZO
Professor of Human Genetics
University of Cambridge

CONFERENCE TOPICS

- Bioinformatics of human genetics and population studies
- Host/pathogen interactions and dynamics of infectious diseases
- Microbiome studies
- Systems biology
- Tools, Pipelines, database and resource development
- Molecular epidemiology and evolution
- Pharmacogenomics, vaccines and drugs design
- Functional, structural, and comparative genomics

SUBMISSION DEADLINES

- Research Talk Abstracts	July 31, 2017
- Poster Abstracts	September 1, 2017

WHEN

October 10-12, 2017

WHERE

Entebbe, Uganda

COST*

ISCB & ASBCB Members

Professional $250 ▎Student & Post Doc $150

Non-Members

Professional $300 ▎Student & Post Doc $175

REGISTER

Register online at
https://www.iscb.org/iscbafrica2017

*Reflects Earlybird rates.
Rates increase on 9/4/2017

MEET THE
2017 ISCB FELLOWS

Alex Bateman, Senior Team Leader, Protein Sequence Resources, European Bioinformatics Institute, EMBL, has made major contributions to Bioinformatics in protein domain research, specifically in providing research infrastructure through major protein and RNA related databases. His work has centered around the idea that there are a finite number of families of protein and RNA genes. He aims to collect and analyze these families to gain an understanding of how complex biological processes have evolved from a relatively small number of components. Alex is an active members of the ISCB community where he currently serves as a member of the Board of Directors, volunteers on numerous committees and is a past ISMB/ECCB conference chair, and Editor of Bioinformatics.

Andrea Califano, Clyde and Helen Wu Professor of Chemical and Systems Biology, Biochemistry and Molecular Biophysics, Biomedical Informatics, Columbia University, is a leader in cancer systems biology. He has pioneered algorithms and technologies for the systematic mapping and interrogation of cancer regulatory/signaling networks that have become a standard in the field and have led to key discoveries. Dr. Califano is currently the founding director and chair of the Columbia Department of Systems Biology, which includes the Sulzberger Columbia Genome Center and the Center for Computational Biology and Bioinformatics (C2B2). He co-founded the DREAM Challenges, which have become a popular and integral part of the RECOMB/ISCB Conference on Regulatory and Systems Genomics.

Daphne Koller, Rajeev Motwani Professor, Computer Science Department, Stanford University has made seminal contributions to machine learning techniques in computational genomics and to education through her founding of Coursera, an innovative model for online learning. Her research focuses on the application of machine learning and Bayesian techniques to problems and interpretation in the biomedical sciences, specifically genomics. Daphne is one of the founders of Coursera, an education platform bringing courses, including from computational biology, from top universities online, free, for anyone who wants to take them. This work is transformative both in how education will be delivered in the future, but also in democratizing accessibility to these courses to the developing world.

Anders Krogh, Professor of Bioinformatics, Head of the Section for Computational and RNA Biology, Department of Biology, University of Copenhagen, initiated the widespread use of hidden Markov models in computational biology and was a key author on one of the most influential textbooks, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. His recent research focuses on analysis of data from high-throughput DNA sequencing with applications to post-transcriptional regulation, ancient genomics, metagenomics, and transcriptome analysis.

William S. Noble, Professor, Department of Genome Sciences, Department of Computer Science and Engineering, University of Washington, has made seminal contributions in both developing and applying statistical and machine learning methods for the analysis of complex biological data sets. He has extensive experience developing novel analytical algorithms, creating user-friendly software implementing those methods, and collaborating with experimentalists. Dr. Noble is a former member of the ISCB Board of Directors (2008-2011) and an Associate or Deputy Editor of PLOS Computational Biology since 2008.

Lior Pachter, Bren Professor of Computational Biology, Division of Biology and Biological Engineering, CalTech, is a leader in both comparative genomics and RNA-Seq data analysis. He is also known for bringing algebraic geometry to biological sequence analysis. Software developed by his group in collaboration with others, such as Cufflinks, Tophat, FSA, MAVID, are used extensively around the world. Dr. Pachter's contribution's to education includes the development of Math courses for biological majors. He serves the public by his famous WordPress blog that advocates for rigorous research approaches to bioinformatics.

Olga Troyanskaya, Professor, Computer Science, Lewis Sigler Institute for Integrative Genomics, Princeton University, has made important contributions to the study of gene function and regulation in biological networks through integrated analysis of biological data from diverse data sources using techniques from computer science and statistics. She translates her work into accessible software for the community. Olga was the 2011 recipient of the ISCB Overton Prize which recognizes outstanding accomplishment of a scientist in the early- to mid-stage of his or her career. She is a former member of the ISCB Board of Directors (2013 – 2016), chaired the ISMB/ECCB 2011 conference and served as ISCB editor for PLOS Computational Biology. She currently serves as deputy director for genomics (2014-present) at the Simons Foundation Center for Computational Biology.

Tandy Warnow, Founder Professor of Engineering, Professor of Bioengineering and Computer Science, University of Illinois, Urbana-Champaign, is a pioneer and leader in the design of algorithms and experimental studies of computational phylogenetics. She and others laid the theoretical foundations of fast convergent phylogenetic algorithms in a series of papers in the late 90s, which led to the development of divide-and-conquer methods that make accurate phylogenetic inference of millions of species practical. Her work in fast convergent phylogenetic inference led to new algorithms for simultaneously estimating multiple sequence alignment and phylogeny. Dr. Warnow was also the Program Chair for the ISCB Great Lakes Bioinformatics Conference and is Conference Chair for ISMB 2018.

THE INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY AND WIKIPROJECT COMPUTATIONAL BIOLOGY: CELEBRATING TEN YEARS OF COLLABORATION TOWARDS OPEN ACCESS

Kieran O'Neill, Vivek Rai, Alastair M. Kilpatrick

Open access to scientific information is a core principle of the International Society for Computational Biology (ISCB). This principle is shared by the the Wikimedia Foundation, with its primary goal to collect, develop and disseminate free and open-access educational content. Consequently, ISCB has and continues to foster strong links with several Wikimedia projects, particularly Wikipedia.

To this end, ISCB works closely with WikiProject Computational Biology (WCB), a group of around 130 editors overseeing Wikipedia articles relating to computational biology and bioinformatics. In 2017, WCB celebrates its 10th anniversary, having grown to cover more than 1,300 articles in the English Wikipedia. This article serves to acknowledge past ISCB-WCB collaborations, officially announce the 2017 ISCB Wikipedia competition, and explore exciting future directions, including the potential role of WCB in classroom education for computational biology.

TOPIC PAGES, COMPETITIONS AND EDITATHONS: A HISTORY OF COLLABORATION

WCB's ten-year history has been marked by a number of collaborative efforts with ISCB. These include PLOS Topic Pages, ISCB's annual Wikipedia competition, and events at ISCB conferences.

Topic Pages are an initiative pioneered in 2012 by PLOS Computational Biology, one of the official journals of ISCB, to create high-quality Wikipedia articles while also providing trainees with an opportunity to build a publication record. A topic page is a review article written for the general public and according to Wikipedia guidelines, that is simultaneously published by PLOS and as a Wikipedia article. Since its inception, ten high-quality, in-depth articles on topics in computational biology have been created.

Also since 2012, ISCB and WCB have held an annual Wikipedia competition, offering cash prizes and memberships to students and trainees for the best contributions to computational biology-related Wikipedia articles and Wikidata entries [1,2]. This competition has been highly successful in driving the improvement of coverage of computational biology within Wikipedia, having drawn a total of 144 entries over just five years.

Beyond the ISCB Wikipedia Competition and PLOS Topic Pages, the partnership between the ISCB and WCB has continued to grow. Following tutorials at ECCB 2012 and ISMB 2014 which provided a practical introduction to editing Wikipedia for scientists, the ISCB held a Wikipedia and Wikidata editathon at ISMB 2016 as part of the celebrations for the Wikipedia Year of Science.

Another editathon will be held at ISMB/ECCB 2017 on an all-day drop-in model, and we invite attendees regardless of their previous experience with Wikipedia editing. We envisage similar joint events in the future which will help to improve the coverage of computational biology and bioinformatics on Wikimedia projects.

THE 2017 ISCB WIKIPEDIA COMPETITION

In 2017, ISCB is running the 6th annual ISCB Wikipedia Competition in collaboration with WCB. Entry to the competition is open internationally to students and trainees of any level, both as individuals and as groups. As in previous years, the ISCB encourages competition entries for contributions to Wikipedia in any language, and contributions to Wikidata items. Further information about the 2017 competition can be found here: https://en.wikipedia.org/wiki/WP:ISCB2017

The 2017 competition will begin on 21 July 2017, coinciding with the ISMB/ECCB 2017 conference, and will end on 31 December 2017. Each article entered in the competition will be reviewed by students nominated by the ISCB Student Council, and a shortlist of entries will be examined by a judging panel. The winners will be presented with their awards at ISMB 2018 in Chicago.

STRENGTHENING LINKS BETWEEN WIKIMEDIA AND ISCB: WIKIPEDIA IN THE (BIOINFORMATICS) CLASSROOM

The ISCB also sees a role for WCB in collaborating with the ISCB Education Committee which, as part of its remit, seeks to define curriculum guidelines for bioinformatics courses [5]. One potential area of work may be to use the current draft guidelines in order to identify a subset of Wikipedia articles which would provide a 'core' set of articles for a bioinformatics curriculum. Clearly these articles should be as complete as possible and should be prioritized for improvement by WCB members. The ISCB suggests that Wikipedia also has scope for helping to refine the curriculum guidelines. As an example, Wikipedia keeps viewing statistics for each of its articles; these show that the Bioinformatics article page was viewed over 41,000 times in January 2017 alone and the most-viewed WCB article (on CRISPR) was viewed almost 140,000 times in the same period. These viewing statistics may play a useful role in identifying areas of the curriculum that are of particular importance and therefore should be emphasized in future versions of the curriculum.

We also encourage teachers, tutors and lecturers at all levels to use the ISCB Wikipedia competition as part of their class assignments. For example, by having students 'claim' a Wikipedia article for the competition, with their contributions over a short, defined period in the fall semester marked by the instructor. Wikipedia provides information and resources for running editing projects as part of classroom activities and the "Ten Simple Rules for Editing Wikipedia" [3] also provides an excellent resource for those new to Wikipedia editing.

Besides the competition, there are a number of ways in which Wikipedia may be used in a classroom setting. For example, both undergraduates and graduate students may 'claim' an article to improve as a short class project to be evaluated by the tutor. Incentives such as the prospect of appearing on the front page of Wikipedia as a "Did you know?" article can help to provide extra motivation. For graduate students, a Wikipedia article can potentially be expanded into a PLOS Topic Page [4], which offers an opportunity to build a publication record, and can grant a head start on writing a thesis introduction. As noted previously, the collaborative writing environment of Wikipedia in particular encourages critical thinking and improves research skills.

CONCLUSIONS

ISCB and WCB have spent the last decade working together to improve access to information about computational biology by fostering the creation of high-quality Wikipedia articles. The results of this have been encouraging. A paper in 2013 [1] reported on the state of articles within the scope of WCB. Since then, almost 200 new articles have been added and many of the shortest articles (known as stubs) have been expanded (Figure 1). However, a significant number of articles still remain at 'Start class' or lower, indicating weaknesses in many areas. ISCB and WCB are keen to expand on the depth and quality of articles relating to computational biology and encourage students and trainees at all levels to take part in the ISCB Wikipedia Competition, write topic pages, and drop in to the Wikipedia Editathon at ISMB 2017. We look forward to continued collaborations and efforts by the entire community towards enhancing and disseminating humanity's knowledge of computational biology.

[1] Bateman A., Kelso J., Mietchen D., Macintyre G., Di Domenico T., Abeel T., Logan D.W., Radivojac P. and Rost B., (2013) ISCB Computational Biology Wikipedia Competition. PLOS Computational Biology 9(9), e1003242.

[2] Kilpatrick A.M., (2016) The 5th ISCB Wikipedia competition: coming to a classroom near you? PLOS Computational Biology 12(12), e1005235.

[3] Logan D.W., Sandal M., Gardner P.P., Manske M., Bateman A., (2010) Ten Simple Rules for Editing Wikipedia. PLOS Computational Biology 6(9): e1000941

[4] Wodak S.J., Mietchen D., Collings A.M., Russell R.B. and Bourne P.E., (2012) Topic Pages: PLoS Computational Biology Meets Wikipedia. PLOS Computational Biology 8(3): e1002446.

[5] Welch L., Brooksbank C., Schwartz R., Morgan S.L., Gaeta B., Kilpatrick A.M., et al. (2016) Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCB's Education Committee). PLOS Computational Biology 12(5): e1004943.

ISCB COMMUNITY JOURNAL UPDATE

The ICJ continues to embrace open science publishing and provides the ISCB community 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.

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.

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 over the past few months:

Optimal threshold estimation for binary classifiers using game theory [version 3; referees: 3 approved]: https://f1000research.com/articles/5-2762/v3.

Transcription factor motif quality assessment requires systematic comparative analysis [version 2; referees: 2 approved]: https://f1000research.com/articles/4-1429/v2.

Over the next few months the ICJ will look forward to hosting published papers and conference presentations from the COSIS, ISCB conferences and the ISCB Student Council. 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 (23) at ISMB 2017 or email us anytime at research@f1000.com.

RSG WITH DREAM 2017

RECOMB/ISCB CONFERENCE on REGULATORY & SYSTEMS GENOMICS with DREAM CHALLENGES

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

NOVEMBER 19-21, 2017 NEW YORK, NY

DETAILS

WHEN

NOVEMBER 19-22, 2017

WHERE

MEMORIAL SLOAN KETTERING
CANCER CENTER

417 E 68TH STREET
NEW YORK, NY 10065

MORE INFO

www.iscb.org/recomb-regsysgen2017

SUBMIT TODAY!

SUBMISSION DEADLINES

Oral presentations & Posters
September 17, 2017
Late Breaking Posters
October 9, 2017

The premier meeting for computational and experimental scientists in regulatory genomics and systems biology!

NEWS FROM THE ISCB STUDENT COUNCIL

By: Dan DeBlasio (SC Representative to the ISCB Board of Directors), Farzana Rahman (SC Chair), Nazeefa Fatima (SC Vice Chair), Gonzalo Parra (SC Secretary), Aishwarya Alex (SC Treasurer), and Sayane Shome (RSG Chair)

The ISCB Student Council (SC) is the student organization within the ISCB. Our mission is to promote the development of the next generation of computational biologists, particularly students and early career researchers in our community. We serve our members by organizing scientific events, offering networking opportunities, softskills training, educational resources, and career advice, while attempting to influence policy processes affecting science and education. Our Student Council Symposium (SCS) series has become our most useful tool in fulfilling our mission. As you will read below, our flagship event at the ISMB continues this year with our 13th SCS. We also organize continental symposia like the European SCS, Latin America SCS and SCS Africa that constitute satellite events to their corresponding continental ISCB conferences, namely ECCB, ISCBLA and ISCB Africa, respectively.

Anne-Claire Martines presents her research to the group of students and postdocs gathered for ESCS 2016 in The Hague

In addition to having a presence at international meetings, the SC has a widespread network of Regional Student Groups (RSGs) around the world; these groups continue our mission on a more local scale. To find out more information about RSGs in your region and upcoming regional events visit our poster in the education section or go to rsg.iscbsc.org.

The Education and Internships Committee within the SC also organizes the highly successful ISCB SC Internships Program. Since 2009 we have helped organize 8 internships with labs in Europe and Australia. We are always looking for participants (both principal investigators and interns) so come find us at our poster or internships.iscbsc.org if you're interested in an internship or just want to know more.

Our members can be found throughout the halls of this week's ISMB/ECCB meeting, make sure you find us and let us know how we can further our mission in creating opportunities for students and researchers or ask us how to get involved. After ISMB/ECCB 2017, don't forget to connect with the Student Council on our website (iscbsc.org) and social media (Twitter: @iscbsc & Facebook: /iscbsc); our main resources for staying in touch with the global computational biology student community. More information about the SC can also be found on Wikipedia [1] (where we welcome your help in keeping our entry up to date).

Student council social events like the one at SCS 2016 in Orlando help to establish robust professional networks

Students were highly engaged with the talks at ESCS 2016 in The Hague

We encourage you to get in touch with your peers to find out about events and initiatives for computational biology students — no matter where in the world you are. If you would like to volunteer in our activities please register at volunteer.iscbsc.org or visit our booth 27!

STUDENT COUNCIL SYMPOSIUM 2017

The ISCB Student Council Symposium is our flagship event. This annual gathering brings together researchers from all subfields of Computational Biology. Organized by student volunteers from all over the world, the event provides, for many, a first opportunity to present their work to an international audience and to network with those that will become their peer and potential collaborators at later career stages.

This year marks the 13th edition of the symposium and we are pleased to be highlighting more than 20 presentations and over 80 posters representing a wide variety of topics from over 38 countries! Our delegates will also have the opportunity to hear from two wonderful and thought provoking keynote speakers: Prof. Christine Orengo (University College London) and Dr. Johannes Söding (Max Planck Institute for Biophysical Chemistry). We look forward to a great meeting on 21 July 2017.

ACTIVITIES AT ISMB/ECCB 2017

- **Student Council Posters** — Visit our posters presented at the ISMB/ECCB 2017.
    - ISCB Student Council Internships Program: Expanding Computational Biology Capacity Worldwide
    - ISCBSC Regional Student Groups: Connecting young computational biologists around the world.
- **Student Council Booth** — Visit the SC at Booth 27 to find more about us and our work!
- **Student Council Symposium** — The event will take place on Friday, July 21 (08:30 –18:00).
- **Student Council Social Event** — After the opening social, keep the conversation going at the Student Council Social Event, Friday July 21, starting around 20:00. Visit the SC booth during the opening reception to find out more.
- **Learning to Grow Your Academic Social Network (BoF B2)** — the Student Council is organizing a panel discussion about how to grow your network and what specific skills you may need when navigating academic and/or industrial career path. Join us Monday, 12:45 – 13:45 in Meeting Hall IV.
- **Job Posting Board** — Located next to the SC booth, you can come advertise your position or search for a job. We provide this service to connect job seekers with job advertisers at the ISMB/ECCB 2017.
- **Student Council Social HQ** — The SC members plan to have an informal gathering, every evening during the ISMB/ECCB 2017, to discuss the day's events. Come to the SC booth 27 to find out more.

---

[1] https://en.wikipedia.org/wiki/International_Society_for_Computational_Biology_Student_Council

MEET YOUR
ISCB BOARD OF DIRECTORS

EXECUTIVE OFFICERS & DIRECTORS

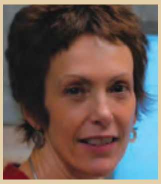
Alfonso Valencia, Ph.D.
President, ISCB
PROFESSOR
Spanish National Cancer Research Centre
SPAIN

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

Bonnie Berger, Ph.D.
Vice President, ISCB
Professor of Applied Mathematics and
Computer Science
MIT
USA

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

Janet Kelso, Ph.D.
Vice President, ISCB
Group Leader
MPI for Evolutionary Anthropology
GERMANY



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

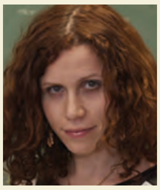
Bruno Gaeta, Ph.D.
Treasurer, ISCB
Senior Lecturer and Bioinformatics Program
Director
University of New South Wales
AUSTRALIA

Scott Markel, Ph.D.
Secretary, ISCB
Director, Life Sciences Modeling and
Informatics
Dassault Systèmes BIOVIA
USA

ISCB DIRECTORS

Alex Bateman, Ph.D.
Head of Protein Sequence Resources
EMBL- EBI
UNITED KINGDOM

Michelle Brazas, Ph.D.
Program Manager
Ontario Institute for Cancer Research
CANADA



Yana Bromberg, Ph.D.
Assistant Professor
Rutgers University
USA

Francisco De La Vega, Ph.D.
ISCB COSI Representative to the Board, ISCB
Consulting Professor
Stanford University
USA

Dan DeBlasio, Ph.D.
Student Council Representative, ISCB
Lane Fellow
Carnegie Mellon University
USA

Iddo Friedberg, Ph.D.
Academic
Iowa State University
USA

Paul Horton, Ph.D.
Senior Researcher
AIST
JAPAN

Nicolas Le Novere, Ph.D.
Senior Group leader
Babraham Institute
UNITED KINGDOM

Francisco Melo Ledermann, Ph.D.
Full Professor
Universidad Catolica de Chile
CHILE

Jill P. Mesirov, Ph.D.
Professor, Associate Vice Chancellor
UC San Diego
USA

Yves Moreau, Ph.D.
Professor
Katholieke Universiteit Leuven R & D
BELGIUM

Nicola Mulder, Ph.D.
Professor
University of Cape Town
SOUTH AFRICA

Predrag Radivojac, Ph.D.
Professor
Indiana University
USA

Burkhard Rost, Ph.D.
Professor
TUM Munich/Columbia Univ NYC
GERMANY

Reinhard Schneider, Ph.D.
Head of Bioinformatics Core Facilities
LCSB
LUXEMBOURG

Hagit Shatkay, Ph.D.
University of Delaware
USA

Lonnie R. Welch, Ph.D.
Stuckey Professor
Ohio University
USA

ISCB APPRECIATES THE SUPPORT OF OUR GENEROUS DONORS!

William McLaughlin
Gloria Franco
Daniel McSkimming
Jyothi Thimmapuram
Stephen Master
Colbie Reed
Farzana Rahman
Janos Binder
Deborah Chasman
Toni Kazic
Dan DeBlasio
Judith Blake
Brent Cochran
Lenore Cowen
Lorena Pantano
Gustavo Stolovitzky
Pier Luigi Martelli
Scott Markel
Bonnie Berger
Patricia Palagi
R. Taylor Raborn
Lukeman Shittu
Nancy Mah
Pierre Baldi
Clare Sansom
Prashanth Suravajhala
Jeffrey Fisk
Peter Ebert

UPCOMING EVENTS
OF INTEREST

5TH RECOMB SATELLITE WORKSHOP ON COMPUTATIONAL METHODS IN GENETICS

United States – CA – Los Angeles
Jul 27, 2017 through Jul 28, 2017

http://computationalgenomics.bioinformatics.ucla.edu

6TH RECOMB SATELLITE WORKSHOP ON COMPUTATIONAL CANCER BIOLOGY

United States – CA – Los Angeles
Jul 28, 2017 through Jul 29, 2017

http://computationalgenomics.bioinformatics.ucla.edu

INCOB 2017 (16TH INTERNATIONAL CONFERENCE ON BIOINFORMATICS)

China – Guangdong – Shenzhen
Sep 20, 2017 through Sep 22, 2017

http://datamining-web.it.uts.edu.au/bioinformatics/index.html

IV COLOMBIAN CONGRESS ON COMPUTATIONAL BIOLOGY AND VIII INTERNATIONAL CONFERENCE SOIBIO 2017

Colombia – Santiago de Cali
Sep 13 through 15, 2017

http://ccbcol.org/

INDIAN CONFERENCE ON BIOINFORMATICS 2017 (INBIX'17)

India – Rajasthan – Jaipur
Nov 07, 2017 through Nov 09, 2017

http://www.inbix.bioclues.org

PACIFIC SYMPOSIUM ON BIOCOMPUTING (PSB)

United States – HI – Kohala Coast
Jan 03, 2018 through Jan 07, 2018

http://psb.stanford.edu/

BIOSTEC'18: INTERNATIONAL JOINT CONFERENCE ON BIOMEDICAL ENGINEERING SYSTEMS AND TECHNOLOGIES

Portugal – Funchal, Madeira
Jan 19, 2018 through Jan 21, 2018

http://www.biostec.org/

INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

www.iscb.org
CONNECTING, TRAINING, EMPOWERING, WORLDWIDE