ISCB Newsletter

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CONFERENCE PROGRAM

CONTENTS

INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
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Featuring the
ISMB 2018
Conference Program

LETTER FROM THE EXECUTIVE DIRECTOR

Dear Members and Colleagues,

As ISCB enters its 21st year being your professional society of choice, I would like to take a moment to welcome our seventh Society president, Thomas Lengauer. Thomas started his three-year term as president on January 21, 2018. Welcome, Thomas! I personally look forward to working with Thomas and am excited to be under his leadership. I would also like to recognize and thank Alfonso Valencia for his leadership and guidance over the course his presidency. Alfonso led with grace and an innovative spirit and we are grateful for his service.

Over the last 21 years, ISCB has grown as an organization. We now have over 3,300 members from 80 plus countries. We continue to strengthen our conference series offering our members and the greater bioinformatics community a platform to present their research, and look for more ways to provide forums for discussion and collaboration. I like to think of us as the little society that could. Each and every year, the many volunteers that are the life-blood behind the organization strengthen who we are as a professional society and greatly impact the scientific community at large. There has been no task too large or difficult and I am honored and appreciative for the daily opportunity of working with so many passionate, dedicated individuals.

At this year's ISMB, we have continued the streamlined thematic organization of our scientific program. We have also added two new Communities of Special Interest (COSIs) - MLCSB: Machine Learning in Computational and Systems Biology and EvolCompGen: Evolution & Comparative Genomics. We hope you find the organization of the program easy to navigate and filled with many opportunities to learn and network.

The ISCB COSI program is designed to foster topically-focused collaborative communities wherein scientists communicate with one another on research problems and/or opportunities in specific areas of computational biology. Conference tracks at ISMB or other ISCB conferences are just one way of offering a forum for these discussions. Many of our COSIs have online groups that allow for continued interaction and collaboration throughout the year. If you haven't found your COSI home yet, I encourage you to take some time to explore the established COSIs. If you find that we are missing an area, please let us know. I would like to thank all of the COSIs leaders for your time, energy, and collaborative spirit as we continue to grow and development this societal program.

If you are attending ISMB 2018 in Chicago, please plan to join us for the ISCB Town Hall, Sunday, July 8 (12:45 PM - 1:45 PM). During this session, you will get to learn a little bit more about our programs as well as new plans and initiatives. We will also celebrate some of our Society achievements. I hope to see you there!

As always, thank you for your continuous support of our Society. We are honored to serve you!

Sincerely

Diane E Kovats

Diane E. Kovats
Executive Director

GET TO KNOW YOUR PRESIDENT
THOMAS LENGAUER

1. CAN YOU TELL US A LITTLE ABOUT YOURSELF AND YOUR BACKGROUND?

I grew up in postwar West-Berlin and studied mathematics in Berlin and Computer Science in Stanford. In the seventies I mostly did research in Theoretical Computer Science. In the eighties I worked on design automation of integrated circuits as a professor of the University of Paderborn, Germany, and in a collaboration with Nixdorf Computer Company, then one of the largest German computer companies. In the beginning of the nineties I moved to the German National Research Center for Information Technology (GMD) in Sankt Augustin near Bonn, Germany, and began my work in computational biology, first on protein structure prediction and protein-ligand docking. In the latter field we developed the first program (FlexX) which could dock fully flexible ligands into protein pockets in a few minutes and were thus able to screen through large ligand libraries. In 2001 three scientists in my lab and I founded the company BiosolveIT GmbH based on our software developments in Computational Chemistry. Around the turn of the millennium I moved to the Max Planck Institute for Informatics in Saarbrücken where a Center for Bioinformatics had been founded together with Saarland University and we started research on computational analysis of viral drug resistance. In collaboration with German (Arevir) and European (Euresist) consortia, my lab developed the software suite geno2pheno which estimates viral resistance based on viral genotype and suggests combination drug therapies based on a data mining paradigm. The server offers analysis of data for the viruses HIV (causing AIDS), HBV (causing hepatitis B) and HCV (causing hepatitis C) and is used to customise treatment plans for patients. Our work is one of the most prominent examples of personalized medicine that has entered the clinic. Around 2004 we entered the field of computational epigenetics and since then we have developed frequently used software for low-level and high-level analysis of epigenomic data (BiQAnalyzer Suite, RnBeads software and more).

I have held several offices in science, such as with the German Informatics Society (GI) (Vice President 1994-1995), with the German National Academy of Sciences Leopoldina (Chair of the Section of Information Sciences 2006-2015, Speaker of the Class of Mathematics, Science and Technology 2013-2016, and Member of the Council since 2015). I cofounded the conference series ESA (European Symposium on Algorithms, 1993), RECOMB (Conference on Research in Computational Biology, 1997) and ECCB (European Conference on Computational Biology, 2002). I am a founding member of ISCB and have had numerous roles in the Society since its inception, among them Scientific Chair of ISMB 1999 in Heidelberg and ISMB/ECCB 2007 in Vienna, member of the Board of Directors, Chair of the Awards Committee and Vice President of the Society.

2. HOW HAS THE FIELD OF COMPUTATIONAL BIOLOGY AND BIOINFORMATICS CHANGED FROM WHEN YOU ENTERED THE FIELD TO NOW?

I decided to enter the field practically as the decision to sequence the human genome was taken. This was early. I formed my first lab nine years before the human genome was published. At the time there was very little molecular data compared with today, both in volume and in variety. We were basically dealing with partial genomic sequences and with a few hundred protein structures. This is also why the first problems we tackled were based on such data: protein structure prediction and docking. The computational biology communitywas very small. Everybody knew basically everybody. However, there was little recognition among our colleagues, either from the methodical or from the biological disciplines. Many people just did not expect the field to grow into anything. Biology was not very quantitative and there was widespread conviction that the data would be too cryptic to be successfully analyzed. Also, research in the field was mostly hypothesis-driven, manual and directed at elucidating causality. The data avalanche and the accompanying development of the field of computational biology turned biology into a quantitative discipline, rendered systematic cell-wide data collection a strong competitor of local and confined analysis and demonstrated the power of associative analysis which affords prediction without necessarily facilitating understanding of causal relationships.

In the past thirty years, the field has blossomed and grown tremendously. The process can be compared to the development of a multicellular organism from the oocyte to the fully differentiated assembly of tissues. This kind of differentiation has happened in our field, regarding data, methods, applications and communities. I consider having been part of this process a great privilege and I believe it was a great source of excitement for all of us.

3. HOW HAS THE SOCIETY HELPED TO GROW THE FIELD?

By fostering communication and exchange. The ISCB community grew out of an artificial intelligence core. This is still reflected by the title of our flagship conference, “Intelligent Systems for Molecular Biology” (ISMB), which Larry Hunter founded in 1993. Today, with the revival of AI in everybody’s mind the title is actually again becoming increasing reflective of much of the content of the conference and is becoming more explanatory to the world than it used to be. It is thereforegood that we stuck to it in the times when the diversification of the field seemed to outgrow it. Anyway, from this AI core the society reached out quickly to the statistical and algorithmic folks on the methodical side and, above all, to the diverse fields in the life sciences. In the early years of ISMB, when computational biology had not that much tradition to show yet and the interdisciplinary expertise of the initially methodically centered community had to be fostered, the keynotes of ISMB were mostly given by stellar researchers from the field of biology. Only after about 15 years of the conference could we change the profile of the keynotes to include more computational biology. This is only one aspect in which ISCB helped uplift the interdisciplinary expertise of the scientific community to which it caters. I believe that this process also helped to give the field an impressive coherence.

Among my informatics colleagues I am frequently envied for being in a field that emerged so quickly to high relevance and that still gained such a strong coherence and feeling of identity. There is not much dissent or discussion on what computational biology does and where it begins and ends. All this has become sort of self-evident. And the questions about its relevance have subsided with the advent of the human genome sequence and the avalanche of gene expression data. This is not so in a number other emerging fields in informatics, some of which disappeared – at least from view – some time after their celebrated appearance. Computational biology is not in this danger. Even though external forces, such as the technical revolution in molecular biology have been major drivers, I believe that ISCB has helped form this identity.

4. WHAT IS YOUR OPINION OF THE PROGRAMS OFFERED BY ISCB?

ISCB was founded to provide a stable base for organizing the ISMB Conference and, I think, ISMB is still ISCB's premier offer. We have tried carefully to develop the conference according to the needs of the computational biology community and there have been a couple of major changes in the conference profile over the years. We continue to keep our ears open and sense needs and desires of the community regarding the conference.

As the Society developed many other programs were added. I think the Fellows and Awards programs are important for providing profile to the community and increasing the standing of the field in the international scientific landscape.

Communities of Special Interest (COSIs) - groups which represent the diverse research themes/interests within our community - have become an increasingly important aspect of ISCB. The latest renewal of the ISMB structure which happened a couple of years ago strengthened the role of the COSIs in the conference and was a step towards making ISCB more coherent while preserving the identities of these groups of special interest.

Our association with premier computational biology journals has also changed over time. We can develop the journal program further – in order to increase the visibility of the society and for the benefit of our members – and there is a continuing discussion of how to do so.

A lot of effort has gone into the development of our website and I am very happy with the multitude of offers members and visitors can find there.

We are spending much thought on how to strengthen the global representation of ISCB, and how best to help developing regions around the world foster the field. The ISCB-X conferences and the regional groups are indications of this effort.

5. WHAT DO YOU BELIEVE IS THE KEY TO THE SUCCESS OF ISCB

ISCB represents a field that has become a pillar of modern life sciences. This is the major external driver of success. Internally, the society was founded at the right time, when the field was still emerging and has continually embraced new developments and communities as the field grew and diversified. Currently we are trying hard to strike the right balance between the different identities of the subcommunities in the field targeted to specific research areas and a common unity representing the field of computational biology, as a whole.

6. WHAT OTHER SOCIETIES ARE YOU A MEMBER OF AND WHAT DO THEY DO WELL?

I am a member of ACM, the premier informatics society of the world. They do a lot of things well and can serve as a role model for ISCB in many aspects. Actually, we are cooperating with ACM and intend to intensify the collaboration in the future. I am also a member of the German Informatics Society (GI) and was their Vice President in 1994-1995. They are the premier informatics society in Germany with around 20,000 members and have increasingly reached out to their non-academic membership in recent years with great web offers.

7. DO YOU HAVE SPECIFIC GOALS FOR THE SOCIETY?

Overall I feel that ISCB is on a good path. Strengthening the involvement of the membership in the activities and further development of the society and increasing communication bandwidth horizontally and vertically will be goals for the coming years. Participation in the ISCB committees and taking responsibility of programmatic elements in the conferences organized by ISCB are good entry points of member involvement. As the field develops further the society will also have to increasingly address medical and especially translational issues. Also, intensifying our relationship with industry while staying independent is an important issue. Our existing and published ethical code is a good basis for delineating this process. Furthermore, we need to further strengthen the international base of ISCB by fostering regional groups and continuing to develop the ISCB-X conferences.

Membership retention is a big issue. While the field of computational biology is clearly defined it is situated between disciplines, and scientists tend to see their primary home in one of the more monodisciplinary societies, be it on the methodical or on the application side. This leads to members floating in and out of ISCB. The Society will be more stable if we can manage to have sustained support by our members. I believe that this is only partly possible via tangible benefits offered by the society. A substantial part is fostering the feeling of belonging to the computational biology community as a premier home for the members. We are discussing what this entails and how it can be managed.

2018 ISCB OVERTON PRIZE
COLE TRAPNELL

Each year the International Society for Computational Biology (ISCB) 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, a respected computational biologist and founding ISCB Board member. The Overton Prize recognizes 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. Cole Trapnell, Assistant Professor of Genome Sciences at the University of Washington as the 2018 winner of the Overton Prize. Trapnell will be presenting a keynote presentation at the 2018 International Conference on Intelligent Systems for Molecular Biology in Chicago, Illinois being held from July 6-10, 2018.

COLE TRAPNELL: BUILDING BRIDGES TO THE LAB BENCH

Cole Trapnell's earliest interest in science began at home. He was born in Cheverly, MD and spent his childhood living in College Park, right near the University of Maryland. His father, Bruce Trapnell, is a physician scientist, and Cole has fond memories of accompanying his father to the lab. Beyond the hands-on experiences of doing restriction digests with his dad as young child, Trapnell most appreciates how his father encouraged him to think scientifically. He recalled, "One time we were playing a board game, and I remarked that because the last dice roll was a six, the next one wouldn't be. My dad decided to correct my thinking, so the next thing I knew, we were flipping a penny 1,000 times to estimate the probability distribution of getting heads vs. tails. I still have the plot that we drew by hand on 1mm graph paper."

Trapnell was first interested in physics and abstract mathematics and was drawn to how these fields tackled complex ideas in terms of "first principles." He began learning programming as a high school student and worked as a student engineer on a robotics project for the US Army. Trapnell honed his coding skills as an undergraduate by working for a startup that developed software for the areas of retail stock, futures and foreign currency trading, and he learned how to develop tools that can do complex calculations with large amounts of data in real time. He completed a dual BS degree in computer science and mathematics at the University of Maryland, College Park in 2005 and then began his PhD in computer science there as well. Trapnell thought he would work on problems in supercomputing, but then he took Steven Salzberg's class on bioinformatics. This brought his attention to the emergence of "next-generation" sequencing technology, and he realized the potential for high throughput computing to handle this sequence data.

Trapnell's PhD research focused on sequence alignment, and he adapted the Bowtie algorithm developed by Ben Langmead into a program called TopHat that could handle transcriptomic data. During this time, Trapnell moved to the University of California, Berkeley, where his wife was pursuing her PhD in mathematics, and he started working with Lior Pachter, who became his co-advisor with Salzberg at UMD. As Trapnell developed TopHat and the companion tool, Cufflinks, he tested them with datasets from Barbara Wold's lab, and he began to develop an appreciation for biological questions, especially in gene regulation. Trapnell was drawn to doing bench research, and his labmate Rob Bradley encouraged him to take that leap. He recalled, "Rob Bradley convinced me that to become a really good biologist, I should learn to do experiments. Rob, who trained as a biophysicist, had gone off to do a postdoc at the bench. I followed suit and joined John Rinn's lab (at Harvard University), where I worked to both do experiments and analyze them myself." Trapnell's time in Rinn's lab not only helped him get his hands dirty doing bench research, but gave him the unique perspective of working under a scientist who pioneered the field of long noncoding RNAs.

Trapnell's postdoctoral training opened his eyes to the realities of experimental biology and he acknowledges that these experiences have made him a better computational biologist. While Cufflinks could help him predict which individual splice isoforms may be elevated under certain disease conditions, he came to realize how hard it can be to validate these observations at the lab bench: a specific antibody may not exist for a western blot or technical difficulties may make it difficult to knock down a gene isoform in a particular model system. Trapnell had to adjust to the different culture associated with working in a wet lab. He recounted, "Computational people are often mystified and frustrated by how often their experiments fail. I like to tell them a story of my own frustration: A little while after starting my wet lab postdoc training, I was complaining to my labmate, Dave Hendrickson, that my experiments were constantly failing. He asked me how long I'd been at it, and I told him about six months. He said, "Well, give it another six months." I thought he meant I would get better at doing experiments but what he actually said next was, "It'll hurt less when they don't work." This was a tremendously eye opening thing for me, because he was trying to tell me that being an effective experimentalist means anticipating failure, planning for it, designing controls that can detect it, and parallelizing work within projects so that you can make progress in one direction even when you're stuck in another. There are similar cultural differences that experimentalists encounter when learning to program." As a PI, Trapnell is supportive of students and trainees that want to gain both experimental and computational experience, but he wants to them to learn to understand the culture of these two realms and not just acquire the necessary skills to do experiments or develop algorithms.

Throughout his training, Trapnell has valued the guidance of his mentors. His current lab is positioned between the labs of Stan Fields and Bob Waterson, both leaders in the field of genomics, and they been invaluable advisors to Trapnell. He said, "Despite their fame and their busy lives, both go way out of their way to advise me on how to bring my research and lab to its potential." All of his mentors have inspired Trapnell to build a lab culture that encourages open, inspiring and rigorous science. As he established his own lab at the University of Washington, he has started to think differently as a PI and said, "I am continually faced with the question: What do I think is the most important scientific contribution I can make?"

Shifting his mindset has been a challenge, but he is still broadly interested in gene regulation, especially gaining a more quantitative understanding of the epigenome. Trapnell considers the advances in single-cell measurements as critical to quantifying aspects of gene regulation, and his team is developing tools for single-cell measurements of gene expression, chromatin accessibility, and other features of the molecular state of the genome. Much of this work is in collaboration with Jay Shendure, whose lab specializes in molecular biotechnology development. Trapnell is keen on this collaboration: "Jay and I have very different approaches but share a common goal to transform our understanding of development and disease using single-cell technologies. Our collaboration has been fantastically productive and fun so far, and there's a lot more to come."

Trapnell is deeply honored to selected for the Overton Prize, and said, "I feel strongly that my success is at least as much a product of my being in the right place at the right time with the right collaborators as from any choices I made. I have been repeatedly given great opportunities and I've tried to make the best use of them, but I would have gotten nowhere if not for the generous help and creativity of a long list of mentors, collaborators and colleagues."

2018 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD
RUTH NUSSINOV

by Christiana N. Fogg[1], Diane Kovats[2*], Ron Shamir[3]

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Each year, the International Society for Computational Biology (ISCB) recognizes a leader in the fields computational biology and bioinformatics with the Accomplishments by a Senior Scientist Award. This is the highest award bestowed by ISCB in recognition of a scientist's significant research, education, and service contributions. Ruth Nussinov, Senior Principal Scientist and Principal Investigator at the National Cancer Institute, National Institutes of Health and Professor Emeritus in the Department of Human Molecular Genetics & Biochemistry, School of Medicine at Tel Aviv University, Israel, is being honored as the 2018 winner of the Accomplishment by a Senior Scientist Award. She will receive her award and present a keynote address at ISCB's premiere annual meeting, the 2018 Intelligent Systems for Molecular Biology (ISMB) conference in Chicago, Illinois, being held on July 6–10, 2018.

RUTH NUSSINOV: IN SEARCH OF BIOLOGICAL SIGNIFICANCE

Ruth Nussinov (Fig. 1) is a computational biologist with research interests that have touched every aspect of the field, from her PhD research on RNA secondary structure prediction to her visionary work on DNA sequence analysis, to proposing that all protein (and other biomacromolecules) conformations preexist and that all dynamic proteins are allosteric, to her current studies focused on Ras signaling in cancer. Nussinov's deep intellectual curiosity has guided her research interests throughout her career.

Fig. 1. Prof. Ruth Nussinov: Cancer and Inflammation Program, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research, National Cancer Institute at Frederick, Frederick, Maryland, United States of America. Sackler Institute of Molecular Medicine, Department of Human Genetics and Molecular Medicine, Sackler School of Medicine, Tel Aviv University, Tel Aviv, Israel

Nussinov was raised in Rehovot, Israel, and attributes her early interest in science to watching her father conduct pioneering agricultural research that focused on adapting crops to the Israeli climate [1,2]. Nussinov's father, Shmuel Hurwitz, was born in Minsk, Russia, and studied chemistry at Moscow University but later immigrated to Palestine (present-day Israel) after his arrest for Zionist activities. It was here he discovered the great need for agricultural research. He pursued these studies at Berlin University but left Nazi Germany after his graduation in 1933 to found the Agricultural Research Station in Rehovot. Hurwitz was a founding member of the Faculty of Agriculture at the Hebrew University and was recognized for his significant contributions to advancing Israel agriculture with the 1957 Israeli Prize. As a child, Nussinov often joined her father on trips to his field sites, and his devotion to research and intense work ethic influenced her deeply and shaped how she approaches her work.

Nussinov also attributes her success as a scientist to the unwavering support from her husband, Shmuel Nussinov. They married just after she completed her service in the Israeli Army, during which time he was pursuing his graduate studies in particle physics at the Weizmann Institute. Her husband's research advisor moved to the University of Washington, so Nussinov continued her undergraduate studies there (in microbiology) and went on to pursue her master's degree in biochemistry at Rutgers University while her husband pursued postdoctoral research at Princeton University. They returned to Israel when Shmuel Nussinov joined the faculty at Tel Aviv University. When they came back to the United States several years later for his sabbatical, Ruth Nussinov enrolled in a PhD program in biochemistry at Rutgers and was mentored by a newly arrived assistant professor named George Pieczenik who had just come from Cambridge (United Kingdom). Nussinov recalled, "He said, 'You know Ruth, Fred Sanger has just developed a DNA sequencing method and consequently there will be RNA sequences, and we will need an algorithm for the prediction of the secondary structure of RNA.'" She ran with this idea and worked tirelessly to develop the foundational Nussinov dynamic programming algorithm that is still in use today [3]. Nussinov's PhD research has driven her career-long search for questions that tackle issues of biological significance. She worked relatively independently on her project and was able to graduate in two years, and this early autonomy was critical to shaping her career path as an independent researcher.

Nussinov and her family returned to Israel, and she pursued postdoctoral studies in the Structural Chemistry Department of the Weizmann Institute and made several seminal contributions to DNA sequence analysis. She also worked as a visiting scientist in the Chemistry Department at the University of California, Berkeley, and in the Biochemistry Department at Harvard University. In spite of her impressive body of work and concept-driven approach to scientific inquiry, Nussinov faced difficulties in securing a position at Tel Aviv University in the mid-1980s due to her husband's existing position at the university and her unconventional, independent career path [4]. In 1985, Nussinov was finally appointed as an associate professor at Tel Aviv University and also became affiliated with the National Cancer Institute (NCI)/National Institutes of Health (NIH). During these early years, she credits her husband for giving her valuable advice about handling criticism from manuscript reviewers. He urged her to trust in her work and to reflect on and revise her manuscripts and resubmit them, as publications matter to the progress of a junior and unknown scientist [2].

One of Nussinov's most profound contributions to the field is the "conformational selection and population shift" model of molecular recognition [5-9]. She and her colleagues first proposed this model in 1999 as an alternative paradigm to the "induced fit" model of protein–protein interactions. The induced-fit model hypothesizes that conformational changes to a protein occur in a stepwise fashion upon binding to a ligand. In contrast, the conformational selection model portends that unbound molecules exist in all possible structural conformations, but some unbound higher-energy conformations preferentially associate with a binding partner and cause a shift in equilibrium that favors this conformation. This model can explain numerous interactions observed for protein–ligand, RNA–ligand, protein–protein, protein–DNA, and protein–RNA interactions and can explain mechanisms of biological regulation, including oncogenic signaling.

Nussinov is currently focused on the Ras protein and its interactions with effectors, with a particular interest in KRAS-driven adenocarcinomas. She observed that self-association of GTP-dependent K-Ras dimers at different interfaces regulates which effectors bind to the dimers, which can alter downstream activity [10]. Nussinov and her team have also described the critical role of calmodulin selectively binding to the GTP-bound K-Ras4B oncogenic isoform, which promotes the initiation and progression of adenocarcinomas due to full activation of PI3Kα/Akt signaling in addition to the mitogen-activated protein kinase (MAPK) pathway. These mechanistic insights are critical to developing better cancer drugs, and this work was recognized in the "Best of the AACR Journals Collection 2015." Nussinov is also starting to explore interactions between the human proteome and pathogens, given the growing appreciation of the microbiome on human health.

Nussinov's impact to the fields of computational biology and bioinformatics is notable. She has published more than 500 articles and has been ranked as a Highly Cited Researcher (ranking among the top 3,000 researchers or 1% across all fields according to Thomson Reuters Essential Science Indicators, http://highlycited.com/ December 2015) with more than 43,000 citations to date. Nussinov has also given over 300 invited talks and continues to maintain an active speaker schedule.

Nussinov serves as the Editor-in-Chief of PLOS Computational Biology, and she has also served as an editor and reviewer for numerous leading journals. Her scientific contributions have been recognized through her election as a Fellow of the Biophysical Society (2011) and an ISCB Fellow (2013). Nussinov has been a devoted mentor and advisor to graduate students and trainees throughout her career, and she has mentored dozens of PhD students, including numerous women. She has tried to model her mentorship to how she was trained, and she said, "I very much encourage independence and like for students to suggest a problem to study."

Nussinov has always felt a close connection with ISCB, and her recognition with the 2018 ISCB Accomplishments by a Senior Scientist Award is a fitting tribute to her contributions to ISCB and to computational biology in general. She said, "I feel that's where I belong and that's where I want to be. I care very much about the development and sustainability and contribution of computational biology to all biological, chemical, and physical sciences."

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2017 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD
RUSS ALTMAN

The Outstanding Contributions to ISCB Award was introduced in 2015 to recognize Society members who have made lasting and beneficial contributions through their leadership, service, and educational work, or a combination of these areas. Russ Altman, Kenneth Fong Professor and Professor of Bioengineering, of Genetics, of Medicine (General Medicine Discipline), of Biomedical Data Science, and, by courtesy, of Computer Science, is the 2018 winner of the Outstanding Contributions to ISCB Award and will be recognized at the 2018 Intelligent Systems for Molecular Biology (ISMB) meeting in Chicago, Illinois being held on July 6 - 10, 2018.

RUSS ALTMAN

Altman's years of dedicated service to ISCB began when he attended the very first ISMB meeting in 1993. As a brand new faculty member, he remembered how he felt at home at ISMB, surrounded by a community of scientists also interested in computational biology and bioinformatics. Altman's enthusiasm at this first ISMB meeting led him to help organize the next ISMB meeting. He recalled, "It became clear that there was no obvious "host" for ISMB 1994, so I volunteered to host it at Stanford, where we had a lovely meeting with a couple of hundred people. We had some extra money after paying our bills, so we wanted to send the money to wherever ISMB 1995 was going to be (UK). For the first few years, this is how ISMB worked—the organizers from one year would send the leftover funds as a seed for the next ISMB. There was no organization, and as the size of the leftover check increased, we started getting nervous and realized we needed to create a legal entity."ISCB was born at ISMB 1997 in Halkidiki, Greece, where organizers of former ISMB meetings and others sat at dinner on the beach and planned the society and figured out how to incorporate it. Altman has warm recollections of that historic gathering and said, "There are pictures of that great dinner and group, and I treasure the memory of that meeting."

Altman has enjoyed serving ISCB at all levels since its inception, from work on the Publications Committee and as a conference organizer, to his tenure on the ISCB Board of Directors (1997-2005) and as ISCB President (2002-2005). Altman's early work on the Publications Committee included applying for PubMED to index the ISMB proceedings, which was a critical step in helping ISCB members receive academic credit for their conference papers. Altman also helped negotiate the agreement to have Bioinformatics named as an official ISCB journal. Beyond ISMB, Altman has been an organizer of the Pacific Symposium on Biocomputing, and has facilitated the relationship between this conference and ISCB.

As computational biology and bioinformatics have grown into stand-alone fields, Altman has made many critical scientific contributions through his research. Altman and his research group have developed numerous computational tools that address problems in basic biology and medicine, with a particular interest in understanding drug responses. His work has included studies of structure-function relationships in macromolecules, understanding RNA structure and folding, and assessing drug responses at the molecular, cellular, organismal, and population levels.

Altman believes that it is critical to bring awareness to the greater scientific community that computational biologists and bioinformaticians are more than just great collaborators, but they also lead major research projects. He considers service to ISCB as a way established PIs, junior faculty, and trainees can help bring about this awareness to advance the field. Altman considers ISCB to be a community that provides both valuable service opportunities and sources of mentorship and collaboration for scientists.

Altman's dedication to the field computational biology has been recognized by his election as an ISCB Fellow (2010), as well as with numerous other honors, including election as a member of the National Academy of Medicine (formerly the Institute of Medicine, 2009) and a Fellow of the American Association for the Advancement of Science (2014). Altman has also worked as an editor and reviewer for numerous scientific journals, including serving as Co-Editor-in-Chief of the Annual Review of Biomedical Data Science.

Altman's many years of service to ISCB have been critical to the very formation and evolution of the Society from its infancy as a small meeting to the globally recognized professional organization that it is today.

M. MADAN BABU

The ISCB Innovator Award 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 of computational biology. The 2018 winner is Dr. M. Madan Babu, Programme Leader at the MRC Laboratory of Molecular Biology, Cambridge, UK. Madan will receive his award and deliver a keynote presentation at the 2018 International Conference on Intelligent Systems for Molecular Biology in Chicago, Illinois being held on July 6-10, 2018.

M. MADAN BABU: PEERING INTO THE REALM OF REGULATION

M. Madan Babu is the head of the Regulatory Genomics and Systems Biology group at the MRC Laboratory of Molecular Biology, Cambridge, UK. His work focuses on understanding how cellular systems are regulated at different scales (molecular, systems, and genomic levels) and how this impacts genome evolution.

Madan grew up in Chennai, India and developed early interests in computer science and biotechnology. As a young child, he has vivid memories of his father bringing home a personal computer, and soon after he became interested in learning to program. He also remembers when his family first started using the internet, and recalled, “In the mid-90’s, we started having access to the Internet. This made a big difference in the days where access to information beyond textbooks was not readily available; so thanks to my father I had these opportunities early in my life.” Madan discovered biotechnology as a high school student, and attributes his lifelong interest in biology to the impact of his biology teacher, Dr. M.C. Aruna, who discussed foundational biological concepts with him, including how genetic information can be used to understand living systems.

Madan went on to pursue a Bachelor of Technology (Biotechnology) degree at Anna University, Center for Biotechnology in Chennai, India. He first became of aware of computational biology during his first year undergraduate research internship, at which time he was exposed to the work of Cyrus Chothia and Arthur Lesk in a course on protein structure. He became fascinated with this research area and then delved into seminal papers on computational genomics, protein engineering, and structural bioinformatics. As an intern, Madan pursued undergraduate research under the guidance of Prof. Balaram and Prof. K. Sankran, and saw this a key turning point in his career path. He recollected, “We started applying methods from computer science to study protein sequences and structures. For the first time, I experienced how to define a scientific problem, develop computational methods to solve it, and write up and defend the findings for publication. This really got me excited and that was when I decided that I would like to pursue a career in computational biology.”

Madan recognizes that his interest in computational biology was fostered by his ability to access publicly-available protein and genomic data on his own computer, as well as the open access he had to lecture materials, methods and algorithms from computational biologists spanning the globe. He said, “I cannot forget the day when I wrote an email to RCSB from India and received a 5-part CD-ROM with coordinate data for all protein structures. Being able to look at protein structures using RASMOL from home and writing FORTRAN programs to analyze structures as an undergraduate student was one of the most exciting experiences that really captured my interest in the field.”

Madan left India in 2001 to pursue his PhD in computational genomics at the MRC Laboratory of Molecular Biology and Trinity College, University of Cambridge, UK under the guidance of Dr. Sarah Teichmann. His PhD research explored various aspects of gene regulatory networks, and marked the beginning of a very fruitful mentorship under Teichmann. Madan carried out his postdoctoral training at the National Center for Biotechnology Information, NIH in Bethesda, MD, USA under the guidance of Dr. L. Aravind, during which time he learned the importance of having broad interests in diverse subject areas as well as critically analyzing the complexity of biological systems at every possible level of detail.

After a brief but extremely productive postdoctoral fellowship, Madan became a group leader at the age of 26 of the Regulatory Genomics and Systems Biology Group at the MRC Laboratory of Molecular Biology in 2006. As a PI, he has come to appreciate how his team of scientists can work together to tackle scientific questions on a much larger scale and shed new light on long-standing, fundamental questions. He said, “One of the things that I really enjoy about the field of computational biology is that you really integrate knowledge from various disciplines-- biology, statistics, computer science, mathematics, physics and chemistry. This means our lab is an amalgamation of people across disciplines that are really passionate about using interdisciplinary approaches to solve the problems they are working on.”

Madan’s group currently focuses on several areas of research, including studies on G-protein coupled receptors (GPCRs), a protein family involved in almost every aspect of human physiology and targeted by numerous drugs. Madan’s group is also using a combination of computational and experimental approaches to discover which parts of unstructured protein regions are functional and understand what makes them functional. His group is interested in applying developments in statistical learning and advances in large-scale genome sequencing to better understand natural variation in the human population as well as gain insight into how genomic variation impact rare and common diseases.

Madan is greatly honored to be selected as the recipient of the 2018 ISCB Innovator Award. He is grateful for his academic mentors and colleagues, including Sarah Teichmann, L. Avarind, Cyrus Chothia, Michael Levitt, Veronica Van Heyningen, Eugene Koonin, Stephen Michnick, Richard Kriwacki, Uri Alon, Arthur Lesk, Alexey Murzin, Julian Gough, Daniela Rhodes, Gebhard Schertler, Peter Wright, Keith Dunker, Janet Thornton, Tom Blundell and Venki Ramakrishnan, who have inspired him through their work and/or provided him valuable advice at various stages of his career. He is also appreciative of his past and present group members, and the MRC Laboratory of Molecular Biology for the freedom to develop new skills and take risks in pursuing research that pushes scientific boundaries. Last but not least, he is grateful to his parents, sister, wife and 2-year old son for their love, support and inspiration.

ISMB 2018

CHICAGO JULY 6-10

CONFERENCE PROGRAM

ISMB 2018
CHICAGO JULY 6-10

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

Welcome to Chicago!

On behalf of the organizing committee of ISMB 2018 and the Board of Directors of the International Society for Computational Biology (ISCB), we wish you a very warm welcome to the conference and the vibrant city of Chicago. This large gathering promises to be the key meeting for computational biologists in 2018.

This year we build on the successful launch last year of a COSI-centric ISMB meeting. COSIs are Communities of Special Interest reflecting most of the major research themes and training in computational biology. We have expanded the number of COSIs to 18 ensuring greater coverage of ISMB by major computational biology themes, so that you can connect more easily to researchers sharing common interests and come together and listen to exciting new developments in your field. Building on the meeting last year, these communities will each run their respective sessions (COSI tracks or workshops) as part of the conference. 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 2018 ISCB award winners, will cover topics as diverse as: 25 years of human gene finding: are we there yet?; Reconstructing and deforming developmental landscapes; Transcription factors and cis-regulatory elements; How does protein disorder enable phenotypic diversity?; A woman's computational biology journey.

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 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. In addition, this year we add a new COSI in Machine Learning, which will present research in this major thematic area. 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 expansion in thematic areas increasing the diversity of options for you and the depth of presented research. We wish you a stimulating and productive time in Chicago.

The program includes

- 5 Keynote addresses, including our 3 2018 ISCB Award Winners
- 18 community-led COSI tracks and workshops
- 7 Special Sessions
- 2 Special Tracks by ELIXIR (EU Life Science Data Infrastructure) and BD2K (NIH Big Data to Knowledge Program)
- 15 Technology Track presentations
- The pre-conference Student Council Symposium organized by and for students
- 8 Pre-conference Tutorials

Equally as important, there are almost 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 2018.

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, Alfonso Valencia and Thomas Lengauer 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 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 Chicago for its welcoming hospitality and wish you all a great conference!

Yours sincerely,

Tandy Warnow
Tandy Warnow
Conference Co-Chair

Christine Orengo.
Christine Orengo
Conference Co-Chair

Gary D. Stormo
Gary Stormo
Honorary Conference Co-Chair

ISMB 2018 Committee Members

ISMB 2018 Conference Chairs

Gary Stormo, Honorary Conference Chair, Washington University Medical School in St Louis, United States

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

Tandy Warnow, Conference Co-chair, University of Illinois at Urbana-Champaign, United States

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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

Thomas Lengauer, President, ISCB, Max Planck Institute for Informatics, Germany

Alfonso Valencia, Past-President, ISCB, Barcelona Supercomputing Center, Spain

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Yana Bromberg, Rutgers University, United States

Predrag Radivojac, Indiana University, United States

Proceedings Area Chairs

Anna Goldenberg, University of Toronto, Canada (Studies of Phenotypes and Clinical Applications)

Carl Kingsford, Carnegie Mellon University, United States (Comparative and Functional Genomics)

Fran Lewitter, Whitehead Institute for Biomedical Research, United States (Bioinformatics Education)

Sriram Sankararaman, University of California, Los Angeles, United States (Genomic Variation Analysis)

Mihai Pop, University of Maryland, United States (Bioinformatics of Microbes and Microbiomes)

Nadia El-Mabrouk, University of Montreal, Canada (Population Genomics and Molecular Evolution)

Charlotte Deane, University of Oxford, United Kingdom (Macromolecular Sequence, Structure, and Function)

Roded Sharan, Tel-Aviv University, Israel (Systems Biology and Networks)

Haixu Tang, Indiana University, United States (Genome Privacy and Security)

Proceedings Area Chairs – COSI (Communities of Special Interest)

Rolf Backhofen, Albert-Ludwigs-University, Germany (RNA)

Jan Baumbach, TU Munich, Germany

Emidio Capriotti, University of Bologna, Italy (VarI)

Ana Conesa, Centro de Investigación Príncipe Felipe, Spain (HiTSeq)

Christophe Dessimoz, University of Lausanne, Switzerland (Evolution)

Jeremy Goecks, Oregon Health & Science University, United States (BioVis)

Paweł P Łabaj, Austrian Academy of Sciences and Jagiellonian University, Poland (CAMDA)

Florian Markowetz, University of Cambridge, United Kingdom (MLCSB)

Nicola Mulder, University of Cape Town, South Africa (Education)

Alice McHardy, Helmholtz Centre for Infection Research, Germany (Microbiome)

Natasa Przulj, University College, London, United Kingdom (NetBio)

Venkata Satagopam, Université du Luxembourg (TransMed)

Saurabh Sinha, University of Illinois at Urbana–Champaign, United States (RegSys)

Karin Verspoor, University of Melbourne, Australia (Bio-Ontologies)

Olga Vitek, Northeastern University, United States (CompMS)

Abstract Chairs

3DSIG: Structural Bioinformatics and Computational Biophysics

Phil Bourne, University of Virginia, United States

Charlotte Deane, Oxford University, United Kingdom

Rafael Najmanovich, University of Montreal, Canada

Bio-Ontologies

Michel Dumontier, Maastricht University, Netherlands

Robert Hoehndorf, King Abdullah University of Science & Technology, Saudi Arabia

Philippe Rocca-Serra, University of Oxford, United Kingdom

Karin Verspoor, University of Melbourne, Australia

BioVis: Biological Data Visualizations

Thomas Höllt, TU Delft, Netherlands

Michael Krone, University of Stuttgart, Germany

CAMDA: Critical Assessment of Massive Data Analysis

David Kreil, Boku University Vienna, Austria

Paweł P Łabaj, Austrian Academy of Sciences, and Jagiellonian University, Poland

CompMS: Computational Mass Spectrometry

Viktoria Dorfer, FH Hagenberg, Austria

William S Noble, U Washington, United States

Oliver Kohlbacher, U of Tübingen, Germany

Education: Computational Biology and Bioinformatics Education and Training

Nicola Mulder, University of Cape Town, South Africa

Russell Schwartz, Carnegie Mellon University, United States

EvolCompGen: Evolution & Comparative Genomics Evolution and Comparative Genomics

Lars Arvestad, Stockholm University, Sweden

Wataru Iwasaki, University of Tokyo, Japan

Function: Gene and Protein Function Annotation

Iddo Friedberg, Iowa State University, United States

Predrag Radivojac, Indiana University Bloomington, United States

Mark N Wass, University of Kent, United Kingdom

HitSeq: High Throughput Sequencing Algorithms & Applications

Can Alkan, Bilkent University, Turkey

Ana Conesa, University of Florida, United States

Francisco M. De La Vega, Stanford University; Fabric Genomics, United States

Dirk J. Evers, Dr. Dirk Evers Consulting, Germany

Kjong Lehmann, ETH-Zürich, Switzerland

Quaid Morris, University of Toronto, Canada

Gunnar Rätsch, ETH-Zürich, Switzerland

Microbiome

Aaron Darling, University of Technology Sydney, Australia

Alice McHardy, Helmholtz Centre for Infection Research, Germany

Mihai Pop, University of Maryland, United States

Thomas Rattei, University of Vienna, Austria

Alexander Sczyrba, Bielefeld University, Germany

MLCSB: Machine Learning in Computational and Systems Biology

Florian Markowetz, University of Cambridge, United Kingdom

Oliver Stegle, European Bioinformatics Institute, United Kingdom

NetBio: Network Biology

Alex Pico, Gladstone Institutes, United States

Natasa Przulj, University College London, United Kingdom

RegSys: Regulatory and Systems Genomics

Stein Aerts, University of Leuven, Belgium

Julia Zeitlinger, Stowers Institute for Medical Research, United States

RNA: Computational RNA Biology

Yoseph Barash, University of Pennsylvania, United States

Eduardo Eyras, Universitat Pompeu Fabra, Spain

Klemens Hertel, University of California, Irvine, United States

SysMod: Computational Modeling of Biological Systems

Andreas Draeger, University of Tübingen, Germany

Tomas Helikar, University of Nebraska - Lincoln, United States

Nicolas Le Novere, Babraham Institute, United Kingdom

TransMed: Translational Medicine Informatics & Applications

Bissan Al-Lazikani, The Institute of Cancer Research, United Kingdom

Wei Gu, Luxembourg Centre For Systems Biomedicine

Venkata Satagopam, University of Luxembourg

VarI: Variant Interpretation

Yana Bromberg, Rutgers, United States

Hannah Carter, UCSD, United States

Emidio Capriotti, University of Bologna, Italy

General Computational Biology

Laxmi Parida, IBM T. J. Watson Research Center, United States

Poster Chairs

Casey Greene, University of Pennsylvania, United States
Arjun Krishnan, Michigan State University, United States

Technology Track Chairs

Dominic Clark, EMBL-EBI, Hinxton, United Kingdom
Jean-Francois Tomb, University of Delaware, United States

Travel Fellowship Chairs

Lucia Peixoto, Washington State University, United States
Catherine Putonti, Loyola University Chicago, United States

Tutorial Chairs

Michelle D. Brazas, Ontario Institute for Cancer Research, Canada
Lonnie Welch, Ohio University, United States

Student Council Chairs

Eli Draizen, National Institutes of Health, United States
Numrah Fadra, University of Minnesota , Mayo Clinic, United States

Communities of Special Interest (COSI) Leadership

ISCB COSI Committee Chair
Christine Orengo

ISCB Board of Directors COSI Representative
Francisco De La Vega

3DSIG: Structural Bioinformatics and Computational Biophysics
Rafael Najmanovich

BIOINFO-CORE
Madelaine Gogol
Brent Richter

Bio-Ontologies
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Christophe Dessimoz

Function: Gene and Protein Function Annotation
Iddo Friedberg

HiTSeq: High Throughput Sequencing Algorithms & Applications
Francisco De La Vega
Dirk Evers

IRB: Integrative RNA Biology
Yoseph Barash
Alex Bateman

JPI: Junior Principal Investigators
Casey Greene
Lucia Peixoto

Microbiome
Thomas Rattei
Alice McHardy
Alexander Sczyrba

MLCSB: Machine Learning in Computational and Systems Biology
Karsten Borgwardt
Katharina Heinrich

NetBio: Network Biology
Alexander Pico
Natasa Przulj

OBF/BOSC: Open Bioinformatics Foundation/Bioinformatics Open Source Conference
Peter Cock
Nomi Harris

RegSys: Regulatory and Systems Genomics
Manolis Kellis
Lonnie Welch

SysMod: Computational Modeling of Biological Systems
Tomáš Helikar
Nicolas Le Novre

TransMed: Translational Medicine Informatics & Applications
Venkata Satagopam

VarI: Variant Interpretation
Hannah Carter
Emidio Capriotti
Yana Bromberg

Posters Display Schedule

EXHIBIT LEVEL, EAST TOWER, HYATT REGENCY CHICAGO

There are two (2) poster sessions at ISMB 2018.

SESSION A

SATURDAY, JULY 7 AND SUNDAY, JULY 8

Session A Posters set up	Saturday, July 7 • 7:30 am - 10:00 am
Poster Help Desk located in Poster Entrance area	*7:30 - 10:00 am*
All Session A Posters on display	July 7 and July 8
Session A Posters should be removed	Sunday, July 8 • 7:30 pm

Authors with Posters

Session A: Odd Numbered	Saturday, July 7 • 6:00 pm - 7:30 pm
Session A: Even Numbered	Sunday, July 8 • 6:00 pm - 7:30 pm

SESSION B

MONDAY, JULY 9 AND TUESDAY, JULY 10

Session B Posters set up	Monday, July 9 • 7:30 am - 10:00 am
Poster Help Desk located in Poster Entrance area	*7:30 - 10:00 am*
All Session B Posters on display	July 9 and July 10
Session B Posters should be removed	Tuesday, July 10 • 2:00 pm

Authors with Posters

Session B: Odd Numbered	Monday, July 9 • 6:00 pm - 7:30 pm
Session B: Even Numbered	Tuesday, July 10 • 12:40 pm - 2:00 pm

Distinguished Keynote Presentations

ROOM: GRAND BALLROOM C-F

FRIDAY JULY 6 • 6:30 PM – 7:30 PM

Steven Salzberg, Bloomberg Distinguished Professor of Biomedical Engineering, Computer Science, and Biostatistics Director; Center for Computational Biology McKusick-Nathans Institute of Genetic Medicine; Johns Hopkins University; Baltimore, United States

25 years of human gene finding: are we there yet?

Introduction By: Tandy Warnow, ISMB 2018 Conference Co-chair

SATURDAY JULY 7 • 8:30 AM – 9:30 AM

ISCB OVERTON PRIZE AWARD KEYNOTE

Cole Trapnell, Assistant Professor, Department of Genome Sciences, University of Washington, United States

Reconstructing and deforming developmental landscapes

Introduction By: Thomas Lengauer, ISCB President

SUNDAY JULY 8 • 8:30 AM – 9:30 AM

Martha L. Bulyk, Division of Genetics, Department of Medicine, Department of Pathology, Brigham & Women's Hospital and Harvard Medical School, Boston, United States

Transcription factors and cis-regulatory elements

Introduction By: Gary Stormo, ISMB 2018 Honorary Chair

MONDAY JULY 9 • 8:30 AM – 9:30 AM

ISCB INNOVATOR AWARD KEYNOTE

M. Madan Babu, Programme Leader, MRC Laboratory of Molecular Biology, Cambridge, United Kingdom

How Does Protein Disorder Enable Phenotypic Diversity?

Introduction By: Christine Oregno, ISMB 2018 Conference Co-chair

TUESDAY JULY 10 • 5:00 PM – 6:00 PM

ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE

Ruth Nussinov, Senior Principal Investigator, National Cancer Institute, National Institutes of Health, United States; Professor, School of Medicine, Department of Human Genetics, Tel Aviv University, Israel

A woman's computational biology journey

Introduction By: Alfonso Valenica, ISCB Past President

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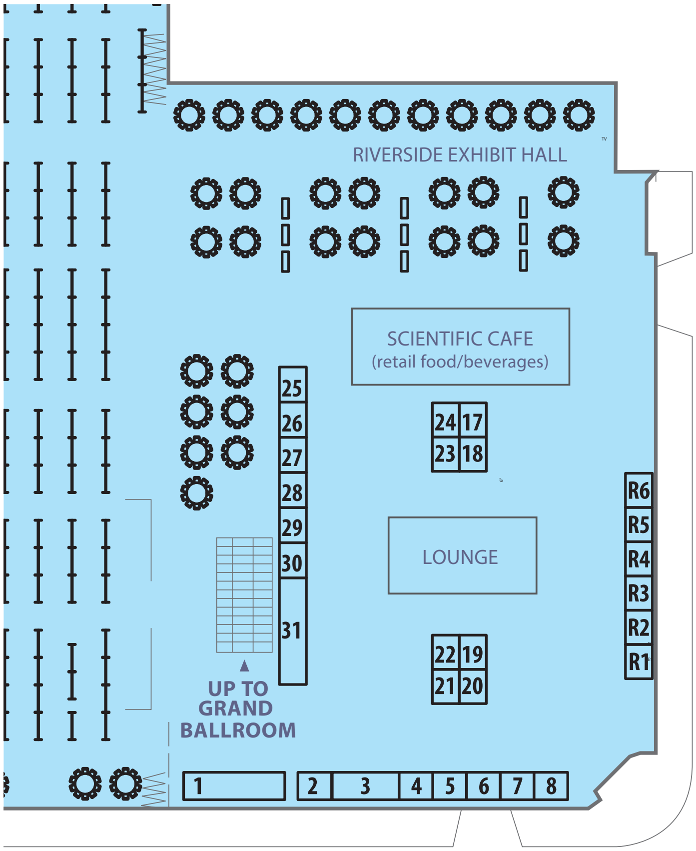
ISMB 2018 Exhibitors and Recruiters Exhibition Floor Plan

RIVERSIDE EXHIBIT HALL



EXHIBITORS

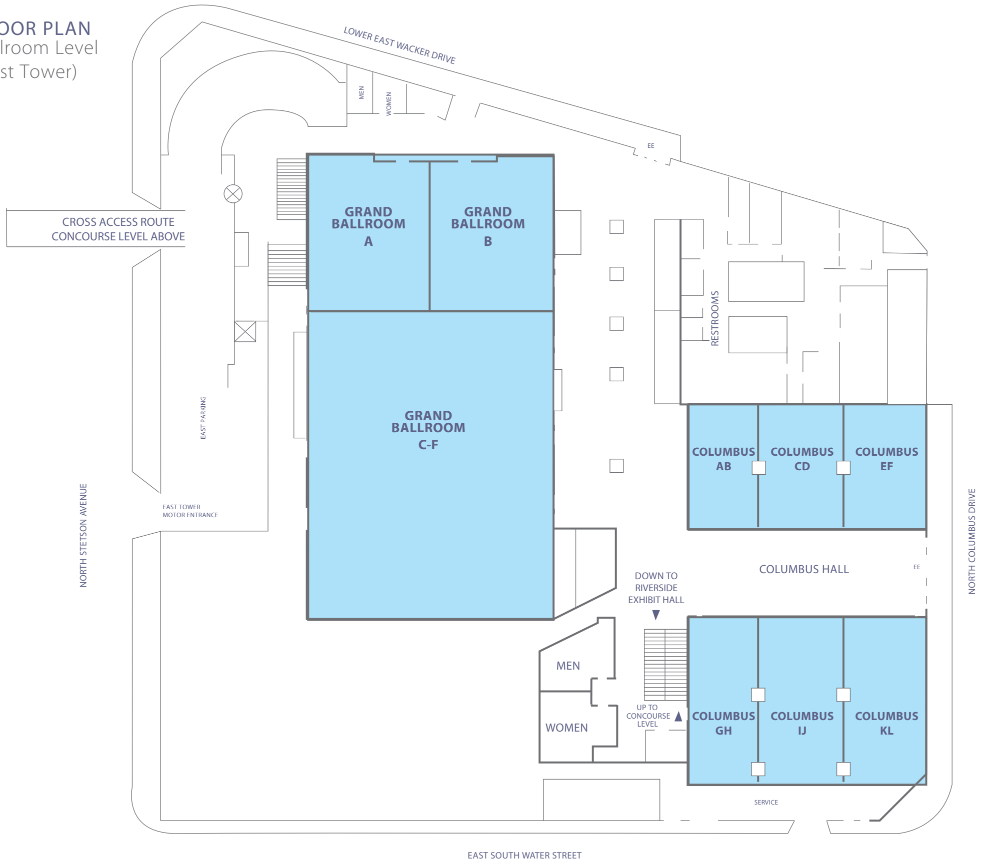
1	INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
2	ISCB TRAVEL FELLOWSHIP
3	ISCB-STUDENT COUNCIL
4	EUROPEAN CONFERENCE ON COMPUTATIONAL BIOLOGY
5	PHRMA FOUNDATION
6-7	ISCB POWER PODS
8	ISMB JOBS BOARD
17	OXFORD UNIVERSITY PRESS
18	LOYOLA UNIVERSITY CHICAGO
19	GENOMICS, PROTEOMICS & BIOINFORMATICS
20	JETSTREAM - INDIANA UNIVERSITY
21	ELIXIR
22	EUROPEAN BIOINFORMATICS INSTITUTE
23	CAMBRIDGE UNIVERSITY PRESS
24	GOBLET & ISCB EDUCATION COSI
25	THE ROYAL SOCIETY
26	PLOS (PUBLIC LIBRARY OF SCIENCE)
27	F1000 RESEARCH
28	ECLIPSE BIOINNOVATIONS
29	MACROGEN
30	HARVARD MEDICAL SCHOOL, DEPARTMENT OF BIOMEDICAL INFORMATICS
31	BD2K

RECRUITER

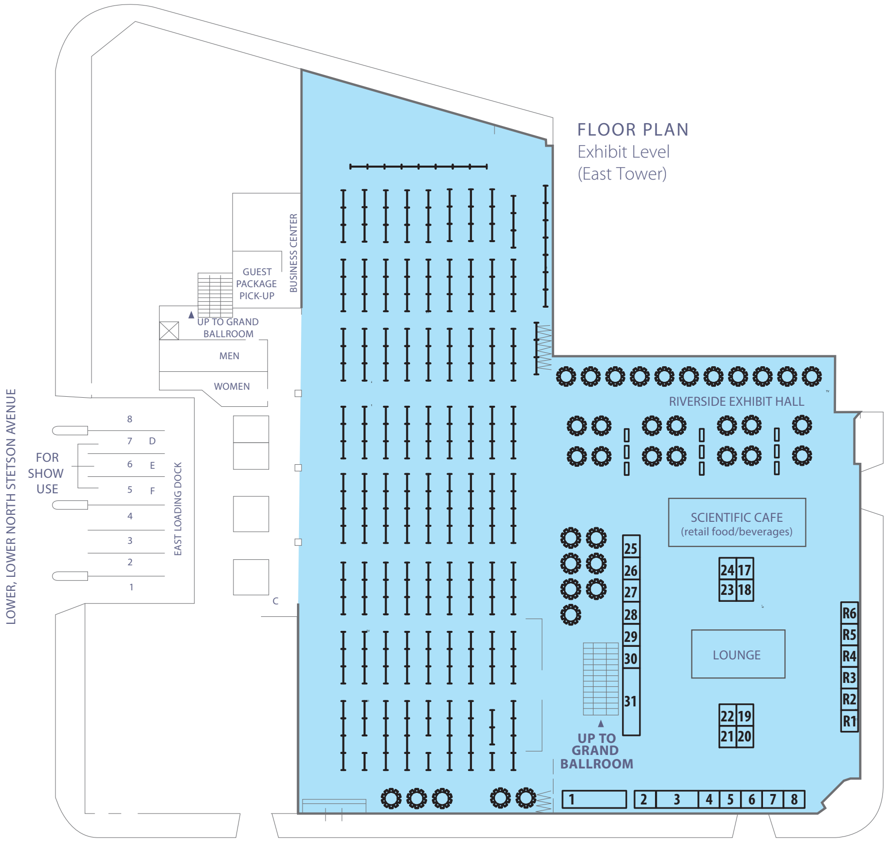
R1	THE JACKSON LABORATORY
R2	ST. JUDE CHILDREN'S RESEARCH HOSPITAL
R3	BIOMEDICAL INFORMATICS AT CINCINNATI CHILDREN'S AND UNIVERSITY OF CINCINNATI
R4	BIOINFORMATICS AND COMPUTATIONAL BIOLOGY AT IOWA STATE UNIVERSITY
R5	BIOSTATISTICS AND MEDICAL INFORMATICS, UNIVERSITY OF WISCONSIN - MADISON
R6	UNIVERSITY OF ALABAMA AT BIRMINGHAM – INFORMATICS INSTITUTE

Hyatt Regency Chicago East Tower

FLOOR PLAN
Ballroom Level
(East Tower)



FLOOR PLAN
Exhibit Level
(East Tower)



ATTENDEE WIFI
Network: Hyatt Conference
Password: Chicago18

Schedule-at-a-Glance • Friday

HYATT REGENCY CHICAGO

ATTENDEE WIFI
Network: Hyatt Conference
Password: Chicago18

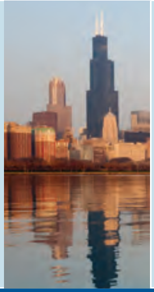
FRIDAY, JULY 6

	GRAND BALLROOM A	GRAND BALLROOM B	COLUMBUS AB	COLUMBUS IJ	COLUMBUS KL
	8:00 AM – 10:00 AM and 3:00 PM - 6:00 PM Conference Registration				GRAND BALLROOM FOYER
9:00 AM	Tutorial AM1: Single cell RNA-seq toolkit	Tutorial AM2: Machine learning methods in the analysis of genomic and clinical data	Student Council Symposium (SCS)	Tutorial AM3: Integrated network analysis: Cytoscape automation using R and Python	Tutorial AM4: Computational methods for comparative regulatory genomics
11:00 AM	COFFEE BREAK – TUTORIALS				
11:15 AM	AM1 continued	AM2 continued	SCS continued	AM3 continued	AM4 continued
1:00 PM	LUNCH BREAK				
2:00 PM	Tutorial PM6: Deep learning for network biology	Tutorial PM7: High-throughput sequencing: Identification of disease variants in exomes and genomes	SCS continued	Tutorial PM5: Visualization of large biological data	Tutorial PM8: Ontologies in computational biology
4:00 PM	COFFEE BREAK – TUTORIALS				
4:15 PM	PM6 continued	PM7 continued	SCS continued	PM5 continued	PM8 continued
6:00 PM	TUTORIALS AND STUDENT COUNCIL SYMPOSIUM END				
6:15 PM 6:30 PM	Conference Welcome **Steven Salzberg,** Johns Hopkins University, United States *25 years of human gene finding: are we there yet?*				Room: Grand Ballroom C-F
7:30 PM	OPENING RECEPTION WITH EXHIBITORS				RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL

Schedule-at-a-Glance • Saturday

HYATT REGENCY CHICAGO

SATURDAY, JULY 7

	GRAND BALLROOM A	GRAND BALLROOM B	GRAND BALLROOM C-F	COLUMBUS AB	COLUMBUS CD	COLUMBUS EF	COLUMBUS GH	COLUMBUS IJ	COLUMBUS KL
	7:30 AM – 7:30 PM Conference Registration GRAND BALLROOM FOYER								
8:15 AM	Morning Welcome and conference updates / Introduction of ISCB 2018 Distinguished Fellows Room: Grand Ballroom C-F								
8:30 AM	**ISCB Overton Prize Award Keynote: Cole Trapnell,** University of Washington, United States *Reconstructing and deforming developmental landscapes*								
9:30 AM	COFFEE BREAK WITH EXHIBITORS RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL								
10:15 AM	SysMod COSI: Computational Modeling of Biological Systems	RNA COSI: Computational RNA Biology	Special Session 3D Genomics: Computational approaches for analyzing the role of three-dimensional chromatin organization in gene regulation	BD2K Special Presentation	CompMS COSI: Computational Mass Spectrometry	Workshop: Bioinformatics training in the FAIR era	CAMDA COSI: Critical Assessment of Massive Data Analysis	Function COSI: Protein Function Annotation	General Computational Biology Talks
12:40 PM	LUNCH (ON OWN) AVAILABLE EXHIBITION / POSTER AREA RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL								
	12:45 PM – 1:45 PM BIRDS OF A FEATHER				BoF: On Leadership and Management: focus on mentorship		BoF: Informatics for Precision Medicine	BoF: Cytoscape Community Meeting: Latest updates and Roadmap	BoF: ISCB Equity, Diversity, and Inclusion Task Force Update and Breakout Sessions
2:00 PM	SysMod COSI Continues	RNA COSI Continues	Special Session: 3D Genomics Continues	BD2K Special Presentation	CompMS COSI Continues	BIOINFO-CORE Workshop: Bioinformatics Core	CAMDA COSI Continues	Function COSI Continues	General Computational Biology Talks
4:00 PM	COFFEE BREAK WITH EXHIBITORS RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL								
4:40 PM	SysMod COSI Continues	RNA COSI Continues	Special Session: 3D Genomics Continues	BD2K Special Presentation	CompMS COSI Continues		CAMDA COSI Continues	Function COSI Continues	General Computational Biology Talks
6:00 PM – 7:30 PM	POSTER PRESENTATIONS (SESSION A, ODD NUMBER POSTERS) RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL								

Schedule-at-a-Glance • Sunday

HYATT REGENCY CHICAGO

ATTENDEE WIFI
Network: Hyatt Conference
Password: Chicago18

SUNDAY, JULY 8

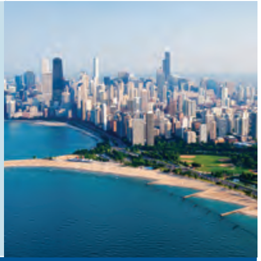
	GRAND BALLROOM A	GRAND BALLROOM B	GRAND BALLROOM C-F	COLUMBUS AB	COLUMBUS CD	COLUMBUS EF	COLUMBUS GH	COLUMBUS IJ	COLUMBUS KL
	7:30 AM – 6:30 PM Conference Registration								**GRAND BALLROOM FOYER**
8:15 AM	Morning Welcome								Room: Grand Ballroom C-F
8:30 AM	**Keynote: Martha L. Bulyk,** Brigham & Women's Hospital and Harvard Medical School, United States *Transcription factors and cis-regulatory elements*								
9:30 AM	**COFFEE BREAK WITH EXHIBITORS**								**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
10:15 AM	HitSeq COSI: High-throughput Sequencing	RNA COSI: Computational RNA Biology	NetBio COSI: Network Biology	BD2K Special Presentation	Education COSI: Computational Biology Education	Special Session: Single-particle Cryo-electron Microscopy, Cryo-electron Tomography, and Integrative/Hybrid Methods Studies of Macromolecular Machines: Opportunities and Challenges for the Bioinformatics Community	CAMDA COSI: Critical Assessment of Massive Data Analysis	TransMed COSI: Translational Medical Informatics	VarI COSI: Variant Interpretation
12:40 PM	**LUNCH (ON OWN)** AVAILABLE EXHIBITION / POSTER AREA								**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
	12:45 PM – 1:45 PM JOIN US FOR THE ISCB TOWN HALL								ROOM: COLUMBUS IJ
2:00 PM	HiTSeq COSI Continues	RNA COSI Continues	NetBio COSI Continues	BD2K Special Presentation	Education COSI Continues	Special Session: Omics Data Compression and Storage: Present and Future	CAMDA COSI Continues	TransMed COSI Continues	VarI COSI Continues
4:00 PM	**COFFEE BREAK WITH EXHIBITORS**								**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
4:40 PM	HiTSeq COSI Continues	RNA COSI Continues	NetBio COSI Continues	BD2K Special Presentation	Education COSI Continues	Special Session: Omics Data Compression and Storage: Present and Future	CAMDA COSI Continues	TransMed COSI Continues	VarI COSI Continues
6:00 PM – 7:30 PM	**POSTER PRESENTATIONS** (SESSION A, EVEN NUMBER POSTERS)								**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**

SCHEDULE SUBJECT TO CHANGE. CHECK ISMB18 APP FOR CURRENT INFORMATION

Schedule-at-a-Glance • Monday

HYATT REGENCY CHICAGO

MONDAY, JULY 9

	GRAND BALLROOM A	GRAND BALLROOM B	GRAND BALLROOM C-F	COLUMBUS AB	COLUMBUS CD
	7:30 AM – 6:30 PM Conference Registration GRAND BALLROOM FOYER				
8:15 AM	Morning Welcome / PhRMA Foundation Award Presentations / ISCB Outstanding Contributions Award Presentation: Russ Altman ROOM: GRAND BALLROOM C-F				
8:30 AM	**Keynote: M. Madan Babu,** MRC Laboratory of Molecular Biology, United Kingdom ISCB Innovator Award Keynote: How Does Protein Disorder Enable Phenotypic Diversity?				
9:40 AM	COFFEE BREAK WITH EXHIBITORS RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL				
10:15 AM	HitSeq COSI: High-throughput Sequencing	RegSys COSI: Regulatory and Systems Genomics	MLCSB COSI: Machine Learning in Computational and Systems Biology	3DSIG COSI: Structural Bioinformatics and Computational Biophysics	EvolCompGen: Evolution and Comparative Genomics COSI
12:40 PM	LUNCH (ON OWN) AVAILABLE EXHIBITION / POSTER AREA RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL				
12:45 PM – 2:00 PM	ISCB CAREER FAIR — RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL				
	12:45 PM – 1:45 PM BIRDS OF A FEATHER	BoF: JPI Career Development: Funding opportunities for Early Career Researchers			
2:00 PM	HiTSeq COSI Continues	RegSys COSI Continues	MLCSB COSI Continues	3DSIG COSI Continues	EvolCompGen COSI Continues
4:00 PM	COFFEE BREAK WITH EXHIBITORS RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL				
4:40 - 5:40 PM	HiTSeq COSI Continues	RegSys COSI Continues		3DSIG COSI Continues	
5:40 - 6:00 PM					
6:00 PM – 7:30 PM	POSTER PRESENTATIONS (SESSION B, ODD NUMBER POSTERS) RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL				

Schedule-at-a-Glance • Monday

HYATT REGENCY CHICAGO

ATTENDEE WIFI
Network: Hyatt Conference
Password: Chicago18

MONDAY, JULY 9

	COLUMBUS EF	COLUMBUS GH	COLUMBUS IJ	COLUMBUS KL
	7:30 AM – 6:30 PM Conference Registration			**GRAND BALLROOM FOYER**
8:15 AM	Morning Welcome / PhRMA Foundation Award Presentations / ISCB Outstanding Contributions Award Presentation: Russ Altman			**ROOM: GRAND BALLROOM C-F**
8:30 AM	**Keynote: M. Madan Babu,** MRC Laboratory of Molecular Biology, United Kingdom ISCB Innovator Award Keynote: How Does Protein Disorder Enable Phenotypic Diversity?			
9:40 AM	**COFFEE BREAK WITH EXHIBITORS**			**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
10:15 AM	Bio-Ontologies COSI	Special Session: Advancing computational biology through critical assessments, community experiments, and crowdsourcing	BioVis COSI: Biological Data Visualization	
10:20 – 10:40 AM				Function COSI (Additional) *Amir Karger*
10:40 – 11:00 AM				TECHNOLOGY TRACK PubMed Labs: An experimental platform
11:00 – 11:20 AM				NetworkAssessor: An interactive visualization tool
11:00 – 11:20 AM				Tibanna: a cloud-based automation system
11:40 AM – 12:00 PM				Deciphering genetic diseases using WGS and ncRNAs
12:00 – 12:20 PM				EBI Search as a Service
12:20 – 12:40 PM				EMBL-EBI Bioinformatics Web Services
12:40 PM	**LUNCH (ON OWN)** AVAILABLE EXHIBITION / POSTER AREA			**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
12:45 PM – 2:00 PM	ISCB CAREER FAIR — RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL			
	12:45 PM – 1:45 PM BIRDS OF A FEATHER			BoF: Critical assessment communities
2:00 PM	Bio-Ontologies COSI	Special Session Continues	BioVis COSI Continues	MICROBIOME COSI
4:00 PM	**COFFEE BREAK WITH EXHIBITORS**			**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
4:40 - 5:40 PM	Bio-Ontologies COSI	TECHNOLOGY TRACKS Jetstream – A national research and education cloud	BioVis COSI Continues	MICROBIOME COSI Continues
5:40 - 6:00 PM		KnowEnG: Knowledge Engine for Genomics		
6:00 PM – 7:30 PM	**POSTER PRESENTATIONS** (SESSION B, ODD NUMBER POSTERS)			**RIVERSIDE EXHIBIT HALL, EXHIBIT LEVEL**

SCHEDULE SUBJECT TO CHANGE. CHECK ISMB18 APP FOR CURRENT INFORMATION

Schedule-at-a-Glance • Tuesday

HYATT REGENCY CHICAGO

ATTENDEE WIFI
Network: Hyatt Conference
Password: Chicago18

TUESDAY, JULY 10

	GRAND BALLROOM A	GRAND BALLROOM B	GRAND BALLROOM C-F	COLUMBUS AB	COLUMBUS EF	COLUMBUS GH	COLUMBUS IJ	COLUMBUS KL
	7:30 AM – 12:00 PM Conference Registration							GRAND BALLROOM FOYER
8:35 AM	ELIXIR Special Presentation	RegSys COSI: Regulatory and Systems Genomics	MLCSB COSI: Machine Learning in Computational and Systems Biology	3DSIG COSI: Structural Bioinformatics and Computational Biophysics	Bio-Ontologies Bio-Ontologies COSI	TECH TRACK Streaming big genomic data with MPEG-G, the emerging ISO standard for genomic information representation	SPECIAL SESSION SCANGEN: Single-cell cancer genomics	Microbiome COSI
9:40 AM	**COFFEE BREAK WITH EXHIBITORS**							**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
10:15 AM	ELIXIR Special Presentation Continues	RegSys COSI Continues	MLCSB COSI Continues	3Dsig COSI continues	Bio-Ontologies COSI Continues		SCANGEN: Single-cell cancer genomics Continues	Microbiome COSI Continues
10:20 - 11:20 AM						TECH TRACK D-SPACE: Deep Semantic Protein Annotation Classification and Exploration		
11:20 - 11:40 AM						DART – a fast and accurate RNA-seq mapper with a partitioning strategy		
11:40 - 12:00 PM						The New PSIPRED Protein Analysis Workbench		
12:00 - 12:20 PM								
12:20 - 12:40 PM								
12:40 PM	**POSTER PRESENTATIONS** (SESSION B, EVEN NUMBER POSTERS) **LUNCH (ON OWN)** AVAILABLE EXHIBITION / POSTER AREA							**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**
2:00 - 2:20 PM		RegSys COSI Continues	MLCSB COSI Continues	3Dsig COSI continues		Phyre2, PhyreRisk and EzMol: Protein structure prediction, variant analysis and visualization made easy	SCANGEN: Single-cell cancer genomics Continues	Microbiome COSI Continues
2:20 - 2:40 PM						The SUPERFAMILY 2.0: HMM library and genome assignments server		
2:40 - 3:00 PM						The Proteins API, Tool Suites for Interpreting the Molecular Mechanisms of Diseases		
4:40 PM	**COFFEE BREAK (ON THE GO) GRAND BALLROOM FOYER**							
5:00 PM	ISCB Accomplishments by a Senior Scientist Award Presentation **Ruth Nussinov,** National Institutes of Health, United States; Tel Aviv University, Israel A woman's computational biology journey							ROOM: GRAND BALLROOM C-F
6:00 – 6:20 PM	**ISMB Awards Ceremony**							ROOM: GRAND BALLROOM C-F

Special Sessions

PRESENTATIONS

SATURDAY JULY 7 • *ROOM: COLUMBUS EF*

https://www.iscb.org/ismb2018-program/ismb2018-special-sessions

10:15 AM - 6:00 PM

3D Genomics: Computational approaches for analyzing the role of three-dimensional chromatin organization in gene regulation.

Organizer(s): **Ferhat Ay,** La Jolla Institute for Allergy and Immunology, United States; **Sushmita Roy,** Biostatistics & Medical Informatics, Wisconsin Institute for Discovery, United States

10:15 - 10:20 AM	3D Genome: Session Overview and Introductions
10:20 - 11:00 AM	**Feng Yue,** Penn State, PA , United States Invited: Impact of structural variants on 3D genome structure in cancer cells
11:00 - 11:10 AM	**Lila Rieber,** The Pennsylvania State University, United States Identification of locus-specific changes in chromosome conformation between cell types reveals enrichment of enhancers
11:10 - 11:20 AM	**Tao Yang,** The Pennsylvania State University, United States Identification of differential TADs across conditions and cell lines
11:20 - 11:30 AM	**Alan Perez-Rathke,** University of Illinois at Chicago, United States Unlocking the TAD: Chromatin folding with CHROMATIX
11:30 - 11:40 AM	**Serhan Yılmaz,** Bilkent University, Turkey SPADIS: An Algorithm for Selecting Predictive and Diverse SNPs in GWAS
11:40 - 11:50 AM	**Da-Inn Lee,** University of Wisconsin-Madison, United States A graph-regularized non-negative matrix factorization method to discover organizational units of chromosomes
11:50 - 12:00 PM	**Duy Nguyen,** University of Wisconsin-Madison, United States TreeHiC: Hierarchical testing for differential chromatin interaction analysis
12:00 - 12:40 PM	**Jian Ma,** Carnegie Mellon University, United States Invited: Continuous-trait probabilistic model for comparing nuclear genome organization of multiple species
2:00 - 2:40 PM	**Mathieu Blanchette,** McGill University, Canada Invited: High-resolution analysis of chromatin conformation capture data
2:40 - 2:45 PM	**Mohamed Nadhir Djekidel,** Tsinghua University, Algeria FIND: difFerential chromatin INteractions Detection using a spatial Poisson process
2:45 - 2:50 PM	**Asa Thibodeau,** Jackson Laboratory, United States Chromatin interaction networks revealed unique connectivity patterns of broad H3K4me3 domains and super enhancers in 3D chromatin
2:50 - 2:55 PM	**Michael Workman,** Cedars-Sinai Medical Center, United States HiCAGE: an R package for large-scale annotation and visualization of 3C-based genomic data
2:55 - 3:00 PM	**Haitham Ashoor,** The Jackson Laboratory for Genomic Medicine, United States CompartmentExplorer: an accurate method for genomic compartments prediction from 3D genome data
3:00 - 3:10 PM	**Sourya Bhattacharyya,** La Jolla Institute for Allergy and Immunology, United States FitHiChIP: Statistical analysis of high-resolution HiChIP and PLAC-seq data
3:10 - 3:20 PM	**Gamze Gursoy,** Yale University, United States Conserved CTCF binding sites act as allosteric hotspots: A computational knock-out study using nC-SAC model
3:20 - 4:00 PM	**William Noble,** University of Washington, United States Invited: Modeling and predicting the 3D genome
4:40 - 5:20 PM	**Geoffrey Fudenberg,** UC San Francisco, CA , United States Invited: Connections between the structure and function of 3D genome folding
5:20 - 5:30 PM	**Subhajyoti De,** Rutgers University, United States Nuclear topology modulates the mutational landscapes of cancer genomes
5:30 - 5:40 PM	**Yong Chen,** The University of Texas at Dallas, United States Computational Detecting Cancer-associated Disorders of Chromatin Interactions from ChIA-PET data
5:40 - 5:45 PM	**Bethany Hall,** Nottingham Trent University, United Kingdom In silico modelling of longevity in Drosophila – a network approach
5:45 - 5:50 PM	**She Zhang,** University of Pittsburgh, United States Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings
5:50 - 5:55 PM	**Ye Zheng,** University of Wisconsin-Madison, United States mHi-C: robust leveraging of multi-mapping reads in Hi-C analysis
5:55 - 6:00 PM	**Brittany Baur,** University of Wisconsin-Madison, United States In silico prediction of high resolution chromosomal contact counts in multiple cell lines

Special Sessions

PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: COLUMBUS EF*

https://www.iscb.org/ismb2018-program/ismb2018-special-sessions

10:15 AM - 12:40 PM

Single-particle Cryo-electron Microscopy, Cryo-electron Tomography, and Integrative/Hybrid Methods Studies of Macromolecular Machines: Opportunities and Challenges for the Bioinformatics Community

Organizer(s): Stephen K. Burley, RCSB Protein Data Bank, United States; **Jose Duarte,** RCSB Protein Data Bank, United States

Jose Duarte, RCSB Protein Data Bank, UC San Diego
Opening Remarks

Yuan He, Department of Molecular Biosciences, Northwestern University, United States
Cryo-EM visualization of eukaryotic transcription initiation machineries

Wei Dai, Rutgers University, United States
Visualizing molecular assemblies inside cells by cryo-electron tomography

Barak Raveh, Department of Bioengineering and Therapeutic Sciences, UC San Francisco, United States
Integrative structural biology

Alexander Rose, RCSB Protein Data Bank, UC San Diego, United States
Web-based 3D visualization and exploration of cryo-electron microscopy and integrative/hybrid methods structures

Stephen K. Burley, RCSB Protein Data Bank, Rutgers University and UC San Diego, United States
Closing remarks

Omics Data Compression and Storage: Present and Future

Organizer(s): Mikel Hernaez, University of Illinois at Urbana-Champaign, United States; **Idoia Ochoa,** University of Illinois at Urbana-Champaign, United States

2:00 - 2:40 PM **Gene Robinson,** University of Illinois at Urbana-Champaign, United States
The Genomics Revolution: Coming to a Neighborhood Near You

2:40 - 3:20 PM **Tsachy Weissman,** Stanford University, United States
Genomic data compression and processing for large and growing databases

3:20 - 4:00 PM **Cenk Sahinalp,** Indiana University, United States
Optimal compressed representation of high throughput sequence data via light assembly

4:00 - 4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 - 5:00 PM **Christian Iseli,** Swiss Bioinformatics Institute, Switzerland
From oak to newborns and viruses : The very diverse use cases of genomic reads

5:00 - 5:20 PM **Jörn Ostermann,** Leibniz Universität Hannover, Germany
MPEG-G and the benefits of the ISO standards development procedure

5:20 - 6:00 PM **Claudio Alberti,** Genomsys, Switzerland
MPEG-G, the compression and transport format for interoperable genomic data sharing

MONDAY JULY 9 • *ROOM: COLUMBUS GH*

Advancing computational biology through critical assessments, community experiments, and crowdsourcing

Organizer(s): Gaia Andreoletti, University of California, Berkeley, United States; **Steven E Brenner,** University of California, Berkeley, United States; **John Moult,** The University of Maryland, United States

10:15 – 10:20 AM **Gaia Andreoletti,** University of California, Berkeley, United States
Introduction

10:20 – 10:40 AM **John Moult,** University of Maryland, United States
CASP: Critical Assessment of protein Structure Prediction

10:40 – 11:00 AM **Ilya Vakser,** The Univrsity of Kansas, United States, **and Michael Sternberg,** Imperial College London, United Kingdom
CAPRI: Critical Assessment of Prediction of Interactions

11:00 – 11:10 AM **Torsten Schwede,** University of Basel, Switzerland
CAMEO: Automated continuous evaluation of protein structure modelling servers

11:10 – 11:20 AM **Sharon Liang,** U.S. Food and Drug Administration, Maryland, United States
pFDA: Precision FDA

11:20 – 11:40 AM **Steven E Brenner,** University of California, Berkeley, United States
CAGI: Critical Assessment of Genome Interpretation

11:40 – 12:00 PM **Laura Almasy** University of Pennsylvania, United States, **Jean MacCluer,** Texas Biomedical Research Institute, United States
GAW: Genetic Analysis Workshop

12:00 – 12:20 PM **James Costello,** University of Colorado Denver, United States
DREAM: Dialogue for Reverse Engineering Assessment and Methods

12:20 – 12:40 PM **Alice McHardy,** Helmholtz Centre for Infection Research
Alexander Sczyrba, Bielefeld University
CAMI: Critical Assessment of Metagenome Interpretation

12:40-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 – 2:20 PM **Alfonso Valencia,** Barcelona Supercomputing Centre, Spain
Elixir

2:20 – 2:40 PM **Iddo Friedberg,** Iowa State University, United States
Predrag Radivojac, Indiana University Bloomington, United States
CAFA: Critical Assessment of Functional Annotation

2:40 - 3:00 PM **Lynnette Hirschmann,** MITRE Corporation
BioCreAtivE: Critical Assessment of Information Extraction in Biology

3:00 – 3:20 PM **Haixu Tang,** Indiana University
iDASH: Integrating Data for Analysis, Anonymization and SHaring (iDASH)

3:20 – 3:30 PM **David Kreil,** Boku University Vienna, Austria, **Joaquin Dopazo,** National Institute of Bioinformatics
CAMDA: Critical Assessment of Massive Data Analysis

3:30 – 3:40 PM **Olivier de Fresnoye**
EPIDEMIUM: A multidisciplinary community to tackle cancer using big and open data

3:40 – 3:50 PM **Carine Poussin,** Philip Morris International Science
sbv-IMPROVER: Systems Biology Verification combined with Industrial Methodology for Process Verification in Research

3:50 – 4:00 PM **Bjoern Peters,** La Jolla institute for allergy & immunology
PLOS Computational Biology: Benchmarking Section

Special Sessions

PRESENTATIONS

TUESDAY JULY 10 • *ROOM: COLUMBUS IJ*

https://www.iscb.org/ismb2018-program/ismb2018-special-sessions

8:35 AM - 4:40 PM

SCANGEN: Single-cell cancer genomics

Organizer(s): Kieran R Campbell, University of British Columbia & BC Cancer Agency, Canada; **Sohrab P Shah,** University of British Columbia & BC Cancer Agency, Canada

8:35-8:40 AM **Introduction**

8:40-9:00 AM **Jean Fan,** Harvard University, United States
Invited: Integrated genetic and transcriptional analysis at the single-cell level

9:00-9:20 AM **Kieran O'Neill,** BC Cancer Agency, Canada
Determing the Mechanism of 5-Azacytidine Response in Myeloid Malignancies Using Single-cell DNA Methylation Sequencing Paired With Flow Cytometry

9:20-9:40 AM **Sombeet Sahu,** Mission Bio, United States
Methods for Identifying Tumor Heterogeneity and Rare Subclones in Single Cell DNA Sequence Data

10:15-10:20 AM **Welcome Back**

10:20-10:40 AM **Chris Yau,** University of Birmingham, United Kingdom
Invited: Scalable Bayesian Tensor Factorization for single-cell Genomics

10:40-11:00 AM **Huidong Chen,** Massachusetts General Hospital Research Institute, United States
STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data

11:00-11:20 AM **Sahar Ansari,** University of Michigan, United States
Leveraging transcription factor networks to identify cell types from single-cell transcriptomes

11:20-11:40 AM **Xun Zhu,** University of Hawaii Cancer Center, United States
Granatum X: A community engaging and flexible scRNA-Seq analysis environment connecting tool developers to bench scientists

11:40 AM-12:00 PM **Wei Vivian Li,** University of California, Los Angeles, United States
scImpute: An accurate and robust imputation method for single-cell RNA-seq data

12:00-12:20 PM **Davis McCarthy,** EMBL-EBI
Invited: An approach to studying clonal cell populations using bulk exome and single-cell RNA sequencing data

12:20-12:40 PM **Simone Ciccolella,** Università degli studi Milano Bicocca, Italy
Inferring Cancer Progression from Single Cell Sequencing while allowing loss of mutations

12:40-2:00 PM **LUNCH (ON OWN) AND SCANGEN POSTERS**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00-2:20 PM **Florian Markowetz,** CR UK Cambridge Institute, United Kingdom
Invited: TBC

2:20-2:40 PM **Mohammed El-Kebir,** University of Illinois at Urbana-Champaign
SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error

2:40-3:00 PM **Violeta Beleva Guthrie,** Johns Hopkins University
Single-cell sequencing analysis of pancreatic cancer precursor lesions reveals convergent evolution and polyclonal origins

3:00-3:20 PM **Haoyun Lei,** Carnegie Mellon University
Deconvolution of tumor copy number data using bulk and single-cell sequencing data

3:20-3:40 PM **Katharina Jahn,** ETH Zurich (invited)
Invited: Modelling tumour evolution from single-cell sequencing data

3:40-4:00 PM **Bojan Losic,** Icahn Institute for Muliscale Biology
Regulatory underpinnings of intra-tumor heterogeneity in HCC liver cancer

4:00-4:20 PM **Sumon Ahmed,** University of Manchester
Investigating Haematopoietic Stem Cells development by single cell sequencing

4:20-4:40 PM **Rui Kuang,** University of Minnesota Twin Cities
A multitask learning approach for clustering multiple single cell RNA-seq datasets

CompMS: Computational Mass Spectrometry

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: COLUMBUS CD*

https://www.iscb.org/cms_addon/conferences/ismb2018/compms.php

10:15 AM-10:20 AM **Oliver Kohlbacher,** University of Tübingen, Germany
Introduction

10:20 AM-11:00 AM **Rebekah L. Gundry,** Medical College of Wisconsin, United States
Expanding our View of the Surfaceome: New Bioinformatic Tools and Technologies for Mapping Glycoproteins from Small Sample Sizes and Human Primary Cells

11:00 AM-11:20 AM **Dai Hai Nguyen,** Kyoto University, Japan
Proceedings Presentation: SIMPLE: Sparse Interaction Model over Peaks of moLEcules for fast, interpretable metabolite identification from tandem mass spectra

11:20 AM-11:40 AM **Ryan Peckner,** Broad Institute of MIT and Harvard, United States
Linear deconvolution for highly sensitive targeted analysis of data-independent acquisition mass spectrometry proteomics

11:40 AM-12:00 PM **Andrew Dowsey,** University of Bristol, United Kingdom
Robust iTraq and TMT proteoform-level quantification and statistical analysis through Bayesian modelling

12:00 PM-12:40 PM **Evgenia Shiskova,** University of Wisconsin, United States
Software solutions for multi-omic research

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:40 PM **Richard LeDuc,** Northwestern University, United States
Proteoform Informatics: Computation in Top-Down Proteomics

2:40 PM-3:00 PM **Marcus Ludwig,** Friedrich-Schiller-University Jena, Germany
Proceedings Presentation: Bayes networks for mass spectrometric metabolite identification via molecular fingerprints

3:00 PM-3:40 PM **Kylie Bemis,** Northeastern University, United States
Computational and Statistical Methods for Mass Spectrometry Imaging

3:40 PM-4:00 PM Poster Flash Presentation

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:20 PM **Joshua Elias,** Stanford University, United States

5:20 PM-6:00 PM **Oliver Kohlbacher,** University of Tübingen, Germany
William Noble, University of Washington, United States
COSI CompMS Business Meeting

Function: Gene and Protein Function Annotation

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • ROOM: COLUMBUS IJ

https://www.iscb.org/cms_addon/conferences/ismb2018/function.php

10:15 AM-10:20 AM	Introduction
10:20 AM-11:00 AM	**Kimberly Reynolds** Using evolutionary information to understand cellular systems
11:00 AM-11:06 AM	**Castrense Savojardo,** University of Bologna, Italy Continuous evaluation of CAFA
11:06 AM-11:13 AM	**Peter Freddolino,** University of Michigan, United States Commonly under-annotated pathways revealed by structure-based proteome annotation
11:13 AM-11:20 AM	**Linhua Wang,** Icahn School of Medicine at Mount Sinai, United States Large-scale assessment of protein function prediction using heterogeneous ensembles
11:20 AM-11:40 AM	**Rachel Kolodny,** University of Haifa, Israel Complex evolutionary footprints revealed in an analysis of reused protein segments of diverse lengths
11:40 AM-12:00 PM	**Magdalena Antczak,** University of Kent, United Kingdom Identifying the unknown functions of the minimal bacterial genome
12:00 PM-12:20 PM	**Nirvana Nursimulu,** University of Toronto, Canada Higher-quality metabolic models through improved enzyme annotation algorithms
12:20 PM-12:40 PM	**Kokulapalan Wimalanathan,** Iowa State University, United States Maize GO Annotation - Methods, Evaluation, and Review (maize-GAMER)
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Yanbin Yin,** Northern Illinois University, United States dbCAN family tools for automated CAZyme (Carbohydrate Active Enzyme) annotation of genomes and metagenomes
2:20 PM-2:40 PM	**Tunca Dogan,** EMBL-EBI, CanSyL, METU, United Kingdom Automated Negative Gene Ontology Based Functional Predictions for Proteins with UniGOPred
2:40 PM-3:00 PM	**Morteza Pourreza Shahri,** Montana State University, United States A Look Back at the Quality of Protein Function Prediction Tools in CAFA
3:00 PM-3:20 PM	**Naihui Zhou,** Iowa State University, United States Updates on CAFA3 and CAFA3.14
3:20 PM-3:40 PM	**Ying Zhang,** University of Rhode Island, United States Visualization and annotation of genome-scale metabolic networks
3:40 PM-4:00 PM	**Vladimir Gligorijevic,** Flatiron Institute, United States Deep Multi-network Embedding for Protein Function Prediction
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Yannick Mahlich,** Technical University of Munich, Germany Proceedings Presentation: HFSP: High speed homology-driven function annotation of proteins
5:00 PM-5:06 PM	**Rabie Saidi,** EMBL-EBI, United Kingdom A New Entropy for Measuring Annotation Consistency with Regards to Protein Signatures
5:06 PM-5:13 PM	**Taylor Brooks,** Bethune Cookman University, United States Predicting the Functions of Actinomyces Universal Stress Proteins
5:13 PM-5:20 PM	**Elad Segev,** Holon Institute of Technology, Israel Identifying protein-protein interaction and protein biochemical cycles based on co-occurrence patterns of orthologous proteins.
5:20 PM-5:40 PM	**Jeffrey Law,** Virginia Tech, United States Network-based Gene Function Prediction for Pathogenic Bacteria
5:40 PM-6:00 PM	**Minsik Oh,** Seoul National University, South Korea Proceedings Presentation: DeepFam: Deep learning based alignment-free method for protein family modeling and prediction

***ADDITIONAL FUNCTION TALK**

MONDAY, JULY 9 • *ROOM: COLUMBUS KL*

10:20 AM-10:40 AM	**Amir Karger,** Harvard University, United States Variation and novelty in evolution: de novo genes arise and enable protein structural innovation

General Computational Biology

PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: COLUMBUS KL*

https://www.iscb.org/cms_addon/conferences/ismb2018/general.php

10:15 AM-10:20 AM	Introduction
10:20 AM-10:40 AM	**Arif Harmanci,** University of Texas Health - Houston, United States Measuring and Closing the Genotype Leakage from Genomic Signal Profiles: Is it Ethical to Share RNA-seq wiggle files?
10:40 AM-11:00 AM	**Rui Hong,** Boston University, United States A Comprehensive Comparison of Gene Set Projection (GSP) Methods
11:00 AM-11:20 AM	**R. Krishna Murthy Karuturi,** The Jackson Laboratory, United States Single Cell-2-Cell Communicator (SC2CC) to Elicit Cell-to-Cell Communication Network using Single Cell RNA-seq (scRNA-seq) Data
11:20 AM-11:40 AM	**Shuhua Fu,** University of Iowa, United States IDP-denovo: de novo transcriptome assembly and isoform annotation by hybrid sequencing
11:40 AM-12:00 PM	**Jan Hasenauer,** Institute of Computational Biology, Helmholtz Zentrum München, Germany Proceedings Presentation: Bayesian parameter estimation for biochemical reaction networks using region-based adaptive parallel tempering
12:00 PM-12:20 PM	**Daniel H. Huson,** University of Tuebingen, Germany SplitsTree5 - a new provenance-graph-based program for calculating and exploring phylogenetic trees and networks
12:20 PM-12:40 PM	**Anqi Wang,** University of Iowa, United States Theoretical analysis of graph-based and alignment-based hybrid error correction methods for error-prone long reads
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Amrita Basu,** UCSF, United States RWEN : Response-Weighted Elastic Net For Prediction of Chemosensitivity of Cancer Cell Lines
2:20 PM-2:40 PM	**Qian Zhu,** Harvard University, United States Decomposing spatially dependent and cell type specific contributions to cellular heterogeneity
2:40 PM-3:00 PM	**Boris Reva,** Icahn School of Medicine at Mount Sinai, United States Computational prediction of natural metabolites for suppression of tumor progression
3:00 PM-3:20 PM	**Yun William Yu,** Harvard Medical School, United States HyperMinHash: MinHash in LogLog space
3:20 PM-3:40 PM	**Sanjana Choudhury,** University of Dhaka, Bangladesh Identification of Candidate Genes Associated with Osteoarthritis by Microarray Data Analysis
3:40 PM-4:00 PM	**Simona Cristea,** Harvard University, United States ModulOmics: Integrating Multi-Omics Data to Identify Cancer Driver Modules
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Negacy Hailu,** University of Colorado, Boulder, United States Biomedical concept normalization using sequence-to-sequence LSTM model
5:00 PM-5:20 PM	**Matthew Bernstein,** University of Wisconsin-Madison, United States MetaSRA: Normalized human sample-specific metadata for the Sequence Read Archive
5:20 PM-5:40 PM	**A. Ercument Cicek,** Bilkent University, Turkey Re-Identification of Individuals in Genomic Data-Sharing Beacons via Allele Inference
5:40 PM-6:00 PM	**Nima Mousavi,** University of California San Diego, United States GangSTR: Genome-wide Analysis aNd Genotyping of Short Tandem Repeats

SysMod: Computational Modeling of Biological Systems

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: GRAND BALLROOM A*

https://www.iscb.org/cms_addon/conferences/ismb2018/sysmod.php

10:15 AM-10:20 AM **Jonathan Karr,** Icahn School of Medicine at Mount Sinai, United States
Introduction to SysMod and Session I Overview: Models of human disease

10:20 AM-11:00 AM **Andre Levchenko**
Variability and phenotype selection in invasive cancer spread

11:00 AM-11:20 AM **Meghna Verma,** Virginia Tech, United States
Advancing systems immunology using a hybrid agent-based model (ABM) of Helicobacter pylori infection

11:20 AM-11:40 AM **Mariko Okada-Hatakeyama,** Osaka University, Japan
Data-driven modeling of cancer subtypes

11:40 AM-12:00 PM **Subhajyoti De,** Rutgers University, United States
A computational model to track patterns of evolutionary dynamics in cancer

12:00 PM-12:20 PM **Beste Turanli,** Science for Life Laboratory, KTH - Royal Institute of Technology, Sweden
Model driven discovery of drug targets for effective treatment of prostate cancer

12:20 PM-12:40 PM **Barbara Niederdorfer,** Norwegian University of Science and Technology, Norway
Logical model simulations predict drug synergies across different cancer cell lines

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:40 PM **Peter Sorger,** Harvard University, United States

2:40 PM-3:00 PM **Matteo Barberis,** University of Amsterdam, Netherlands
Deciphering cell's robustness by a multi-scale framework integrating cell cycle and metabolism in budding yeast

3:00 PM-3:20 PM **Kenneth Wertheim,** University of Nebraska–Lincoln, United States
Towards a Virtual Immune System: Multi-scale Modeling of CD4+ T Lymphocytes

3:20 PM-3:40 PM **Peter Karp,** SRI International, United States
How Accurate is Automated Gap Filling of Metabolic Models?

3:40 PM-4:00 PM **Saahith Pochiraju,** Icahn School of Medicine at Mount Sinai, United States
Datanator: Toolkit for Discovering and Aggregating Data for Whole-Cell Modeling

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:00 PM **Ulrike Münzner,** Kyoto University, Japan
Cyclic attractor estimation in Boolean networks

5:00 PM-5:05 PM **Aditya Pratapa,** Virginia Tech, United States
CrossPlan: systematic planning of genetic crosses to validate mathematical models

5:05 PM-5:10 PM **Gregor Neuert,** Vanderbilt University, United States
Distribution Shapes Govern the Discovery of Predictive Models for Gene Regulation

5:10 PM-5:15 PM **Benjamin Kellman,** University of California San Diego, United States
Metabolic modeling of human milk oligosaccharide biosynthesis and implications for maternal blood groups

5:15 PM-5:20 PM **Carolin Loos,** Institute of Computational Biology, Helmholtz Zentrum München, Germany
A hierarchical, data-driven approach to modeling single-cell populations predicts latent causes of cell-to-cell variability

5:20 PM-6:00 PM **John Tyson,** Virginia Tech, United States
The Cell Division Cycle: A Closed Loop of Switches Embedded in Switches

6:00 PM-6:10 PM **Tomáš Helikar,** University of Nebraska-Lincoln, United States
Session closing

Workshops

SATURDAY, JULY 7 • *ROOM: COLUMBUS EF*

https://www.iscb.org/ismb2018-program/ismb2018-workshop

10:15 AM – 12:40 PM

Bioinformatics training in the FAIR era

Organized by the ISCB Education Committee:
Annette McGrath, CSIRO, Australia;
Michelle Brazas, Ontario Institute for Cancer Research, Canada

10:20 - 10:50 AM **Ben Busby,** NCBI, United States
What is FAIR and why we should be aware of it?

10:50 - 11:20 AM **Erin Becker,** The Carpentries, United States
The Data Carpentry model

11:20 - 11:50 AM **Michel Dumontier,** Maastricht University, Netherlands
FAIR Guiding Principles for scientific data management and stewardship

11:50 - 12:20 PM Experience Exchange Panel: Growing awareness of the value of data and its reuse and what role we as trainers, play in this effort
Annette McGrath, CSIRO, Australia
Ben Busby, NCBI, United States
Erin Becker, The Carpentries, United States
Michel Dumontier, Maastricht University, Netherlands

12:20 - 12:40 PM **Michelle Brazas,** Ontario Institute for Cancer Research, Canada
Wrap up and future directions discussion

2:00 PM – 4:00 PM

Bioinformatics Core Workshop

Organizer: Madelaine Gogol, Stowers Institute, United States; **Hemant Kelkar,** UNC-Chapel Hill, United States; **Alastair Kerr,** University of Edinburgh; **Brent Richter,** Partners HealthCare of Massachusetts General and Brigham and Women's Hospitals, United States; **Alberto Riva,** University of Florida, United States

2:00 PM - 2:08 PM LIGHTNING TALKS A
Sara Grimm, NIEHS, United States
Bioinformatics Core Staffing

2:08 PM - 2:16 PM **Brent Richter,** Partners HealthCare, United States
Characteristics of a highly successful candidate and how to find them

2:16 PM - 2:24 PM LIGHTNING TALKS B
Alexander Peltzer Quantitative Biology Center, Tübingen, Germany
nf-core: community-driven best-practice Nextflow pipelines

2:24 PM - 2:32 PM **Ben Busby,** NCBI, United States
Data Science in the 21st Century: Streaming Public Data into Containerized Workflows

2:32 PM - 2:40 PM **Lars Jorgensen,** OICR, Canada
Shesmu – An analysis orchestration system designed for FAIR standards and the GA4GH cloud ecosystem

2:40 PM - 2:48 PM **Divy Kangeyan,** Harvard University, United States
A (Fire)Cloud-Based DNA Methylation Data Preprocessing and Quality Control Platform

2:48 PM - 2:56 PM LIGHTNING TALKS C
Jyothi Thimmapuram, Purdue University, United States
Usability of Marginal Data

2:56 PM - 3:04 PM **Krishna Karuturi,** The Jackson Laboratory, United States
Experimental Failures

3:04 PM - 3:20 PM Small Group Discussions

3:20 PM - 4:00 PM Report to all present the insights obtained within the small group discussions

MARK YOUR CALENDAR

BASEL

JULY 21–25

ISMB ECCB

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CONFERENCE CHAIRS

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University of Cape Town, South Africa

Torsten Schwede
Biozentrum, University of Basel & SIB Swiss Institute of Bioinformatics, Switzerland

WWW.ISCB.ORG/ISMBECCB2019

BD2K

SPECIAL TRACK PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: COLUMBUS AB*

https://www.iscb.org/cms_addon/conferences/ismb2018/bd2k.php

BD2K YOUNG PI SESSION

10:15 AM-10:40 AM **Willem Van Panhuis,** University of Pittsburgh, United States
Project Tycho 2.0: A New Repository for the Integration and Reuse of Global Health Data

10:40 AM-11:00 AM **Ana Stanescu,** University of West Georgia, United States
Integrating Heterogeneous Predictive Models Using Reinforcement Learning

11:00 AM-11:20 AM **Gamze Gursoy,** Yale University, United States
Quantification of Private Information Leakage and Privacy-Preserving File Formats for Functional Genomics Data

11:40 AM-12:00 PM **John Lawson,** University of Virginia, United States
Principal Component Region Set Analysis: Facilitating Interpretation of PCA Dimensions for DNA Methylation Data

12:00 PM-12:20 PM **Matthew Bernstein,** University of Wisconsin-Madison, United States
MetaSRA: Normalized Human Sample-Specific Metadata for the Sequence Read Archive

12:20 PM-12:40 PM **Charles Blatti,** University of Illinois at Urbana-Champaign, United States
Integrating Knowledge-Guided Analysis into Novel Genomic Data Ecosystems Using FAIR Principles

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

BUILDING THE FAIR DATA ECOSYSTEM FOR DISCOVERY TO HEALTH

2:00 PM-2:15 PM **Avi Ma'Ayan,** Icahn School of Medicine at Mount Sinai, United States
Practical Strategies towards Making Biomedical Research Data more FAIR

2:15 PM-2:30 PM **Dina Paltoo,** NIH Office of Science Policy, United States
NIH Data Sharing Policies

2:30 PM-2:45 PM **Haixu Tang,** Indiana University Bloomington, United States
Privacy-Preserving Techniques for Analyzing and Sharing Biomedical Data

2:45 PM-3:00 PM **Chunlei Wu,** The Scripps Research Institute (TSRI), United States
SmartAPI: Building a FAIR API Ecosystem for Biomedical Knowledge

3:00 PM-3:15 PM **Tim Clark,** University of Virginia, United States
Implementing FAIR Principles on Protected Health Information

3:15 PM-3:30 PM **Lucila Ohno-Machado,** University of California, San Diego, United States
Towards a Data Discovery Index: Lessons Learned by the bioCADDIE Consortium

3:30 PM-4:00 PM Panel Discussion

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

MACHINE LEARNING APPROACHES TO ENABLE BIOMEDICAL DISCOVERIES

4:40 PM-4:55 PM **Joseph Picone,** Temple University, United States
Automated Cohort Retrieval from EEG Medical Records

4:55 PM-5:10 PM **Cathy Wu,** University of Delaware, United States
Big Data to Knowledge: Integrative Literature Mining and Knowledge Networks for Drug Analytics in Precision Medicine

5:10 PM-5:25 PM **Wei Wang,** HeatBD2K, UCLA, United States
Learning from Text: Translating Clinical Case Reports into Structured Knowledge

5:25 PM-5:40 PM **Larry Hunter,** CU-Denver Anschutz Medical Campus, United States
The Role of Prior Knowledge in Machine Learning and Biomedical Data Science

5:40 PM-6:00 PM **Greg Cooper,** University of Pittsburgh , United States
Causal Network Discovery from Biomedical Data

BD2K

SPECIAL TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: ROOM: COLUMBUS AB*

https://www.iscb.org/cms_addon/conferences/ismb2018/bd2k.php

BIOMEDICAL DATA SCIENCE IN ACTION

10:15 AM-10:45 AM	NIH Introduction
10:45 AM-11:05 AM	**Christina Yung,** University of Chicago, United States PanCancer Analysis of Whole Genomes using Multi-Cloud Strategy
11:05 AM-11:25 AM	**Greg Stupp,** The Scripps Research Institute, United States Wikidata for Biomedical Knowledge Integration and Curation
11:25 AM-11:45 AM	**Jack Van Horn,** University of Southern California , United States Toward the FAIRness of Data Science Training Resources
11:45 AM-12:05 PM	**Ben Busby,** NCBI, United States The Future is Now! Engaging Biomedical Data Scientists in the 21st Century
12:05 PM -12:40 PM	Panel Discussion
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

BD2K POWER TOOLS: MOVING TO THE CLOUD WITH INDUSTRIAL STRENGTH DATA

2:00 PM-2:20 PM	**Brian D. O'Connor,** University of California, United States Scaling Analysis on the Cloud
2:20 PM-2:40 PM	**Saurabh Sinha,** University of Illinois at Urbana-Champaign, United States KnowEnG: A Cloud-based Framework for Genomics Data Analysis
2:40 PM-3:00 PM	**Jianhao Peng,** UIUC, United States The Three Faces of Genomic Data Compression
3:00 PM-3:20 PM	**Mark Musen,** Stanford University, United States Cloud Computing Alone Will Not Make Experimental Data FAIR. We Need Better Metadata First
3:20 PM-4:00 PM	Panel Discussion
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

BD2K DATA VISUALIZATION TOOLS & FUTURE DIRECTIONS

4:40 PM-6:00 PM	**Nils Gehlenborg,** Harvard Medical School, United States **Griffin M. Weber,** Harvard Medical School, United States; **Alistair Ward,** Frameshift, United States

CAMDA: Critical Assessment of Massive Data Analysis

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: COLUMBUS GH*

https://www.iscb.org/cms_addon/conferences/ismb2018/camda.php

10:15 AM-10:20 AM	**David P. Kreil,** Boku University Vienna, Austria Data Analysis Challenges of the CAMDA Contest 2018
10:20 AM-11:20 AM	**Lawrence J. Lesko,** University of Florida, United States Why You Should Care (A Lot) About Real World Evidence
11:20 AM-11:40 AM	**Weida Tong,** National Center for Toxicological Research, United States The CMap Drug Safety Challenge
11:40 AM-12:20 PM	**Leihong Wu,** NCTR, FDA, United States IS-DILI: Drug-Induced Liver Injury Inference in Big Data era
12:20 PM-12:40 PM	**Witold R. Rudnicki,** Institute of Informatics and Computational Centre, University of Białystok; ICM, University of Warsaw, Poland Predicting Drug Induced Liver Injury from gene expression profiles in cancer cell lines using machine learning algorithms.
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:40 PM	**Margherita Francescatto,** Fondazione Bruno Kessler, Italy Deep Learning for drug-induced liver injury prediction
2:40 PM-3:00 PM	**Glen Rex Sumsion,** Brigham Young University, United States An Ensemble Approach to Predicting Drug-induced Liver Injury based on RNA Expression Levels
3:00 PM-3:20 PM	**Zhixiu Lu,** University of South Dakota, United States Predicting Drug Induced Liver Injury Through Combined Genomics Indicator and Ensemble Machine Learning Approaches
3:20 PM-4:00 PM	**Maciej M. Kandula,** Boku University Vienna, Austria Metrics for clinically relevant characterization of patient stratification
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-4:50 PM	**Paweł P. Łabaj, MCB UJ,** Kraków, Poland & Austrian Academy of Sciences, Vienna, Austria Short highlight talks
4:50 PM-5:00 PM	**Anish Datta,** Indian Institute of Engineering Science and Technology, Shibpur, India Connecting Expression Profiles in Cancer Cell Lines with Drug Induced Liver Injury
5:00 PM-5:10 PM	**Yasser El-Manzalawy,** The Pennsylvania State University, United States Multi-view feature selection for multi-omics data integration and its application in cancer survival prediction
5:10 PM-5:20 PM	**Dimitar Vassilev,** Sofia University "St. Kliment Ohridski", Faculty of Mathematics and Informatics, Bulgaria Data integration and survival time prediction models in cancer studies
5:20 PM-5:30 PM	Clinical and molecular markers for the prediction of clinical endpoints in breast cancer patients
5:30 PM-5:40 PM	**Gabriele Franch,** Fondazione Bruno Kessler, Italy Metagenomic fingerprints reveal geographic origin of biological samples collected in mass-transit areas
5:40 PM-5:50 PM	**Alejandro Walker,** University of Florida, United States Deciphering bacterial signatures from WGS metagenomics data from multiple subway stations through MetaSUB International Consortium
5:50 PM-6:00 PM	**Zachary Harris,** Saint Louis University, United States Massive Metagenomic Data Analysis using Abundance-Based Machine Learning

CAMDA: Critical Assessment of Massive Data Analysis

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: COLUMBUS GH*

https://www.iscb.org/cms_addon/conferences/ismb2018/camda.php

10:15 AM-10:20 AM **Joaquin Dopazo,** Fundacion Progreso y Salud, Spain
Data Analysis Challenges of the CAMDA Contest 2018. (II)

10:20 AM-11:20 AM **Daniel H. Huson,** University of Tuebingen, Germany
Computational analysis of short and long microbiome sequencing reads - Keynote

11:20 AM-12:00 PM **Joaquin Dopazo,** Fundacion Progreso y Salud, Spain
Functional biomarkers for precise simple classification in the MetaSUB Forensic Challenge

12:00 PM-12:20 PM **Chengsheng Zhu,** Rutgers University, United States
mi-faser deciphers city subway microbiome functional fingerprints

12:20 PM-12:40 PM **Jolanta Kawulok,** Silesian University of Technology, Poland
Environmental Metagenome Classification for construction of a microbiome fingerprint

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:20 PM **Paweł P Łabaj,** Austrian Academy of Sciences and Jagiellonian University, Poland
Meta-analysis of the MetaSUB forensics challenge, and Outlook: Follow-on challenges 2019

2:20 PM-3:00 PM **Tyler Grimes,** University of Florida, United States
Meta-analysis of Breast Cancer and Neuroblastoma through the integration of RNA-seq network analysis, clinical data, and known signaling pathways

3:00 PM-3:40 PM **Maarten Larmuseau,** Ghent University, Belgium
Pair-based Integration of Gene Expression and CNV Data

3:40 PM-4:00 PM **Ben Lengerich,** Carnegie Mellon University, United States
Proceedings Presentation: Personalized Regression Enables Sample-Specific Pan-Cancer Analysis

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:20 PM **So Yeon Kim,** Ajou University, South Korea
Robust Pathway-based Multi-Omics Data Integration using Directed Random Walk and a Denoising Autoencoder for Survival Prediction in Cancer Studies

5:20 PM-5:40 PM **Shraddha Thakkar,** NCTR, FDA, United States
FDA Meta-analysis of the CMap Drug Safety Challenge, and Outlook: Follow-on Challenges 2019

5:40 PM-6:00 PM **Wenzhong Xiao,** Harvard Medical School & Stanford, United States;
David P. Kreil, Boku University Vienna, Austria
Contest voting, awards, and outlook

RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS

SATURDAY, JULY 7 • *ROOM: GRAND BALLROOM B*

https://www.iscb.org/cms_addon/conferences/ismb2018/rna.php

10:15 AM-10:20 AM Introduction

10:20 AM-11:00 AM **Michael Seiler,** H3 Biomedicine, United States
Invited Talk I

11:00 AM-11:20 AM **Ammar Naqvi,** Children's Hospital of Philadelphia, United States
Aberrant splicing in B-cell acute lymphoblastic leukemia

11:20 AM-11:40 AM **Marina Reixachs,** Universitat Pompeu Fabra, Spain
Measuring ribosome profiling at isoform level: towards unveiling the functional impact of alternative splicing

11:40 AM-12:00 PM **Auinash Kalsotra,** University of Illinois at Urbana-Champaign, United States
Overexpression of a non-muscle Rbfox2 splice isoform drives cardiac dysfunctions in Myotonic Dystrophy type 1

12:00 PM-12:10 PM **Pooja Sethiya,** University Of Macau, Macao
Integrating different transcription profiling data to determine mRNA stability upon host-pathogen interaction

12:10 PM-12:20 PM **Weizhong Li,** Sun Yat-sen University, China
ncRPheDB: identify and prioritize associations between noncoding RNAs and disease phenotypes based on novel evidential metrics

12:20 PM-12:30 PM **Vanessa Aguiar-Pulido,** Cornell University, United States
High-throughput single-cell transcriptomics profiling interneuron specification during brain development

12:30 PM-12:40 PM **Zhen Tan,** University of Rochester, United States
TurboFold II: RNA Structural Alignment and Secondary Structure Prediction Informed by Multiple Homologs

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:20 PM **Jean-Pierre Glouzon,** University of Sherbrooke, Canada
Proceedings Presentation: aliFreeFold: an alignment-free approach to predict secondary structure from homologous RNA sequences

2:20 PM-2:40 PM **Dezhong Deng,** School of EECS, Oregon State University, United States
LinearFold: Linear-Time Prediction of RNA Secondary Structures

2:40 PM-3:00 PM **Anton Petrov,** EMBL-EBI, United Kingdom
Rfam: The transition to a genome-centric sequence database

3:00 PM-3:20 PM **Jan Gorodkin,** University of Copenhagen, Denmark
Enhanced prediction of CRISPR-Cas9 off-targets through modeling of nucleic acid duplex interactions

3:20 PM-3:40 PM **Lucia Lorenzi,** Ghent University, Belgium
RNA atlas: a nucleotide resolution map of the human transcriptome

3:40 PM-4:00 PM **Vincent Boivin,** Université de Sherbrooke, Canada
Uncovering new non-coding RNA genes in human with TGIRT-Seq.

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:00 PM **Yasubumi Sakakibara, Keio University, Japan**
Proceedings Presentation: Convolutional neural networks for classification of alignments of non-coding RNA sequences

5:00 PM-5:20 PM **Jean-Michel Garant, Université de Sherbrooke, Canada**
RNA G-quadruplex prediction to investigate a novel RNA regulation model.

5:20 PM-6:00 PM **Stirling Churchman, Harvard University, United States**
Exploring the nascent transcriptome with direct RNA nanopore sequencing

RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: GRAND BALLROOM B*

https://www.iscb.org/cms_addon/conferences/ismb2018/rna.php

10:15 AM-10:20 AM	Introduction
10:20 AM-11:00 AM	**Gene Yeo,** UCSD University, United States Large-scale studies of RNA binding proteins by eCLIP and proximity labeling
11:00 AM-11:20 AM	**Mark Gerstein,** Yale University, United States RADAR: Annotation and prioritization of variants in the post-transcriptional regulome for RNA-binding proteins
11:20 AM-11:40 AM	**Reazur Rahman,** Brandeis University, United States Identification of RNA-Binding Protein Targets with HyperTRIBE
11:40 AM-12:00 PM	**Carla Mann,** Iowa State University, United States RPIDisorder: A machine learning method for improved prediction of RNA-Protein interaction partners
12:00 PM-12:10 PM	**Bojan Losic,** Icahn School of Medicine at Mount Sinai Hospital, United States Using co-expression networks and predictive models to infer circular RNA regulatory function in colitis models
12:10 PM-12:20 PM	**Hendrik Weisser,** STORM Therapeutics Limited, United Kingdom New tools for RNA epigenetics: an open-source approach to RNA modification analysis
12:20 PM-12:30 PM	**Renana Sabi,** Tel Aviv University, Israel Novel Insights into Gene Expression Regulation during Meiosis Revealed by Translation Elongation Dynamics
12:30 PM-12:40 PM	**Dimitra Karagkouni,** University of Thessaly, Hellenic Pasteur Institute, Greece Ushering in a new era of CLIP-guided detection of miRNA targets
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:10 PM	**Dana Wyman,** University of California, Irvine, Center for Complex Generating full-length, high quality human transcriptomes from PacBio Iso-seq data
2:10 PM-2:20 PM	Long noncoding RNA (lncRNA)-Protein coding gene (PCG) regulatory networks responsive to diverse xenobiotics in rat liver
2:20 PM-2:40 PM	**Tilgner Hagen,** Cornell University, United States A deep long-read sequencing technology reveals coordination of distant exons on RNA molecules to be widespread.
2:40 PM-3:00 PM	**Mingfu Shao,** Carnegie Mellon University, United States Accurate assembly of transcripts through phase-preserving graph decomposition
3:00 PM-3:20 PM	**Christopher Jürges,** Institut für Virologie und Immunbiologie, Julius-Maximilians-Universität Würzburg, Germany Proceedings Presentation: Dissecting newly transcribed and old RNA using GRAND-SLAM
3:20 PM-3:40 PM	**Andrew Thurman,** University of Iowa, United States Gene isoform abundance quantification with third generation transcriptome sequencing
3:40 PM-4:00 PM	**Steven E. Brenner,** University of California, Berkeley, United States Revealing the hidden transcriptome: Analysis of nonsense-mediated mRNA decay target reveals mechanistic insights
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Donny Licatalosi,** Case Western Reserve University, United States Stage-specific mRNA regulatory programs drive mammalian gametogenesis
5:00 PM-5:20 PM	**Namshik Han,** University of Cambridge, United Kingdom Genomic positional conservation identifies topological anchor point RNAs linked to developmental loci
5:20 PM-6:00 PM	**Chaolin Zhang,** Columbia University, United States Modeling RNA-binding protein specificity using single-nucleotide-resolution binding maps: a case study of LIN28 and two subclasses of let-7 microRNAs

Birds of a Feather (BoF)

https://www.iscb.org/ismb2018-program/ismb2018-bof

SATURDAY, JULY 7 • 12:45 PM – 1:45 PM

ROOM: COLUMBUS CD

On Leadership and Management: focus on mentorship

Leader: Lucia Peixoto, Washington State University, United States

Panel
Trey Ideker, University of California San Diego, United States
Casey Green, University of Pennsylvania, United States
Lucia Peixoto, Washington State University, United States
Terry Gaasterland, University of California San Diego, United States

ROOM: COLUMBUS GH

Informatics for Precision Medicine

Leader: Jake Chen, University of Alabama at Birmingham, United States

ROOM: COLUMBUS KL

ISCB Equity, Diversity, and Inclusion Task Force Update and Breakout Sessions

Leader: Madelaine Gogol, Kieran O'Neill, Aurora Blucher

Co-Leaders:
Madelaine Gogol, Stowers Institute for Medical Research
Kieran O'Neill, University of British Columbia / BC Cancer
Aurora Blucher, Oregon Health & Science University

ROOM: COLUMBUS IJ

Cytoscape Community Meeting: Latest updates and Roadmap

Leader: Barry Demchak, University of California at San Diego

MONDAY, JULY 9 • 12:45 PM – 1:45 PM

ROOM: GRAND BALLROOM B

JPI Career Development: Funding opportunities for Early Career Researchers

Leader: Lucia Peixoto, Washington State University, United States

Panelists:
Jennifer Walsh Weller,PhD National Science Foundation, United States
Xujing Wang, PhD NIH/NIDDK, United States
Haluk Resat, PhD NIH/NIGMS, United States

ROOM: COLUMBUS KL

Critical assessment communities

Leader: Steven E Brenner, University of California Berkeley, United States

Education: Computational Biology and Bioinformatics Education and Training

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: COLUMBUS CD*

https://www.iscb.org/cms_addon/conferences/ismb2018/education.php

10:15 AM-10:20 AM **Russell Schwartz,** Carnegie Mellon University, United States
Introduction

10:20 AM-11:00 AM **Keynote: Phillip Compeau,** Carnegie Mellon University, United States
Establishing a computational biology flipped classroom

11:00 AM-11:20 AM **Tomas Helikar,** University of Nebraska-Lincoln, United States
Innovating life sciences education with computational modeling and simulations

11:20 AM-11:40 AM **William Pearson,** U. of Virginia, United States
Teaching BLAST

11:40 AM-12:00 PM **Serghei Mangul,** University of California, Los Angeles, United States
Involving undergraduates in genomics research to narrow the education-research gap

12:00 PM-12:20 PM **Joshua Kangas,** Carnegie Mellon University, United States
A multidisciplinary wet-lab course for computational biology students

12:20 PM-12:40 PM **K. Anton Feenstra,** Vrije Universiteit Amsterdam, Netherlands
Proceedings Presentation: Training for translation between disciplines: A philosophy for life and data sciences curricula

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:40 PM **Keynote: Anne Rosenwald,** Georgetown University, United States
Bioinformatics in the Undergraduate Classroom: Barriers to Integration

2:40 PM-3:00 PM **Vera Matser,** EMBL-EBI, United Kingdom
Implementing a competency-based training strategy for biomolecular researchers with high computational needs

3:00 PM-3:20 PM **Shaun Aron,** University of the Witwatersrand, South Africa
Implementation and evaluation of different training modalities in resource limited settings

3:20 PM-3:40 PM **Shannon McWeeney,** Oregon Health and Science University, United States
Mapping the interdisciplinary landscape to leverage community educational efforts

3:40 PM-4:00 PM **Invited: Allegra Via,** Sapienza University, Rome, Italy
Cognitive psychology in the bioinformatics learning enterprise

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:00 PM **Invited: Bill Morgan,** The College of Wooster, United States
Development of the NIBLSE Learning Resource Collection and Incubators

5:00 PM-5:40 PM **Keynote: Russ Altman,** Stanford University, United States
The Stanford Biomedical Informatics Curriculum: Early results from use in qualifying exams

5:40 PM-6:00 PM Panel Discussion + Wrapup

NetBio: Network Biology

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: GRAND BALLROOM C–F*

https://www.iscb.org/cms_addon/conferences/ismb2018/netbio.php

10:15 AM-10:20 AM	Introduction
10:20 AM-10:40 AM	**Sushant Patkar,** University of Maryland, United States Proceedings Presentation: An optimization framework for network annotation
10:40 AM-11:00 AM	**Scott Simpkins,** University of Minnesota, United States Functional annotation of chemical libraries across diverse biological processes
11:00 AM-11:20 AM	**Aaron Baker,** University of Wisconsin-Madison, United States Pathway-Regularized Matrix Factorization
11:20 AM-11:26 AM	**Phan Nguyen,** Northwestern University, United States Time-lagged ordered lasso for network inference
11:26 AM-11:33 AM	**Jake Crawford,** Tufts University, United States Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases
11:33 AM-11:40 AM	**Mehmet Eren Ahsen,** Icahn School of Medicine at Mount Sinai, United States The transcriptome of a synergistic drug combination emerges from correlated single-drug gene expression via a transcriptional cascade
11:40 AM-12:20 PM	**Anna Goldenberg,** University of Toronto, Canada Keynote: Being Bayesian about gene networks to discover disease mechanisms for complex human diseases
12:20 PM-12:40 PM	Poster Highlights
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Karel Kalecky,** Baylor University, United States Proceedings Presentation: PrimAlign: PageRank-Inspired Markovian Alignment for Large Biological Networks
2:20 PM-2:40 PM	**Shawn Gu,** University of Notre Dame, United States From homogeneous to heterogeneous biological network alignment
2:40 PM-2:46 PM	**Omer Basha,** Ben-Gurion University of the Negev, Israel Expanding the paradigm of differential network analyses toward comparisons between multiple human tissue interactomes highlights tissue-selective processes and disease genes
2:46 PM-2:53 PM	**Nadezhda T. Doncheva,** University of Copenhagen, Denmark Tissue- and organism-specific comparison of mammalian pathways
2:53 PM-3:00 PM	**Jake Chen,** University of Alabama at Birmingham, Informatics Institute, United States Integrated gene ontology, network, and pathway analysis using PAGER
3:00 PM-3:20 PM	**Wei Zhang,** University of California San Diego, United States Proceedings Presentation: Classifying tumors by supervised network propagation
3:20 PM-3:40 PM	**Shuzhao Li,** Emory University, United States Multi-omics, multiscale networks of human immune responses to vaccination and infection
3:40 PM-3:46 PM	**Mohamed Hamed Fahmy,** Rostock University Medical Center, Germany Functional analysis of miRNA-transcription factor synergistic regulatory motifs in Parkinson disease.
3:46 PM-3:53 PM	**George Acquaah-Mensah,** Massachusetts College of Pharmacy & Health Sciences, United States HER2: differences in transcriptional regulation between breast cancer molecular subtypes
3:53 PM-4:00 PM	**Alice Yu,** Stanford University, United States Network-based approach to identifying cell-cell interactions within the lung tumor microenvironment
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-4:46 PM	**Robin Haw,** Ontario Institute for Cancer Research - Reactome, Canada The Reactome Pathway Knowledgebase
4:46 PM-4:53 PM	**Guanming Wu,** Oregon Health and Science University, United States Visualization of Cancer Targetome in the Contexts of Pathways and Networks
4:53 PM-5:00 PM	**Florian Auer,** University Medical Center Göttingen, Germany Composing a dockerized Ecosystem for the Exchange and Visualization of Biological Networks
5:00 PM-5:40 PM	**Trey Ideker,** University of California San Diego, United States Keynote: Decoding patient genomes through the hierarchical pathway architecture of the cancer cell
5:40 PM-6:00 PM	Closing Discussions

TransMed: Translational Medicine Informatics & Applications

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: COLUMBUS IJ*

https://www.iscb.org/cms_addon/conferences/ismb2018/transmed.php

10:15 AM-10:20 AM **Venkata Satagopam,** University of Luxembourg
Introduction

10:20 AM-10:30 AM **Reinhard Schneider,** University of Luxembourg
Opening talk on behalf of the organizing committee

10:30 AM-11:10 AM **Steven E. Brenner,** University of California, Berkeley United States
Interpreting newborn genomes

11:10 AM-11:20 AM **Viji Nair,** University of Michigan, United States
A systematic computational approach in translational medicine to integrate transcriptional profiles to clinical and structural changes for outcome prediction in Diabetic Kidney Disease

11:20 AM-11:40 AM **Christian Bock,** ETH Zurich, Switzerland
Proceedings Presenation: Association Mapping in Biomedical Time Series via Statistically Significant Shapelet Mining

11:40 AM-12:00 PM **Alexander J. Paul,** Saint Louis University, United States
Proceedings Presenation: LONGO: An R Package for Interactive Gene Length Dependent Analysis for Neuronal Identity

12:00 PM-12:20 PM **Wensheng Zhang,** Xavier University of Louisiana, United States
Proceedings Presenation: Driver gene mutations based clustering of tumors: methods and applications

12:20 PM-12:40 PM **Anna Cichonska,** University of Helsinki, Finland
Proceedings Presenation: Learning with multiple pairwise kernels for drug bioactivity prediction

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:40 PM **Maria Secrier,** University College London, United Kingdom
Tracing genomic histories and environmental influences in cancer development

2:40 PM-3:00 PM **Rani Powers,** University of Colorado, United States
Proceedings Presenation: GSEA-InContext: Identifying novel and common patterns in expression experiments

3:00 PM-3:20 PM **Bristena Oprisanu,** University College London, United Kingdom
Proceedings Presenation: AnoniMME: Bringing Anonymity to the Matchmaker Exchange Platform for Rare Disease Gene Discovery

3:20 PM-3:30 PM **Chen Meng,** Technical University of Munich, Germany
Activity landscapes of cancer cell lines predict drug response

3:30 PM-3:40 PM **Aly Khan,** Toyota Technological Institute at Chicago, United States
A generalizable and interpretable deep learning model for predicting microsatellite instability from routine histopathology images

3:40 PM-3:50 PM **Zeeshan Ahmed,** University of Connecticut Health Center, United States
PROMIS-Med: Precise and Reproducible OMICS-Data Management and Integrative System for Precision Medicine

3:50 PM-4:00 PM **Lei Huang,** University of Chicago, United States
Integrative Genomics Analysis Identifies Distinct Prognostic Subgroups In Pediatric Cancers

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-4:50 PM **Francisco Ortuno,** University of Chicago, United States
Building and Using a Gen3 Data Commons for Translational Medicine

4:50 PM-5:00 PM **Yanran Wang,** Rutgers University, United States
Identifying Crohn's disease signal from variome analysis

5:00 PM-5:10 PM **Hyunghoon Cho,** Massachusetts Institute of Technology, United States
Secure genome crowdsourcing for million-individual association studies

5:10 PM-5:50 PM **Jessie Tenenbaum,** Duke University, United States
Clinical and translational informatics: An overview

5:50 PM-6:00 PM Concluding Remarks

VarI: Variant Interpretation

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: COLUMBUS KL*

https://www.iscb.org/cms_addon/conferences/ismb2018/vari.php

10:15 AM-10:20 AM **Introduction**

10:20 AM-10:30 AM **Elizabeth White,** CU-Denver Anschutz Medical Campus, United States
Integration of protein modifications, localizations, and pathways in a biological knowledge base

10:30 AM-11:00 AM **Bonnie Berger,** Massachusetts Institute of Technology, United States
Genomic Crowdsourcing with Privacy

11:00 AM-11:20 AM **Yoonjoo Choi,** Korea Advanced Institute of Science and Technology, South Korea
Proceedings Presentation: DisruPPI: Structure-based computational redesign algorithm for protein binding disruption

11:20 AM-11:40 AM **Maximilian Miller,** Rutgers University, United States
Identifying protein positions for variation driven functional tuning

11:40 AM-12:00 PM **Barthélémy Caron,** Institut Imagine, France
Prediction of non-coding variants causing Mendelian diseases through an integrative supervised learning approach mining signals of ongoing purifying selection in humans

12:00 PM-12:20 PM **Adriana Sperlea,** University of California, Los Angeles, United States
Systematic Discovery of Conservation States for Single-Nucleotide Annotation of the Human Genome

12:20 PM-12:30 PM **Fabrizio Pucci,** Université Libre de Bruxelles, Belgium
Probing the effect of mutations on the interactome

12:30 PM-12:40 PM **Jennifer Poitras,** QIAGEN, United States
Rapid Variant Interpretation and Reporting Using the QIAGEN Knowledgebase and QIAGEN Clinical

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:10 PM **Farhad Hormozdiari,** Harvard University, United States
Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits

2:10 PM-2:40 PM **Mona Singh**
Variation in protein interactions, with applications to disease

2:40 PM-3:00 PM **Lisa Gai,** University of California, Los Angeles, United States
Proceedings Presentation: Finding associated variants in genome-wide association studies on multiple traits

3:00 PM-3:20 PM **Poulami Chaudhuri,** Innovation Lab, Tata Consultancy services, India
An approach to discover branchpoint variants and assess the functional consequences

3:20 PM-3:40 PM **Rachel Marty,** University of California San Diego, United States
Computational modeling of genomic immune variation to deduce role of MHC Class II in cancer susceptibility and evolution

3:40 PM-3:50 PM **Emidio Capriotti,** University of Bologna, Italy
Predicting gene expression changes in E. coli from mRNA sequence information

3:50 PM-4:00 PM **Alex Kaplun,** Variantyx
Detection of pathologic short tandem repeat extensions using Whole Genome Sequencing

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-4:50 PM **Cong Ma,** Carnegie Mellon University, United States
SQUID: Transcriptomic structural variation detection from RNA-seq

4:50 PM-5:20 PM **Olga Troyanskaya,** Princeton University, United States
Decoding the human genome with deep learning models.

5:20 PM-5:40 PM **Hsuan-Lin Her,** Taipei Medical University, Taiwan
Proceedings Presentation: A pan-genome-based machine learning approach for predicting antimicrobial resistance activities of the Escherichia coli strains

5:40 PM-6:00 PM **Bjoern Stade,** Fabric Genomics Inc., United States
Phenotype-driven variant prioritization significantly improves over impact and prevalence scores in a large-scale analysis of 2,408 cases of Mendelian disease diagnostics by whole-genome sequencing

HitSeq: High Throughput Sequencing Algorithms & Applications

COSI TRACK PRESENTATIONS

SUNDAY, JULY 8 • *ROOM: GRAND BALLROOM A*

https://www.iscb.org/cms_addon/conferences/ismb2018/hitseq.php

10:15 AM-10:20 AM	Welcome
10:20 AM-11:20 AM	**Nancy Cox,** Vanderbilt University, United States Using Biobanks to swim upstream: phenome risk scores as a way to start with function and move to phenotype
11:20 AM-11:40 AM	**Ibrahim Numanagić,** Massachusetts Institute of Technology, United States Allelic decomposition and exact genotyping of highly polymorphic and structurally variant genes
11:40 AM-12:00 PM	**Jorge Duitama,** Universidad de los Andes, Colombia Realignment of short reads around short tandem repeats significantly improves accuracy of genomic variants detection
12:00 PM-12:20 PM	**Hugues Richard,** University Pierre and Marie Curie, France Jointly aligning a group of DNA reads improves accuracy of identifying large deletions
12:20 PM-12:40 PM	**Yun Feng,** University of Oxford, United Kingdom Convolutional filtering for mutation signature detection
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Weihua Pan,** University of California, Riverside, United States Proceedings Presentation: Novo&Stitch: Accurate Reconciliation of Genome Assemblies via Optical Maps
2:20 PM-2:40 PM	**Shilpa Garg,** MPI-INF, Germany Proceedings Presentation: A graph-based approach to diploid genome assembly
2:40 PM-3:00 PM	**Tobias Marschall,** Max Planck Institute for Informatics, Center for Bioinformatics, Saarland Proceedings Presentation: Strand-seq Enables Reliable Separation of Long Reads by Chromosome via Expectation Maximization
3:00 PM-3:20 PM	**Fatemeh Almodaresi,** Stony Brook University, United States Proceedings Presentation: A space and time-efficient index for the compacted colored de Bruijn graph
3:20 PM-3:40 PM	**Jay Ghurye,** University of Maryland, United States Integrating Hi-C links with assembly graphs for chromosome-scale assembly
3:40 PM-4:00 PM	**Mohamed Gunady,** University of Maryland, United States Bridging Linear to Graph-based Alignment with Whole Genome Population Reference Graphs
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**A. Ercument Cicek,** Bilkent University, Turkey Hercules: a profile HMM-based hybrid error correction algorithm for long reads
5:00 PM-6:00 PM	**Ekta Khurana,** Weill Cornell Medical College, United States Non-coding genetic variation in cancer

HitSeq: High Throughput Sequencing Algorithms & Applications

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: GRAND BALLROOM A*

https://www.iscb.org/cms_addon/conferences/ismb2018/hitseq.php

10:15 AM-11:20 AM	**Cenk Sahinalp,** Indiana University, United States **Coordinated evolution of tumor phylogeny inference methods and sequencing technologies**
11:20 AM-11:40 AM	**Gryte Satas,** Brown University, United States **Proceedings Presentation: Haplotype Phasing in Single-Cell DNA Sequencing Data**
11:40 AM-12:00 PM	**Yves Moreau,** Katholieke Universiteit Leuve, Belgium **HiVA: a web platform for haplotyping and copy number analysis of single-cell genomes and mosaicism detection in bulk DNA**
12:00 PM-12:20 PM	**Kieran Campbell,** The University of British Columbia, Canada **Probabilistic inference of clonal gene expression through integration of RNA & DNA-seq at single-cell resolution**
12:20 PM-12:40 PM	**Ka Ming Nip,** BC Cancer Genome Sciences Centre, Canada **De novo single-cell transcript sequence reconstruction with Bloom filters**
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Benjamin Vandervalk,** BC Cancer Genome Sciences Centre, Canada **ABySS-LR: de novo Assembly Pipeline for Linked Reads**
2:20 PM-2:40 PM	**Heewook Lee,** Carnegie Mellon University, United States **Kourami: Graph-guided assembly for novel HLA allele discovery**
2:40 PM-3:00 PM	**Alexey Gurevich,** St. Petersburg State University, St. Petersburg, Russia, Russia **Proceedings Presentation: Versatile genome assembly evaluation with QUAST-LG**
3:00 PM-3:20 PM	**Kendell Clement,** Harvard University, United States **Proceedings Presentation: AmpUMI: Design and analysis of unique molecular identifiers for deep amplicon sequencing**
3:20 PM-3:40 PM	**Nima Nouri,** Yale School of Medicine, United States **Proceedings Presentation: A Spectral Clustering-Based Method for Identifying Clones from High-throughput B cell Repertoire Sequencing Data**
3:40 PM-4:00 PM	**Kristoffer Sahlin,** Pennsylvania State University, United States **IsoCon: Deciphering highly similar multigene family transcripts from Iso-Seq data**
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Alex Zelikovsky,** Georgia State University, United States **CliqueSNV: Scalable Reconstruction of Intra-Host Viral Populations from NGS Reads**
5:00 PM-5:20 PM	**Martin Steinegger,** Max-Planck-Institute, Republic of Korea **MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets**
5:20 PM-5:40 PM	**Gamze Gursoy,** Yale University, United States **Quantification of private information leakage and privacy-preserving file formats for functional genomics data**
5:40 PM-6:00 PM	**Guillaume Marçais,** Carnegie Mellon University, United States **Proceedings Presentation: Asymptotically optimal minimizers schemes**

BioVis: Biological Data Visualizations

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: COLUMBUS IJ*

https://www.iscb.org/cms_addon/conferences/ismb2018/biovis.php

10:15 AM-10:20 AM	**Marc Streit,** Johannes Kepler University Linz, Germany Opening Remarks
10:20 AM-11:20 AM	**Keynote: Martin Krzywinski,** BC Cancer Agency, Canada 0ne successful data exploration—many explanations
11:20 AM-11:40 AM	**Marwan Abdellah,** Blue Brain Project/EPFL, Switzerland Proceedings Presentation: NeuroMorphoVis: a collaborative framework for visualization and analysis of neuronal morphology skeletons reconstructed from microscopy stacks
11:40 AM-11:50 AM	**Joshua W. K. Ho,** Victor Chang Cardiac Research Institute, Australia starmap: Immersive visualisation of single cell data using smartphone-enabled virtual reality
11:50 AM-12:00 PM	**Thomas Höllt,** Delft University of Technology, Leiden University Medical Center, Netherlands Interactive Visual Analysis of Mass Cytometry Data by Hierarchical Stochastic Neighbor Embedding Reveals Rare Cell Types
12:00 PM-12:10 PM	**Karsten Schatz,** University of Stuttgart, Germany Visual Analysis of Enzyme-Substrate Interactions
12:10 PM-12:20 PM	**Michael J.E. Sternberg,** Imperial College London, United Kingdom BioBlox – A suite of computer games for protein docking for crowd-sourcing scientific solutions and education via mobiles and virtual reality
12:20 PM-12:30 PM	**Lindsay Rutter,** Iowa State University, United States Visualization methods for RNA-sequencing data analysis
12:30 PM-12:40 PM	**Hani Girgis,** University of Tulsa, United States HebbPlot: A new tool for visualizing histone signatures
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-3:00 PM	**Keynote: Sheelagh Carpendale,** University of Calgary, Canada The Changing Nature of Collaboration in Visualization
3:00 PM-3:20 PM	**Pierre Boutillier,** Harvard University, United States Proceedings Presentation: The Kappa platform for rule-based modeling
3:20 PM-3:30 PM	**Fritz Lekschas,** Harvard University, United States Feature-Centric Visual Exploration of Genome Interaction Maps
3:30 PM-3:40 PM	**Danielle Nguyen,** Harvard University, United States Scaling Up the Genome Browser
3:40 PM-3:50 PM	**Javi Zhang,** University of Toronto, Canada PopNetD3: An accessible web tool for the analysis and visualization of population structure
3:50 PM-4:00 PM	**Kunal Kundu,** University of Maryland, United States MecCog: A framework for representing human genetic disease mechanisms
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:20 PM	**Invited: Nils Gehlenborg,** Harvard University, United States Mining Gems from the Data Visualization Literature
5:20 PM-5:30 PM	**Kyoung Tak Cho,** Iowa State University, United States MaizeDIG: A mechanism for connecting gene models to phenotypes at MaizeGDB
5:30 PM-5:40 PM	**Alida Palmisano,** National Cancer Institute, DCTD/BRP, United States D3Oncoprint: Standalone software to visualize and dynamically explore annotated genomic mutation files
5:40 PM-5:50 PM	**Theresa Anisja Harbig,** University of Tübingen, Germany Visualization of Longitudinal Cancer Genomics Data
5:50 PM-6:00 PM	**Kay Nieselt,** University of Tübingen, Germany Closing Remarks

EvolCompGen: Evolution and Comparative Genomics

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: COLUMBUS CD*

https://www.iscb.org/cms_addon/conferences/ismb2018/evolution.php

10:15 AM-10:20 AM Introduction

10:20 AM-10:40 AM **Edward L. Braun,** University of Florida, United States
Proceedings Presentation: An evolutionary model motivated by physico-chemical properties of amino acids reveals variation among proteins

10:40 AM-10:50 AM **Daniella F Lato,** McMaster University, Canada
Spatial Patterns of Substitutions in Bacterial Genomes

10:50 AM-11:00 AM **Huy Nguyen,** Iowa State University, United States
Tracing the Ancestry of Operons in Bacteria

11:00 AM-11:10 AM **Ana Maria Rojas,** CSIC-IBIS, Spain
A novel MMR pathway in prokaryotes

11:10 AM-11:20 AM **Wataru Iwasaki,** The University of Tokyo, Japan
Generalist species drive microbial dispersion and evolution.

11:20 AM-11:30 AM **Itamar Sela,** NCBI/NIH, United States
Evolution of the pangenome and core genome in prokaryotes

11:30 AM-11:40 AM **Louxin Zhang**
A package for computing distance metrics for phylogenetic networks

11:40 AM-12:00 PM **Jesse Eaton,** Carnegie Mellon University, United States
Proceedings Presentation: Deconvolution and phylogeny inference of structural variations in tumor genomic samples

12:00 PM-12:10 PM **Mohammed El-Kebir,** University of Illinois at Urbana-Champaign, United States
Inferring Parsimonious Migration Histories for Metastatic Cancers

12:10 PM-12:20 PM **Benjamin Siranosian,** Harvard University, United States
Genetic and transcriptional instability alters cancer cell line drug response

12:20 PM-12:30 PM **Zena Lapp,** University of Michigan, United States
Regional transmission and antibiotic resistance evolution of the hospital pathogen Klebsiella pneumoniae

12:30 PM-12:40 PM **Giltae Song,** Pusan National University, South Korea
A non-parametric statistical test for determining fine-scale temporal variation patterns in evolving populations

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:20 PM **Manuel Lafond,** University of Ottawa, Canada
Proceedings Presentation: Accurate prediction of orthologs in the presence of divergence after duplication

2:20 PM-2:30 PM **Tina Begum,** University of Lausanne, Switzerland
Testing the "ortholog conjecture" with phylogenetic and pairwise methods under realistic simulations of evolution after duplication, and after fish whole genome duplication

2:30 PM-2:40 PM **Nadia El-Mabrouk,** University of Montreal, Canada
Reconstructing the history of syntenies through SuperReconciliation

2:40 PM-2:50 PM **Christophe Dessimoz,** University of Lausanne, SwitzerlandRe
OMA standalone: orthology inference among public and custom genomes and transcriptomes

2:50 PM-3:00 PM **Urminder Singh,** Iowa State University, United States
Characterization of human orphan genes and its functions using annotated and unannotated genomic and massive RNA-seq data and metadata

3:00 PM-3:20 PM **Jiafan Zhu,** Rice University, United States
Proceedings Presentation: Inference of Species Phylogenies from Bi-allelic Markers Using Pseudo-likelihood

3:20 PM-3:30 PM **Kenneth B. Hoehn,** Yale University, United States
A unified maximum likelihood approach to B cell repertoire phylogenetics

3:30 PM-3:40 PM **Alex Nord,** University of Montana, United States
Mirage: Splice-Aware Multiple Sequence Alignment of Protein Isoforms

3:40 PM-3:50 PM **Gon Carmi,** Bar-Ilan University, Israel
Protein-Protein Interactions of Stress-Response Genes are Conserved in Subterranean and Fossorial Animals and Cluster Unambiguously to their Shared Ecology

3:50 PM-4:00 PM **Janani Ravi,** Michigan State University, United States
The evolution, conservation, and covariation of the Psp envelope-stress-response system

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

3DSIG: Structural Bioinformatics and Computational Biophysics

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: COLUMBUS AB*

https://www.iscb.org/cms_addon/conferences/ismb2018/3dsig.php

10:15 AM-10:20 AM	Introduction
10:20 AM-11:00 AM	**Christine Orengo,** University College London, United Kingdom Structural insights into the impacts of genetic variations in splicing and disease
11:00 AM-11:20 AM	**Debswapna Bhattacharya,** Auburn University, United States scoreD: Deep discriminative ensemble classifiers for protein scoring
11:20 AM-11:40 AM	**Khalique Newaz,** University of Notre Dame, United States Network approach integrates 3D structural and sequence data to improve protein structural comparison
11:40 AM-12:00 PM	**Florian Kaiser,** University of Applied Sciences Mittweida, Germany Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases
12:00 PM-12:20 PM	**John-Marc Chandonia,** Berkeley National Lab, United States Structural Classification of Proteins in the post-Structural Genomics era
12:20 PM-12:40 PM	**Jianlin Cheng,** University of Missouri - Columbia, United States Improved protein contact prediction using two-level deep convolutional neural networks
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Jinbo Xu,** Toyota Technological Institute at Chicago, United States Proceedings Presentation: Protein threading using residue co-variation and deep learning
2:20 PM-2:40 PM	**Witold Dyrka,** Wroclaw University of Science and Technology, Poland Where the context-free grammar meets the contact map: a probabilistic model of protein sequences aware of contacts between amino acids
2:40 PM-3:00 PM	**Charlotte Deane,** University of Oxford, United Kingdom Predicting Loop Conformational Ensembles
3:00 PM-3:20 PM	**Antoniya Aleksandrova,** NINDS – NIH, United States Systematic Analysis of Symmetry and Pseudo-Symmetry in Membrane Protein Structures
3:20 PM-3:40 PM	**Philippe Youkharibache,** NCI/NIH, United States Pseudo-Symmetry in 7 Transmembrane Helix (7TMH) Proteins: Intragenic Duplication of Protodomains with Evolutionary Balance of Structural Constraints and Functional Divergence
3:40 PM-4:00 PM	**Daisuke Kihara,** Purdue University, United States Predicting the assembly order of multimeric heteroprotein complexes
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Genki Terashi,** Purdue University, United States MAINMAST: De novo Main-chain Modeling for EM maps Using Tree-graph optimization.
5:00 PM-5:20 PM	**Xiangrui Zeng,** Carnegie Mellon University, United States Proceedings Presentation: An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification
5:20 PM-5:40 PM	**Alexey Porollo,** Cincinnati Children's Hospital Medical Center, United States Metalloproteome landscape from the amino acid covariance perspective
5:40 PM-6:00 PM	**Vivek Modi,** Fox Chase Cancer Center, United States Clustering and classification of active and inactive protein kinase structures

3DSIG: Structural Bioinformatics and Computational Biophysics

COSI TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: COLUMBUS AB*

https://www.iscb.org/cms_addon/conferences/ismb2018/3dsig.php

8:35 AM-8:40 AM	Introduction
8:40 AM-9:00 AM	**Bhumika Arora,** Indian Institute of Technology, Monash University, and IITB-Monash Research Academy, India Improving the prediction of loops and drug binding in GPCR structure models
9:00 AM-9:20 AM	**Marcel S. Frenkel,** Duke University, United States OSPREY 3.0: Open-Source Protein Redesign for You, with Powerful New Features
9:20 AM-9:40 AM	**Yang Shen,** Texas A&M University, United States iCFN: an efficient exact algorithm for multistate protein design
9:40 AM-10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:15 AM-10:20 AM	Introduction
10:20 AM-11:20 AM	**Philip E. Bourne,** School of Medicine, University of Virginia, United States Towards Better Reproducibility (Discussion led by Philip E. Bourne)
11:20 AM-11:40 AM	**Adnan Sljoka,** Kwansei Gakuin University, Japan High throughput analysis of allostery through propagation of rigidity
11:40 AM-12:00 PM	**Janez Konc,** National Institute of Chemistry, Slovenia ProBiSdock: flexible docking using existing knowledge from the Protein Data Bank
12:00 PM-12:20 PM	Energetic conflicts in catalytic sites of protein enzymes
12:20 PM-12:40 PM	**Louis-Philippe Morency,** University of Montreal, Canada The Impact of Conformational Entropy on the Accuracy of the Molecular Docking Software FlexAID in Binding Mode Prediction
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-3:00 PM	**Fergus Boyles,** University of Oxford, United Kingdom; **Fergus Imrie,** University of Oxford, United Kingdom Collaborative structural biology using machine learning and Jupyter notebook
3:00 PM-3:20 PM	**Hakime Öztürk,** Bogazici University, Turkey Proceedings Presentation: A novel methodology on distributed representations of proteins using their interacting ligands
3:20 PM-3:40 PM	**Leandro Radusky,** CRG, Spain FoldX accurate biomolecular binding prediction using PADA1 (Protein Assisted DNA Assembly v1)
3:40 PM-4:00 PM	**Henry Martell,** The University of Kent, United Kingdom Investigating the molecular determinants of ebolavirus pathogenicity
4:20 PM-4:40 PM	**Hongjun Bai,** WRAIR, Henry M. Jackson Foundation for the Advancement of Military Medicine, United States The breadth of HIV broadly neutralizing antibodies depends on how they engage key epitope sites

Bio-Ontologies

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: COLUMBUS EF*

https://www.iscb.org/cms_addon/conferences/ismb2018/bioontologies.php

10:15 AM-10:20 AM	Introduction
10:20 AM-11:20 AM	**Nicola Mulder,** University of Cape Town, South Africa The use of existing and new ontologies in African biomedical research
11:20 AM-11:40 AM	**Yisu Peng,** Indiana University Bloomington, United States Proceedings Presentation: Enumerating consistent subgraphs of directed acyclic graphs: an insight into biomedical ontologies
11:40 AM-12:00 PM	**Randi Vita,** La Jolla Institute for Allergy & Immunology, United States Standardizing ontology metadata in the OBO registry and beyond
12:00 PM-12:06 PM	Ontology-based Semantic Mapping of Chemical Toxicities
12:06 PM-12:13 PM	FAIRShake: Toolkit to Enable the FAIRness Compliance Assessment of Biomedical Digital Objects
12:13 PM-12:20 PM	Minimum Information Required: Guideline for Stroke Research and Clinical Data Reporting
12:20 PM-12:26 PM	Structuring Genetic Disease Complexity & Environmental Drivers
12:26 PM-12:33 PM	Automated Negative Gene Ontology Based Functional Predictions for Proteins with UniGOPred
12:33 PM-12:40 PM	PyxisMap: Phenotype Rankings for Genomic Sequencing Variants
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:10 PM	Ontology application at the ENCODE portal
2:10 PM-2:20 PM	An Unsupervised Probabilistic Method for Automatically Integrating Multiple Disease Terminologies
2:20 PM-2:40 PM	**Fatima Zohra Smaili,** King Abdullah University of Science and Technology, Saudi Arabia Proceedings Presentation: Onto2Vec: joint vector-based representation of biological entities and their ontology-based annotations
2:40 PM-3:00 PM	**Lucy Lu Wang,** University of Washington, United States Ontology-based annotation and integration of pathway databases
3:00 PM-4:00 PM	**Volker Tresp** Deep X: Deep Learning with Deep Knowledge
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
5:00 PM-6:00 PM	The Role of Ontologies in Artificial Intelligence (and Machine Learning)

Bio-Ontologies

COSI TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: COLUMBUS EF*

https://www.iscb.org/cms_addon/conferences/ismb2018/bioontologies.php

Bio-Ontologies

8:35 AM-8:40 AM	Introduction
8:40 AM-9:00 AM	**Sara Althubaiti,** King Abdullah University of Science and Technology, Saudi Arabia Ontology-Based Concept Recognition by Using Word Embeddings
9:00 AM-9:20 AM	**Arjun Magge,** ASU, United States Proceedings Presentation: Deep neural networks and distant supervision for geographic location mention extraction
9:20 AM-9:26 AM	**Willem Van Panhuis,** University of Pittsburgh, United States Project Tycho 2.0: a new repository for the integration and reuse of global health data
9:26 AM-9:33 AM	Computational Classification of Phenologs across Biological Diversity
9:33 AM-9:40 AM	**Tunca Dogan,** EMBL-EBI, CanSyL, METU, United Kingdom HPO2GO: Prediction of Human Phenotype Ontology Term Associations for Proteins Using Cross Ontology Annotation Co-occurrences
9:40 AM-10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:15 AM-10:20 AM	Introduction
10:20 AM-10:40 AM	**Wenhui Xing,** Wuhan University of Technology, China Proceedings Presentation: A Gene-Phenotype Relationship Extraction Pipeline from the Biomedical Literature Using a Representation Learning Approach
10:40 AM-11:00 AM	**Senay Kafkas,** King Abdullah University of Science and Technology, Saudi Arabia Ontology based mining of pathogen-disease associations from literature
11:00 AM-11:20 AM	**Josef Hardi,** Stanford BMIR, United States Assessing Schema.org's Coverage of Terms from Key Biomedical Datasets
11:20 AM-11:40 AM	**Michael Sinclair,** University of Utah, United States Intelligently Designed Ontology Alignment: A Case Study from the Sequence Ontology
11:40 AM-11:46 AM	Establishing the framework for an African Genome Archive
11:46 AM-11:53 AM	Predicting new relationships between genes and Human Phenotype Ontology terms
11:53 AM-12:00 PM	OntoloBridge – A Semi-Automated Ontology Update Request System
12:00 PM-12:10 PM	One Minute Short Talks
12:10 PM-12:20 PM	Closing

Microbiome

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: COLUMBUS KL*

https://www.iscb.org/cms_addon/conferences/ismb2018/microbiome.php

MICROBIOME
COMMUNITY OF SPECIAL INTEREST

2:00 PM-2:40 PM **Adam Phillippy,** National Human Genome Research Institute, National Institutes of Health, United States
Keynote I: Why is species-level classification so hard and how can we make it easy?

2:40 PM-3:00 PM **Alice McHardy,** Helmholtz Centre for Infection Research, Germany
CAMI Overview, Introduction CAMI II challenges

3:00 PM-3:10 PM **Adrian Fritz,** Helmholtz Centre for Infection Research, Germany
CAMISIM: Simulating metagenomes and microbial communities

3:10 PM-3:20 PM **Fernando Meyer,** Helmholtz Centre for Infection Research, Germany
AMBER: Assessment of Metagenome BinnERs

3:20 PM-3:40 PM **Alexander Sczyrba,** Bielefeld University, Germany
CAMI Evaluation Metrics: Assembly, Profiling

3:40 PM-4:00 PM **Aaron E. Darling,** University of Technology, Sydney, Australia
A CAMI metagenomic Hi-C challenge: what should it look like?

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:20 PM **Curtis Huttenhower,** Harvard University, United States
Keynote II: Methods for multi'omics in microbial community population studies

5:20 PM-5:40 PM **Haris Vikalo,** The University of Texas at Austin, United States
Proceedings Presentation: Viral quasispecies reconstruction via tensor factorization with successive read removal

5:40 PM-5:50 PM **Zhenwei Dai,** The Chinese University of Hong Kong, Hong Kong
Batch Effects Correction for Microbiome Data with Dirichlet-multinomial Regression

5:50 PM-6:00 PM **Xiyu Peng,** Iowa State University, United States
Ampliclust: A Fully Probabilistic Model-Based Approach Denoising Illumina Amplicon Data

Microbiome

COSI TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: COLUMBUS KL*

https://www.iscb.org/cms_addon/conferences/ismb2018/microbiome.php

MICROBIOME
COMMUNITY OF SPECIAL INTEREST

8:35 AM-8:40 AM	Session Overview and Introductions
8:40 AM-9:20 AM	**Katherine Pollard,** Gladstone Institutes and University of California, San Francisco, United States Keynote III: Metagenotyping Reveals Cryptic Functional Variation in the Human Microbiome
9:20 AM-9:30 AM	**Himel Mallick,** Harvard University, United States Multivariable Association in Population-scale Meta'omic Surveys
9:30 AM-9:40 AM	**Jason Lloyd-Price,** Harvard University, United States Gaussian process models for microbial dynamics in the expanded Human Microbiome Project
9:40 AM-10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:15 AM-10:20 AM	Session Continuation and Introductions
10:20 AM-11:20 AM	CAMI – how to get involved
11:20 AM-11:40 AM	**Ehsaneddin Asgari,** University of California, Berkeley, United States Proceedings Presentation: MicroPheno: Predicting environments and host phenotypes from 16S rRNA gene sequencing using a k-mer based representation of shallow sub-samples
11:40 AM-11:50 AM	**Daniel H. Huson,** University of Tuebingen, Germany MEGAN-LR: New algorithms allow accurate binning and easy interactive exploration of metagenomic long reads and contigs
11:50 AM-12:00 PM	**Andreas Bremges,** Helmholtz Centre for Infection Research, Germany Probabilistic abundance estimation accelerates metagenome binning by orders of magnitude
12:00 PM-12:20 PM	**ZhengZheng Tang,** University of Wisconsin-Madison, United States Zero-Inflated Generalized Dirichlet Multinomial (ZIGDM) Regression Model for Microbiome Compositional Data
12:20 PM-12:30 PM	**Gholamali Rahnavard,** Broad Institute of MIT and Harvard, United States Identifying important uncharacterized genes using metagenomes and metatranscriptomes
12:30 PM-12:40 PM	Predicting Microbial Ecology from Shotgun Metagenomic Data
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:40 PM	**Murat Eren,** University of Chicago, United States Keynote IV: Metagenomic insights into ecology, evolution, and biochemistry of single environmental populations through single-amino acid variants.
2:40 PM-2:50 PM	**Tiffany Hsu,** Harvard University, United States Identifying novel lateral gene transfer events from assembled metagenomes
2:50 PM-3:00 PM	**Siyuan Ma,** Harvard University, United States Population structure discovery in meta-analyzed microbial communities
3:00 PM-3:10 PM	**Stefan Janssen,** University of California San Diego, United States Phylogenetic placement of exact amplicon sequences improves associations with clinical information
3:10 PM-3:20 PM	**Derek Reiman,** University of Illinois at Chicago, United States PopPhy-CNN: A Convolutional Neural Network Approach Using Embedded Phylogenetic Trees for Analyzing the Association of Host Microbiome and Phenotype
3:20 PM-3:30 PM	**Peter Karp,** SRI International, United States Computing Metabolic Routes in the Human Microbiome
3:30 PM-3:40 PM	**Dmitry Rodionov,** Sanford Burnham Prebys Institute and IITP RAS, United States Genomics-based prediction of metabolic phenotypes in microbial communities
3:40 PM-4:00 PM	**Lars Juhl Jensen,** University of Copenhagen, Denmark Text-mining-based interpretation of microbiome data
4:20 PM-4:40 PM	Outlook / Community Input

MLCSB: Machine Learning in Computational and Systems Biology

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: GRAND BALLROOM C–F*

https://www.iscb.org/cms_addon/conferences/ismb2018/mlcsb.php

10:15 AM-10:20 AM	Introduction
10:20 AM-11:20 AM	**Olga Troyanskaya,** Princeton University, United States Keynote:
11:20 AM-11:40 AM	**Seonwoo Min,** Seoul National University, South Korea Deep-learning improves prediction of CRISPR-Cpf1 guide RNA activity
11:40 AM-12:00 PM	**Dan DeBlasio,** Carnegie Mellon University, United States Automatically eliminating errors induced by suboptimal parameter choices in transcript assembly
12:00 PM-12:20 PM	**Jacob Schreiber,** University of Washington, United States Multi-scale Deep Tensor Factorization Learns a Latent Representation of the Human Epigenome
12:20 PM-12:40 PM	**Maziyar Baran Pouyan,** University of Pittsburgh, United States Proceedings Presentation: Random forest based similarity learning for single cell RNA sequencing data
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Emmi Jokinen,** Aalto University, Finland Proceedings Presentation: mGPfusion: Predicting protein stability changes with Gaussian process kernel learning and data fusion
2:20 PM-2:40 PM	**Yu Li,** KAUST, Saudi Arabia Proceedings Presentation: DLBI: Deep learning guided Bayesian inference for structure reconstruction of super-resolution fluorescence microscopy
2:40 PM-3:00 PM	**Hannes Bretschneider,** University of Toronto, Canada Proceedings Presentation: COSSMO: Predicting Competitive Alternative Splice Site Selection using Deep Learning
3:00 PM-4:00 PM	**Matthew Stephens,** University of Chicago, United States Keynote: Adventures with sparsity and structure in computational biology
4:00 PM-4:40 PM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
4:40 PM-5:00 PM	**Hee June Choi,** Worcester Polytechnic Institute, United States A Machine learning approach to dissect subcellular protrusion heterogeneity and the underlying actin regulator dynamics
5:00 PM-5:20 PM	**Hatice Osmanbeyoglu,** MSKCC, United States Inferring transcriptional regulatory programs in gynecological cancers
5:20 PM-5:40 PM	**Paul Stapor,** Helmholtz Center for Environmental Health, Germany Proceedings Presentation: Optimization and profile calculation of ODE models using second order adjoint sensitivity analysis
5:40 PM-6:00 PM	**Sumana Srivatsa,** ETH Zurich, Switzerland Proceedings Presentation: Improved pathway reconstruction from RNA interference screens by exploiting off-target effects

MLCSB: Machine Learning in Computational and Systems Biology

COSI TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: GRAND BALLROOM C–F*

https://www.iscb.org/cms_addon/conferences/ismb2018/mlcsb.php

8:35 AM-8:40 AM	Introduction
8:40 AM-9:40 AM	**Quaid Morris** Keynote: Machine learning in cancer genomics
9:40 AM-10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:20 AM-10:40 AM	**Ahmet Süreyya Rifaioğlu**, Middle East Technical University, Turkey Drug-Target Interaction Prediction with Deep Convolutional Neural Networks Using Compound Images
10:40 AM-11:00 AM	**Andrew Rouillard,** GSK, United States Can Deep Learned Omic features predict clinically successful therapeutic targets?
11:00 AM-11:20 AM	**Samuel Kaski,** Aalto University, Finland Proceedings Presentation: Improving genomics-based predictions for precision medicine through active elicitation of expert knowledge
11:20 AM-11:40 AM	**Mehmet Gönen,** Koç University, Turkey Proceedings Presentation: Discriminating early- and late-stage cancers using multiple kernel learning on gene sets
11:40 AM-12:00 PM	**Francesca Petralia,** Mount Sinai Medical School, United States Proceedings Presentation: A new method for constructing tumor specific gene co-expression networks based on samples with tumor purity heterogeneity
12:00 PM-12:20 PM	**Yves Moreau,** Katholieke Universiteit Leuven, Belgium Proceedings Presentation: Gene Prioritization Using Bayesian Matrix Factorization with Genomic and Phenotypic Side Information
12:20 PM-12:40 PM	**Marinka Zitnik,** Stanford University, United States Proceedings Presentation: Modeling Polypharmacy Side Effects with Graph Convolutional Networks
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-3:00 PM	**Alexis Battle** Keynote: Context-specific and dynamic effects of genetic variation
3:00 PM-3:20 PM	**Ana Stanescu,** University of West Georgia, United States Integrating heterogeneous predictive models using Reinforcement Learning
3:20 PM-3:40 PM	**Tahmid Mehdi,** University of Toronto, Canada Applying semi-supervised variational inference to heterogeneous genomic data predicts heart enhancers
3:40 PM-4:00 PM	**Yue Wu,** University of California, Los Angeles, United States Proceedings Presentation: A scalable estimator of SNP heritability for Biobank-scale data
4:20 PM-4:40 PM	**Ruth Johnson,** University of California, Los Angeles, United States Proceedings Presentation: A unifying framework for joint trait analysis under a non-infinitesimal model

RegSys: Regulatory and Systems Genomics

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 • *ROOM: GRAND BALLROOM B*

https://www.iscb.org/cms_addon/conferences/ismb2018/regsys.php

10:15 AM-10:20 AM **Julia Zeitlinger,** Stowers Institute, United States
Welcome to RegSys Day 1

10:20 AM-10:50 AM **Remo Rohs,** University of Southern California, United States
Keynote: A tale of DNA shape analysis: a user manual and next steps

10:50 AM-11:00 AM **Raluca Gordan,** Duke University, United States
Divergence in DNA specificity among paralogous transcription factors contributes to their differential in vivo binding

11:00 AM-11:20 AM **Ariel Afek,** Duke University, United States
Mismatched base-pairs locally distort DNA structure and can induce increased DNA-binding by transcription factor proteins

11:20 AM-11:40 AM **Robin Dowell,** University of Colorado, Boulder, United States
Enhancer RNA profiling predicts transcription factor activity

11:40 AM-12:00 PM **Ivan G. Costa,** RWTH Aachen University, Germany
Identification of Transcription Factor Binding Sites using ATAC-seq

12:00 PM-12:20 PM **Jinfeng Xiao,** University of Illinois at Urbana-Champaign, United States
Proceedings Presentation: SigMat: A Classification Scheme for Gene Sig-nature Matching

12:20 PM-12:30 PM **Juri Reimand,** Ontario Institute for Cancer Research, Canada
Candidate non-coding driver mutations in super-enhancers and long-range chromatin interaction networks

12:30 PM-12:31 PM **Dennis Kostka,** University of Pittsburgh, United States
What We Talk About When We Talk About Enhancers

12:31 PM-12:32 PM **Verena Heinrich,** Max Planck Institute for Molecular Genetics, Germany
Differential Analysis of Regulatory Elements Based on ChIP-seq Data

12:32 PM-12:33 PM **Matteo Barberis,** University of Amsterdam, Netherlands
ChIP-exo analysis highlights Fkh transcription factors as hubs that integrate multi-scale networks in budding yeast

12:33 PM-12:34 PM **Joydeep Mitra,** Albert Einstein College of Medicine, United States
Genome-wide identification of enhancer release and retargeting, a novel disease mechanism involving enhancer-gene target switching

12:34 PM-12:35 PM **Atul Deshpande,** University of Wisconsin Madison; Morgridge Institute of Research, United States
Network Inference from Single-Cell Transcriptomic Data Using Granger Causality

12:35 PM-12:36 PM **Yungil Kim,** Icahn School of Medicine at Mt. Sinai, United States
Novel normalization and clustering methods for accurately identifying subtypes of single cells in fresh human brains

12:36 PM-12:37 PM **Konstantine Tchourine,** NYU – Center for Genomics and Systems Biology, United States
Bridging the Gap Between Detailed Biophysical Modeling and Large-Scale Inference of Expression Regulation

12:37 PM-12:38 PM **Aleksander Jankowski,** EMBL, Germany
Functional impact of genomic rearrangements on gene expression and chromatin organization

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:30 PM **Smita Krishnaswamy,** Yale School of Medicine, United States
Keynote: Using Manifold learning to Gain Insights Into Complex Biological Systems from Single-Cell Data

2:30 PM-2:40 PM **Vivekanandan Ramalingam,** Stowers Institute, United States
Single-cell RNA-seq reveals two types of tissue-specific promoters with different expression characteristics

MONDAY, JULY 9 *continued • ROOM: GRAND BALLROOM B*

RegSys: Regulatory and Systems Genomics

COSI TRACK PRESENTATIONS

MONDAY, JULY 9 *continued • ROOM: GRAND BALLROOM B*

https://www.iscb.org/cms_addon/conferences/ismb2018/regsys.php

2:40 PM-3:00 PM **Yue Zhang,** University of Washington, United States
Proceedings Presentation: Scalable preprocessing for sparse scRNA-seq data exploiting prior knowledge

3:00 PM-3:20 PM **Michael Kleyman,** Carnegie Mellon University, United States
Bulk Regulatory Peak Deconvolution using Single Cell RNA-seq

3:20 PM-3:40 PM **Jie Liu,** University of Washington, United States
Proceedings Presentation: Unsupervised embedding of single-cell Hi-C data (2)

3:40 PM-4:00 PM **Joshua Welch,** Broad Institute of MIT and Harvard, United States
Manifold Alignment Reveals Correspondence between Single Cell Transcriptome and Epigenome Dynamics

4:00 PM-4:40 PM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

4:40 PM-5:10 PM **Katie Pollard,** University of California San Francisco, United States
Keynote: Chromatin boundaries are under strong negative selection

5:10 PM-5:20 PM **Lin An,** The Pennsylvania State University, United States
Hierarchical Domain Structure Reveals the Divergence of Activity among TADs and Boundaries

5:20 PM-5:40 PM **Ruochi Zhang,** Carnegie Mellon University, United States
Proceedings Presentation: Predicting CTCF-mediated chromatin loops using CTCF-MP

5:40 PM-5:41 PM **Alexander Fine,** The Jackson Laboratory & Tufts University, United States
Uncoupling of transcription and cytodifferentiation in mouse spermatocytes with impaired meiosis

5:41 PM-5:42 PM **Olivier Gevaert,** Stanford University, United States
Module Analysis Captures Pancancer Genetically and Epigenetically Deregulated Cancer Driver Genes for Smoking and Antiviral Response

5:42 PM-5:43 PM **Donghoon Lee,** Yale University, United States
The Epigenomic Landscape of Aberrant Splicing in Cancer

5:43 PM-5:44 PM **Andre Kahles,** ETH Zurich, Switzerland
Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients

5:44 PM-5:45 PM **Heather Wheeler,** Loyola University Chicago, United States
Imputed gene associations identify replicable trans-acting genes enriched in transcription pathways

5:45 PM-5:46 PM **Michael Scherer,** Max-Planck Institute for Informatics, Germany
RnBeads 2018 – comprehensive analysis of DNA methylation data

5:46 PM-5:47 PM **John Lawson,** University of Virginia, United States
Principal Component Region Set Analysis: Facilitating Interpretation of PCA Dimensions for DNA Methylation Data

5:47 PM-5:48 PM **Valeriya Malysheva,** The Babraham Institute, United Kingdom
Highly dynamic chromatin interactions drive neurogenesis through gene regulatory networks

5:48 PM-5:49 PM **Kellen Cresswell,** Virginia Commonwealth University, United States
SpectralTAD: identification of topologically associated domaints (TADs) using spectral clustering

5:49 PM-5:50 PM **Christopher Jf Cameron,** McGill University, Canada
Prediction of complete Hi-C contact maps from genomic sequence

5:50 PM-5:51 PM **Konstantin Okonechnikov,** German Cancer Research Center (DKFZ), Germany
Identification of enhancer target genes by correlating gene expression and epigenetic modifications within topologically associated domains

5:51 PM-5:52 PM **Aparna Gorthi,** University of Texas Health San Antonio, United States
Genome-wide analysis of EWS-FLI1 driven transcription reprogramming: impact on dna damage response in ewing sarcoma

RegSys: Regulatory and Systems Genomics

COSI TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: GRAND BALLROOM B*

https://www.iscb.org/cms_addon/conferences/ismb2018/regsys.php

8:35 AM-8:40 AM Welcome to RegSys Day 2

8:40 AM-9:10 AM **Yoav Gilad,** University of Chicago, United States
Keynote: What are the big barriers to a complete understanding of gene regulation?

9:10 AM-9:20 AM **Chao-Chung Kuo,** RWTH Aachen Medical Faculty, Germany
Long noncoding RNAs as sequence-specific DNA-binding factors

9:20 AM-9:40 AM **Siamak Zamani Dadaneh,** Texas A&M University, United States
Proceedings Presentation: Covariate-Dependent Negative Binomial Factor Analysis of RNA Sequencing Data

9:40 AM-10:15 AM **COFFEE BREAK WITH EXHIBITORS**
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

10:15 AM-10:45 AM **Jun Song,** University of Illinois at Urbana-Champaign, United States
Keynote: Predictive local sequence features can distinguish the binding specificity of transcription factor family members

10:45 AM-11:00 AM **Timothy Durham,** University of Washington, United States
PREDICTD: PaRallel Epigenomics Data Imputation with Cloud-based Tensor Decomposition

11:00 AM-11:20 AM **Akshay Balsubramani,** Stanford University, United States
Systematic evaluation of multimodal approaches to predict in vivo transcription factor binding across cell types

11:20 AM-11:40 AM **Shaun Mahony,** The Pennsylvania State University, United States
Deep neural networks for characterizing sequence and chromatin pre-determinants of transcription factor binding

11:40 AM-12:00 PM **Artur Jaroszewicz,** University of California, Los Angeles, United States
Fine Mapping of Chromatin Interactions via Neural Networks

12:00 PM-12:20 PM **Jun Ding,** Carnegie Mellon University, United States
Reconstructing differentiation networks and their regulation from time series single-cell expression data

12:20 PM-12:40 PM **Jingyi Jessica Li,** University of California, Los Angeles, United States
Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them

12:40 PM-2:00 PM **LUNCH (ON OWN)**
Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL

2:00 PM-2:30 PM **Manolis Kellis,** Massachusetts Institute of Technology, United States
Keynote: From Genetics To Therapeutics: Uncovering And Manipulating The Circuitry Of Non-coding Disease Variants

2:40 PM-3:00 PM **Wouter Meuleman,** Altius Institute for Biomedical Sciences, United States
Consensus architectures of regulatory DNA actuation across 420 human cell types and states

3:00 PM-3:20 PM **Yang Yang,** Carnegie Mellon University, United States
Continuous-trait probabilistic model for comparing multi-species functional genomic data

3:20 PM-3:40 PM **Deborah Chasman,** University of Wisconsin-Madison, United States
Dynamic Regulatory Module Networks for integrative inference of cell type-specific regulatory programs

3:40 PM-4:00 PM **Kjong-Van Lehmann,** ETH Zurich, Switzerland
Assessing the Gene Regulatory Landscape in 1,188 Human Tumors

4:20 PM-4:40 PM **Natalie Sauerwald,** Carnegie Mellon University, United States
Proceedings Presentation: Quantifying the similarity of topological domains across normal and cancer human cell types

Technology Track

PRESENTATIONS

https://www.iscb.org/cms_addon/conferences/ismb2018/technologytrack.php

MONDAY, JULY 9 • *ROOM: COLUMBUS KL*

10:40 AM-11:00 AM	**Zhiyong Lu,** NCBI, NLM, NIH, United States PubMed Labs: An experimental platform for improving biomedical literature search
11:00 AM-11:20 AM	**Anna Calinawan,** Icahn School of Medicine at Mount Sinai, United States NetworkAssessor: An interactive visualization tool for ranking the significance of canonical cancer pathways in gene networks
11:20 AM-11:40 AM	**Soohyun Lee,** Harvard Medical School, United States Tibanna: a cloud-based stand-alone workflow automation system for data processing at the 4D Nucleome Data Coordination and Integration Center
11:40 AM-12:00 PM	**Marilyn Safran,** Weizmann Institute of Science, China Deciphering genetic diseases using WGS regulatory elements and ncRNAs
12:00 PM-12:20 PM	**Young mi Park,** EMBL-EBI, United Kingdom EBI Search as a Service
12:20 PM-12:40 PM	**Fábio Madeira,** EMBL-EBI, United Kingdom Bioinformatics Web Services at the EMBL-EBI

MONDAY, JULY 9 • *ROOM: COLUMBUS GH*

4:40 PM-5:40 PM	**Sanjana Sudarshan,** Jetstream – Indiana University, United States Jetstream — A national research and education cloud
5:40 PM-6:00 PM	**Colleen Bushell,** University of Illinois, NCSA, United States KnowEnG: Knowledge Engine for Genomics

TUESDAY, JULY 10 • *ROOM: COLUMBUS GH*

8:40 AM-9:40 AM	**Claudio Alberti,** GenomSys, Switzerland Streaming big genomic data with MPEG-G, the emerging ISO standard for genomic information representation
9:40 AM-10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:20 AM-11:20 AM	**Matthew LaFave,** Synthetic Genomics, Inc., United States D-SPACE: Deep Semantic Protein Annotation Classification and Exploration
11:20 AM-11:40 AM	**Wen-Lian Hsu,** Academia Sinica, Taiwan DART – a fast and accurate RNA-seq mapper with a partitioning strategy
11:40 AM-12:00 PM	**Daniel Buchan,** University College London, United Kingdom The New PSIPRED Protein Analysis Workbench
12:40 PM-2:00 PM	**LUNCH (ON OWN)** Available Exhibition / Poster Area — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
2:00 PM-2:20 PM	**Michael Sternberg,** Imperial College, United Kingdom Phyre2, PhyreRisk and EzMol: Protein structure prediction, variant analysis and visualization made easy
2:20 PM-2:40 PM	**Arun Prasad Pandurangan,** MRC Laboratory of Molecular Biology, United Kingdom The SUPERFAMILY 2.0: HMM library and genome assignments server
2:40 PM-3:00 PM	**Benoit Bely,** EMBL-EBI, United Kingdom The Proteins API, Tool Suites for Interpreting the Molecular Mechanisms of Diseases

ELIXIR

SPECIAL TRACK PRESENTATIONS

TUESDAY, JULY 10 • *ROOM: GRAND BALLROOM A*

https://www.iscb.org/cms_addon/conferences/ismb2018/elixir.php

European and global lifes sciences core data resources: managing funding for big data

8:35 - 8:40 AM	**Chuck Cook** ELIXIR: Session Overview and Introductions
8:40 - 9:00 AM	**Niklas Blomberg,** Elixir, United Kingdom Introduction to ELIXIR and Core Data Resources
9:00 - 9:20 AM	**Christine Orengo,** University College London, United Kingdom CATH protein structure classification databases
9:20 - 9:40 AM	**Cathy Wu,** University of Delaware, United States UniProt: A global hub of protein information
9:40 - 10:15 AM	**COFFEE BREAK WITH EXHIBITORS** RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
10:15 - 10:20 AM	**Chuck Cook** ELIXIR: Session Continuation and Introductions
10:20 - 10:40 AM	**Rolf Apweiler** The Global Coalition for Life Sciences Data Resources
10:40 - 11:00 AM	**Francis Ouellette** Life sciences data resources: a funder's perspective
11:00 - 11:20 AM	Panel discussion: for Life Sciences Data Resources: Funding and a Global Coalition
11:20 - 11:40 AM	**Niklas Blomberg,** Elixir, United Kingdom ELIXIR Core Data Resource Indicators
11:40 - 12:00 PM	**Stephen Burley,** RCSB PDB, UCSD, Rutgers University, United States RCSB topic
12:00 - 12:20 PM	**Judy Blake** The Alliance of Genome Resources: Visions of the Future
12:20 - 12:40 PM	Panel discussion indicators for data resources

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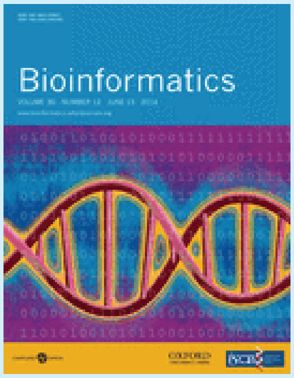
BIOINFORMATICS UPDATE



Bioinformatics has had a very busy and successful 2017. We continue to serve the computational biology community and we thank our authors, reviewers, and readers for the continued support. Our levels of online readership and citation remain high, reflecting the value of our papers to the field.

The following papers from 2017 and 2018 have been particularly popular with our readership in the past twelve months.

Deep learning with word embeddings improves biomedical named entity recognition by M Habibi et al. Volume 33, Issue 14, 15 July 2017, Pages i37–i48

An introduction to deep learning on biological sequence data: examples and solutions by VI Jurtz et al. Volume 33, Issue 22, 15 November 2017, Pages 3685–3690

UpSetR: an R package for the visualization of intersecting sets and their properties by JR Conway et al. Volume 33, Issue 18, 15 September 2017, Pages 2938–2940

SPRING: a kinetic interface for visualizing high dimensional single-cell expression data by C Weinreb et al. Volume 34, Issue 7, 1 April 2018, Pages 1246–1248.

We track and display article-level metrics, as well as Altmetrics alongside articles. The following articles have had particularly high Altmetric scores in the past twelve months:

Minimap2: pairwise alignment for nucleotide sequences by H Li, bty191, 10 May 2018

heatmaply: an R package for creating interactive cluster heatmaps for online publishing by T Galili et al. Volume 34, Issue 9, 1 May 2018, Pages 1600–1602

The submission rate in 2017 exceeded 2,000 papers with an acceptance rate in the region of 35%. Of our published papers, around 33% have been published open access in 2017, with authors choosing either CC-BY-NC and CC-BY licences. Our publication speed remains very fast – accepted articles are online within 1 week and are published in an issue within 23 weeks. Review time is also fast, with time to first decision averaging 46 days.

In the autumn of 2017, *Bioinformatics* started a new policy of accepting **Format-Free submissions**. Accepted manuscripts will need to be formatted on revision, but this will ease the burden on authors and the editorial team at the point of first submission.

Bioinformatics is now integrated with **Publons** to recognise our expert peer reviewers and raise the status of peer review. Reviewers of manuscripts for *Bioinformatics*, will be asked whether they wish to instantly add a verified record of that review to their Publons profile in ScholarOne Manuscripts. Once a first review has been added, the reviewer can elect to have all future reviews performed for Bioinformatics automatically added to their profile by enabling the "Automatically add reviews for partnered journals" option in their profile settings.

As always, we very much welcome your suggestions for new developments, review or editorial topics, and feedback on any aspect of the journal.

ISCB MEMBER DISCOUNT FOR OPEN ACCESS

Members of the ISCB are now eligible for a **15% discount** to publish open access in Bioinformatics. In order to receive this discount, ISCB members must claim this discount prior to signing a license to publish. Please do so by contacting the production editor <bioinformatics@oup.com> and informing them that you are an ISCB member.

ISCB ARTICLES

Bioinformatics is an official journal of ISCB, and we have collected together the ISCB articles published in the journal over the past several years: bit.ly/2j3uc0w

As ever, we welcome comments or feedback on any aspect of the journal — please do not hesitate to get in touch with us <bioinformatics.editorialoffice@oup.com> or visit us at the OUP booth at ISMB 2018 in Chicago—see you there!

With best wishes,
The Bioinformatics Editorial team

MEET THE
2018 ISCB FELLOWS

ISCB created the Fellows program in 2009 to recognize members that make outstanding contributions to the fields of computational biology and bioinformatics. Each year, the ISCB Fellows Selection Committee reviews nominations submitted by members and selects eligible ISCB members that have made significant scientific contributions and have served ISCB in some manner. In 2018, eight Fellows were selected and will be recognized at the annual ISMB meeting in Chicago, Illinois in July.

Patricia C Babbitt, Ph.D. Professor, Department of Bioengineering and Therapeutic Sciences, and Department of Pharmaceutical Sciences, University of California, San Francisco. Babbitt is being recognized for her pioneering work in developing computational methods to understand the relationship between protein structure and function. Her research has focused on understanding enzyme reactions in particular, and she has applied this knowledge to rational protein design and improvements in protein function prediction. Babbitt has served as the Director of the Graduate Program in Biological and Medical Informatics at UCSF and has also held scientific board roles within ISCB, HHMI and NIH.

Terry Gaasterland, Ph.D. Professor of Computational Biology and Genomics, University of California, San Diego, and Director, Scripps Genome Center. Gaasterland is being recognized for her seminal work developing tools for genome annotation, including the MAGPIE system, and her work as one of the first computer scientists to collect and combine molecular biology data and annotate pathway data. Gaasterland has served ISCB in many capacities, including being the first female member on the ISMB Board of organizers and serving as one of the first female ISCB Board members.

RSG WITH DREAM 2018

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

DECEMBER 8-10, 2018 NEW YORK, NY

KEYNOTE SPEAKERS

Ross Cagan, PhD
Senior Associate Dean for the Graduate School of Biomedical Sciences, Icahn School of Medicine at Mount Sinai, USA

Aravinda Chakravarti, PhD
NYU Langone Health, USA

Barbara Engelhardt, PhD
Princeton University, USA

Peter Kharchenko, PhD
Assistant Professor of Biomedical Informatics, Harvard University, USA

Daphne Koller, PhD
Stanford University, USA

Xiaole Shirley Liu, PhD
Professor of Statistics, Biostatistics, and Computational Biology, Harvard University, Dana-Farber Cancer Institute, USA

Miriam Merad, PhD
Icahn School of Medicine at Mount Sinai, USA

Ana Pombo, PhD
Berlin Institute for Medical Systems Biology, at the Max Delbrueck Center, Germany

Bing Ren, PhD
Professor of Cellular and Molecular Medicine, UC San Diego, USA

Adam Siepel, PhD
Professor, Watson School of Biological Sciences
Chair, Simons Center for Quantitative Biology
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DECEMBER 8-10, 2018

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Professional $400
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Student $275

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MORE INFO
www.iscb.org/recomb-regsysgen2018

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Featuring a Special Session on Single Cell Analysis

GLBIO

GREAT LAKES BIOINFORMATICS CONFERENCE May 19-22, 2019
The University of Wisconsin-Madison

ISCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
Official Conference

Call for GLBIO 2019 Special Session Proposals!

Due to the overwhelming enthusiasm for special sessions, GLBIO 2019 will again feature

Special Sessions

Special sessions will focus on new and emerging problems in bioinformatics and will be organized by members of the research community.

Special sessions will be of three broad categories:
- ☐ Focused workshops on specific research problems in computational biology and bioinformatics
- ☐ Software schools, aimed at providing training in new methods
- ☐ Activities focused on students and postdocs, or on non-academic career opportunities

Interested in organizing a Special Session?

Check out the website for more information and submit today!

Deadline: September 17, 2018

https://www.iscb.org/glbio2019

Hanah Margalit, Ph.D. Professor of Computational Molecular Biology, Department of Microbiology and Molecular Genetics, Faculty of Medicine, The Hebrew University of Jerusalem. Margalit is a pioneer in the field bioinformatics through her early work that was critical to establishing the sub-field of computational systems biology, and her current work on gene expression regulation, with a particular interest in regulation mediated by non-coding RNAs. Margalit has served on multiple editorial boards and conference organization committees, and she was instrumental in developing and launching the bioinformatics graduate program at the Hebrew University of Jerusalem.

Yves Moreau, Ph.D. Professor, Department of Electrical Engineering, Katholieke Universiteit Leuven. Moreau has made fundamental research contributions to microarray data analysis, and to disease gene prioritization and genomic variants analysis with respect to rare genetic diseases. Moreau has been integral in bringing together the European bioinformatics community through his role in coordinating the interdisciplinary SymBioSys Center for Computational Systems, and his work on developing and directing the Masters program in computational biology at KU Leuven. He has served in organizational positions for ECCB and ISMB and currently holds a position on the ISCB Board of Directors.

Bernard M.E. Moret, Ph.D. Professor Emeritus of Computer Science, École Polytechnique Fédérale de Lausanne, Switzerland. Moret is being recognized for his significant contributions to the areas of phylogeny estimation, comparative genomics, and regulatory genomics through his work on developing mathematical models, algorithms and software. Moret has served the computational biology community through his work on founding and organizing several meetings, including, the Workshop on Algorithms in Bioinformatics, RECOMB-Comparative Genomics, and IEEE/ACM Transactions on Computational Biology and Bioinformatics. He also founded the ACM Journal of Experimental Algorithmics, has chaired committees for NIH and directed the NSF-funded CIPRES project.

William Pearson, Ph.D. Professor, Biochemistry and Molecular Genetics, University of Virginia School of Medicine. Pearson is being recognized for his instrumental role in developing widely used methods for analyzing and understanding protein sequence information. His early work includes contributing to the development of the FASTP and FASTA sequence similarity search programs, and he has continued to develop and improve FASTA and other similarity search methods. Pearson is also recognized for his many years of service to the bioinformatics community through the numerous sequence analysis workshops he has taught at meetings and International courses.

Mona Singh, Ph.D. Professor, Lewis-Sigler Institute for Integrative Genomics, Department of Computer Science, Princeton University. Singh is being recognized for her visionary work in bringing machine learning and sophisticated algorithmic techniques to computational biology. She has made seminal contributions to cellular network analysis, protein interaction and specificity predictions, and functional annotation. Singh has served as an NIH Study Section Chair, and has worked in various positions on conference planning committees and as a member of the ISCB Board of Directors.

Mike Steel, Ph.D. Distinguished Professor, Department of Mathematics and Statistics, and Director of Biomathematics Research Centre, University of Canterbury, Christchurch, New Zealand. Steel is being recognized for his outstanding contributions to mathematical and computational phylogenetics, including his work on mathematical characterizations of phylogenetic trees and networks, models of sequence evolution, and models of speciation. Steel has been a leader in the evolutionary biology community and has served as an Associate Editor of Algorithms in Molecular Biology, and Evolutionary Bioinformatics. Steel has organized numerous phylogenetics meetings and is a Fellow of the Royal Society of New Zealand.

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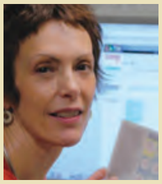

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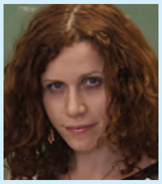

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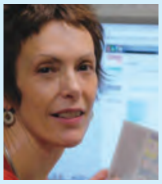

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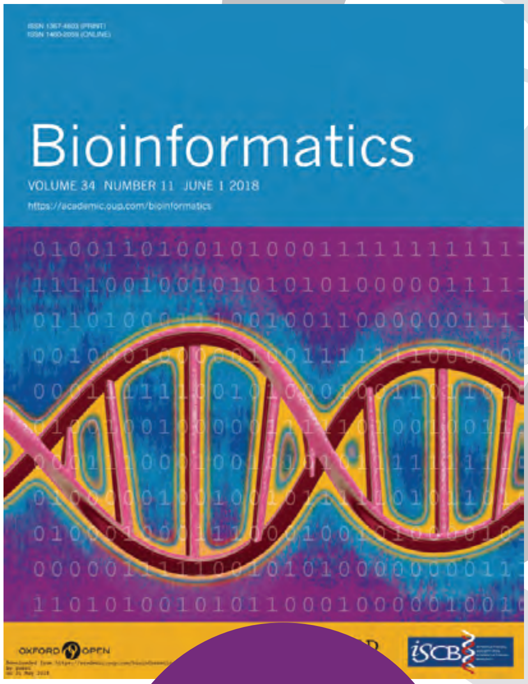

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NEWS FROM THE
ISCB STUDENT COUNCIL

THE 2018 ISCB STUDENT COUNCIL SYMPOSIUM SERIES

ISCB Student Council's flagship event, the 14th Annual Student Council Symposium (SCS), was held on 8 July 2018 directly preceding ISMB 2018, Chicago. This annual event gathered students and young scientists from across the globe. The highlight of the SCS includes two keynotes from Debora Marks (Harvard University) and Lucia Peixoto (Washington State University), 13 student presentations and 50 poster presentations and industry talk. Information and recorded presentations can be found at symposium.iscbsc.org.

The 5th European Student Council Symposium is once again going to be held in the days preceding ECCB in Athens, Greece. The ESCS keynotes will be Anna Zhukova (University of Bordeaux) and Julio Saez-Rodriguez (Aachen University). Registration for the event is still open! The organizing committee is looking forward to an an exciting event comprising student talks, a poster session, scientific networking and more on 8 September 2018! Information can be found at escs.iscbsc.org.

Once again, the Latin American Student Council Symposium will be held along with ISCB-LA on 6 November 2018 in Viña del Mar, Chile. Abstracts are being welcomed through 21 September 2018 for those wanting to participate by giving an oral or poster presentation. More information about the meeting will be posted online as the date approaches at lascs.iscbsc.org.

More information about all of our symposia as well as a peak behind the scenes of organizing a meeting like SCS can be found in the preprint of our upcoming publication at iscbsc.org/scs17_preprint. In addition, we look forward to seeing everyone at the 15th Annual Student Council Symposium in Basel next year!

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SEP 08, 2018 THROUGH SEP 12, 2018
http://eccb18.org

INCOB2018
INDIA - NEW DELHI

SEP 26, 2018 THROUGH SEP 28, 2018
http://sciwhylab.org/incob2018/index.php

WORKSHOP ON THE FUTURE OF ALGORITHMS IN BIOLOGY
UNITED STATES - PA - PITTSBURGH

SEP 28, 2018 THROUGH SEP 29, 2018
http://fab2018.cbd.cmu.edu/

RECOMB
COMPARATIVE GENOMICS 2018
CANADA - QUEBEC - MAGOG-ORFORD

OCT 09, 2018 THROUGH OCT 12, 2018
https://recombcg2018.usherbrooke.ca/

PACIFIC SYMPOSIUM ON BIOCOMPUTING 2019
UNITED STATES - HI - KOHALA COAST

JAN 03, 2019 THROUGH JAN 07, 2019
http://psb.stanford.edu/

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