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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
Executive Director
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 Algorithmics, 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 community was 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 therefore good 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.
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.”
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 Pienzenik 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 step-wise 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 oncoprotein isoform, which promotes the initiation and progression of adenocarcinomas due to full activation of PI3Ka/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.”

References
http://en.hafakulta.agri.huji.ac.il/people/shmuel-hurwitz
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.
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. Sankaran, 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. L. Aravind. 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.

“The PhRMA Foundation grant is making a significant impact in our efforts to move forward personalized cancer treatment research.”

Daniel Lobo, PhD | University of Maryland

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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 Conference 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
Conference Co-Chair

Christine Orengo
Conference Co-Chair

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

ISMB 2018 Steering Committee
Bruno Gaëta, Treasurer, University of New South Wales, Australia
Janet Kelso, Conference Advisory Council Co-chair, Max Planck Institute for Evolutionary Anthropology, Germany
Diane E. Kovals, ISCB Executive Director, United States
Steven Leard, ISMB Conference Director, Canada
Tang Lengauer, President, ISCB, Max Planck Institute for Informatics, Germany
Alfonso Valencia, Past-President, ISCB, Barcelona Supercomputing Center, Spain

Proceedings Chairs
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)
Frän 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)
Haiyu 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 Capiotti, University of Bologna, Italy (Yarl)
Ana Comesa, Centro de Investigacion Principe Felipe, Spain (HiTFreq)
Christophe Dessimoz, University of Lauzanne, Switzerland (Evolution)
Jeremy Goecks, Oregon Health & Science University, United States (BioVis)
Pawel P Labaj, 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)
Olga Vital, Northern University, United States (CompMS)

Abstract Chairs
3DBiG: 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
Karim Vergoor, University of Melbourne, Australia

BioVis: Biological Data Visualizations
Thomas Höllt, TU Delft, Netherlands
Michael Krone, University of Stuttgart, Germany

CAMDA: Critical Assessment of Mass Data Analysis
David Kreil, Boku University Vienna, Austria
Pawel P Labaj, 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 Tubingen, 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
Watari 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 Comesa, 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 Zurich, Switzerland
Quaid Morris, University of Toronto, Canada
Gunna Metlsch, ETH Zurich, 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
Joseph 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 Tuebingen, Germany
Tomas Helikar, University of Nebraska - Lincoln, United States
Nicolas Le Novère, Babraham Institute, United Kingdom

TransMed: Translational Medicine Informatics & Applications
Bissar 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 Capiotti, 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

**BIONFO-CORE**
Madalaine Gogol
Brent Richter

**Bio-Ontologies**
Michel Dumontier
Karim Verspoor

**BioVis: Biological Data Visualizations**
Jan Aerts
Nils Gehlenborg

**CAMDA: Critical Assessment of Massive Data Analysis**
David Kreil
Pawel Labaj

**CompMS: Computational Mass Spectrometry**
Oliver Kohlbacher

**Education: Computational Biology and Bioinformatics Education and Training**
Teresa Attwood
Fran Lewitter
Lonnie Welch

**EvolCompGen: Evolution & Comparative Genomics**
Christophe Dessizmoz

**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 Barasch
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
Nomii Harris

**RegSys: Regulatory and Systems Genomics**
Manolis Kellis
Lonnie Welch

**SysMed: Computational Modeling of Biological Systems**
Tomáš Helík
Nicolas Le Novre

**TransMed: Translational Medicine Informatics & Applications**
Venkata Satagopam

**Varti: Variant Interpretation**
Hannah Carter
Emidio Capriotti
Yana Bromberg

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**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 Valencia, ISCB Past President
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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**

## FRIDAY, JULY 6

<table>
<thead>
<tr>
<th>Time</th>
<th>Grand Ballroom A</th>
<th>Grand Ballroom B</th>
<th>Columbus AB</th>
<th>Columbus IJ</th>
<th>Columbus KL</th>
<th>Grand Ballroom Foyer</th>
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</thead>
<tbody>
<tr>
<td>10:00 AM</td>
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<tr>
<td>11:00 AM</td>
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<tr>
<td>11:15 AM</td>
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<tr>
<td>1:00 PM</td>
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<tr>
<td>2:00 PM</td>
<td>Tutorial PM6: Deep learning for network biology</td>
<td>Tutorial PM7: High-throughput sequencing: Identification of disease variants in exomes and genomes</td>
<td>Student Council Symposium (SCS)</td>
<td>Tutorial PM5: Visualization of large biological data</td>
<td>Tutorial PM8: Ontologies in computational biology</td>
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<tr>
<td>4:00 PM</td>
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</tr>
<tr>
<td>4:15 PM</td>
<td>PM6 continued</td>
<td>PM7 continued</td>
<td>Student Council Symposium (SCS)</td>
<td>PM5 continued</td>
<td>PM8 continued</td>
<td></td>
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<tr>
<td>6:00 PM</td>
<td>Tutorials and Student Council Symposium End</td>
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<tr>
<td>6:15 PM</td>
<td>Conference Welcome</td>
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<tr>
<td>6:30 PM</td>
<td>Steven Salzberg, Johns Hopkins University, United States</td>
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<tr>
<td>7:30 PM</td>
<td>25 years of human gene finding: are we there yet?</td>
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<tr>
<td>7:30 PM</td>
<td>Opening Reception with Exhibitors</td>
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</tbody>
</table>

**ATTENDEE WIFI**

Network: Hyatt Conference
Password: Chicago18
# Schedule-at-a-Glance • Saturday

**HYATT REGENCY CHICAGO**

## SATURDAY, JULY 7

<table>
<thead>
<tr>
<th>Time</th>
<th>Location/Session</th>
</tr>
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<tbody>
<tr>
<td>7:30 AM</td>
<td>Conference Registration</td>
</tr>
<tr>
<td>8:15 AM</td>
<td>Morning Welcome and conference updates / Introduction of ISCB 2018 Distinguished Fellows</td>
</tr>
<tr>
<td>8:30 AM</td>
<td>ISCB Overton Prize Award Keynote: Cole Trapnell, University of Washington, United States</td>
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<tr>
<td></td>
<td>Room: Grand Ballroom C-F</td>
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<tr>
<td>9:30 AM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
</tr>
<tr>
<td>10:15 AM</td>
<td>RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL</td>
</tr>
<tr>
<td>12:40 PM</td>
<td>LUNCH (ON OWN)</td>
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<tr>
<td></td>
<td>RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL</td>
</tr>
<tr>
<td>2:00 PM</td>
<td>3D Genomics: Computational approaches for analyzing the role of three-dimensional chromatin organization in gene regulation</td>
</tr>
<tr>
<td>4:00 PM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
</tr>
<tr>
<td>4:40 PM</td>
<td>RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>POSTER PRESENTATIONS (SESSION A, ODD NUMBER POSTERS)</td>
</tr>
<tr>
<td>8:15 AM</td>
<td>ISCB Overton Prize Award Keynote: Cole Trapnell, University of Washington, United States</td>
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<tr>
<td></td>
<td>Reconstructing and deforming developmental landscapes</td>
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<td>9:30 AM</td>
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</tr>
<tr>
<td>12:40 PM</td>
<td>LUNCH (ON OWN)</td>
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<tr>
<td></td>
<td>RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL</td>
</tr>
<tr>
<td>2:00 PM</td>
<td>3D Genomics: Computational approaches for analyzing the role of three-dimensional chromatin organization in gene regulation</td>
</tr>
<tr>
<td>4:00 PM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
</tr>
<tr>
<td>4:40 PM</td>
<td>RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>POSTER PRESENTATIONS (SESSION A, ODD NUMBER POSTERS)</td>
</tr>
</tbody>
</table>

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**ISMB 2018 APP**: Check ISMB18 app for current information.
SUNDAY, JULY 8

<table>
<thead>
<tr>
<th>TIME</th>
<th>SESSION / ACTIVITY</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30 AM</td>
<td>Conference Registration</td>
</tr>
<tr>
<td>8:15 AM</td>
<td>Morning Welcome</td>
</tr>
<tr>
<td>8:30 AM</td>
<td>Keynote: Martha L. Bulyk, Brigham &amp; Women’s Hospital and Harvard Medical School, United States</td>
</tr>
<tr>
<td>9:30 AM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
</tr>
<tr>
<td>10:15 AM</td>
<td>HitSeq COSI: High-throughput Sequencing</td>
</tr>
<tr>
<td>12:40 PM</td>
<td>LUNCH (ON OWN)</td>
</tr>
<tr>
<td>2:00 PM</td>
<td>HITSeq COSI Continues</td>
</tr>
<tr>
<td>4:00 PM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>POSTER PRESENTATIONS (SESSION A, EVEN NUMBER POSTERS)</td>
</tr>
</tbody>
</table>

**GRAND BALLROOM**

- **A**
- **B**
- **C-F**

**COLOMBUS**

- **AB**
- **CD**
- **EF**
- **GH**
- **IJ**
- **KL**

**RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL**

- **COFFEE BREAK WITH EXHIBITORS**
- **LUNCH (ON OWN)**
- **COFFEE BREAK WITH EXHIBITORS**
- **POSTER PRESENTATIONS**
# Schedule-at-a-Glance • Monday

**HYATT REGENCY CHICAGO**

## MONDAY, JULY 9

<table>
<thead>
<tr>
<th>Time</th>
<th>Event Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>7:30 AM</td>
<td>Conference Registration</td>
</tr>
<tr>
<td>8:15 AM</td>
<td>Morning Welcome / PhRMA Foundation Award Presentations / ISCB Outstanding Contributions Award Presentation: Russ Altman</td>
</tr>
<tr>
<td>8:30 AM</td>
<td><strong>Keynote: M. Madan Babu</strong>, MRC Laboratory of Molecular Biology, United Kingdom</td>
</tr>
<tr>
<td></td>
<td>ISCB Innovator Award Keynote: How Does Protein Disorder Enable Phenotypic Diversity?</td>
</tr>
<tr>
<td>9:40 AM</td>
<td><strong>COFFEE BREAK WITH EXHIBITORS</strong></td>
</tr>
<tr>
<td>10:15 AM</td>
<td><strong>LUNCH (ON OWN)</strong></td>
</tr>
<tr>
<td>12:45 PM</td>
<td>ISCB CAREER FAIR — RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL</td>
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<tr>
<td>12:45 PM</td>
<td>BoF: JPI Career Development: Funding opportunities for Early Career Researchers</td>
</tr>
<tr>
<td>2:00 PM</td>
<td><strong>COFFEE BREAK WITH EXHIBITORS</strong></td>
</tr>
<tr>
<td>4:00 PM</td>
<td><strong>COFFEE BREAK WITH EXHIBITORS</strong></td>
</tr>
<tr>
<td>4:40 - 5:40 PM</td>
<td>HitSeq COSI Continues</td>
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<tr>
<td>5:40 - 6:00 PM</td>
<td>HitSeq COSI Continues</td>
</tr>
<tr>
<td>6:00 PM</td>
<td>POSTER PRESENTATIONS (SESSION B, ODD NUMBER POSTERS)</td>
</tr>
</tbody>
</table>

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*SCHEDULE SUBJECT TO CHANGE. CHECK ISMB18 APP FOR CURRENT INFORMATION*
## Schedule-at-a-Glance • Monday

**HYATT REGENCY CHICAGO**

### MONDAY, JULY 9

<table>
<thead>
<tr>
<th>Time</th>
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<tbody>
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<td><strong>Keynote:</strong> M. Madan Babu, MRC Laboratory of Molecular Biology, United</td>
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<td>Kingdom</td>
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<tr>
<td>9:40 AM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
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<tr>
<td>10:15 AM</td>
<td>Bio-Ontologies COSI</td>
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<tr>
<td>10:20 – 10:40 AM</td>
<td>Special Session: Advancing</td>
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<tr>
<td></td>
<td>computational biology through</td>
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<td></td>
<td>critical assessments, community</td>
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<td>experiments, and crowdsourcing</td>
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<tr>
<td>10:40 – 11:00 AM</td>
<td>BioVis COSI: Biological Data</td>
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<td></td>
<td>Visualization</td>
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<tr>
<td>10:40 – 11:00 AM</td>
<td>Function COSI (Additional)</td>
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<td></td>
<td>Amir Karger</td>
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<tr>
<td>11:00 AM</td>
<td>TECHNOLOGY TRACK</td>
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<td></td>
<td>PubMed Labs: An experimental platform</td>
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<tr>
<td>11:00 AM</td>
<td>NetworkAssessor: An interactive</td>
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<td>visualization tool</td>
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<tr>
<td>11:00 – 12:00 PM</td>
<td>Tibanna: a cloud-based automation system</td>
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<tr>
<td>12:00 – 12:20 PM</td>
<td>Deciphering genetic diseases using WGS and ncRNAs</td>
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<tr>
<td>12:20 – 12:40 PM</td>
<td>EBI Search as a Service</td>
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<tr>
<td>12:40 PM</td>
<td>LUNCH (ON OWN)</td>
</tr>
<tr>
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<tr>
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<td>Special Session Continues</td>
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<td>4:00 PM</td>
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<tr>
<td>4:40 – 5:40 PM</td>
<td>TECHNOLOGY TRACK</td>
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<td>Jetstream – A national research and education cloud</td>
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<td>5:40 – 6:00 PM</td>
<td>KnowEnG: Knowledge Engine for</td>
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<tr>
<td></td>
<td>Genomics</td>
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<tr>
<td>6:00 PM</td>
<td>POSTER PRESENTATIONS</td>
</tr>
<tr>
<td></td>
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</tr>
</tbody>
</table>
TUESDAY, JULY 10

7:30 AM – 12:00 PM Conference Registration

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 COSI

9:40 AM
COFFEE BREAK WITH EXHIBITORS
RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL

10:20 - 11:20 AM
ELIXIR Special Presentation Continues
RegSys COSI Continues
MLCSB COSI Continues
3DSig COSI continues
Bio-Ontologies COSI Continues

11:20 - 12:00 PM
TECH TRACK
D-SPACE: Deep Semantic Protein Annotation Classification and Exploration
DART – a fast and accurate RNA-seq mapper with a partitioning strategy
The New PSIRED Protein Analysis Workbench

12:00 - 12:20 PM
Phyre2, PhyreRisk and EzMol: Protein structure prediction, variant analysis and visualization made easy

12:20 - 12:40 PM
The SUPERFAMILY 2.0: HMM library and genome assignments server
The Proteins API, Tool Suites for Interpreting the Molecular Mechanisms of Diseases

12:40 PM
POSTER PRESENTATIONS
RIVERSIDE EXHIBIT HALL – EXHIBIT LEVEL
(SESSION B, EVEN NUMBER POSTERS)
LUNCH (ON OWN) AVAILABLE EXHIBITION / POSTER AREA

2:00 - 2:20 PM
RegSys COSI Continues
MLCSB COSI Continues
3DSig COSI continues
Bio-Ontologies COSI Continues
Phyre2, PhyreRisk and EzMol: Protein structure prediction, variant analysis and visualization made easy

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

6:00 – 6:20 PM
ISMB Awards Ceremony
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
Feng Yue, Penn State, PA, United States
Invited: Impact of structural variants on 3D genome structure in cancer cells

10:20 - 11:00 AM
Feng Yue, Penn State, PA, United States
Invited: Impact of structural variants on 3D genome structure in cancer cells

10:30 - 11:40 AM
Serhan Yılmaz, Bilkent University, Turkey
SPADIS: An Algorithm for Selecting Predictive and Diverse SNPs in GWAS

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 - 11:50 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 - 2:20 PM
Mathieu Blanchette, McGill University, Canada
Invited: High-resolution analysis of chromatin interaction capture data

2:20 - 2:50 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 n-SAC model

3:20 - 4:00 PM
William Noble, University of Washington, United States
Invited: Modeling and predicting the 3D genome

4:00 - 4:20 PM
Mathieu Blanchette, McGill University, Canada
Invited: High-resolution analysis of chromatin interaction capture data

4:20 - 4:50 PM
Sourya Bhattacharyya, La Jolla Institute for Allergy and Immunology, United States
FitHiChIP: Statistical analysis of high-resolution HiChIP and PLAC-seq data

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 - 5:55 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; Iddo Friedberg, University of Maryland, 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 Moul, 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 Moul, University of Maryland, United States
CASP: Critical Assessment of protein Structure Prediction
10:40 – 11:00 AM
Ilya Vakser, The University 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, and 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 Radijovic, 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
Determining 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 Multiscale 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

Special Sessions
PRESENTATIONS
TUESDAY JULY 10 • ROOM: COLUMBUS IJ
https://www.iscb.org/ismb2018-program/ismb2018-special-sessions
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)**

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**

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


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 Cookey 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


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

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

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

12:40 PM-2:00 PM  Lunch (on own)

2:00 PM-2:40 PM  Peter Sorger, Harvard University, United States
Deciphering cell’s robustness by a multi-scale framework integrating cell cycle and metabolism in budding yeast

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

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  Caroline 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

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
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
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
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
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

BASSEL
JULY 21-25
2019

ISMB ECCB

CONFERENCE CHAIRS

Nicola Mulder
University of Cape Town, South Africa

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

WWW.ISCB.ORG/ISMBECCB2019
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

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

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 Sumision, 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. Labaj, 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 Franchi, 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
<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:15 AM</td>
<td>Joaquin Dopazo, Fundacion Progreso y Salud, Spain</td>
<td>Data Analysis Challenges of the CAMDA Contest 2018. (II)</td>
</tr>
<tr>
<td>10:20 AM</td>
<td>Daniel H. Huson, University of Tuebingen, Germany</td>
<td>Computational analysis of short and long microbiome sequencing reads - Keynote</td>
</tr>
<tr>
<td>11:20 AM</td>
<td>Joaquin Dopazo, Fundacion Progreso y Salud, Spain</td>
<td>Functional biomarkers for precise simple classification in the MetaSUB Forensic Challenge</td>
</tr>
<tr>
<td>12:00 PM</td>
<td>Chengsheng Zhu, Rutgers University, United States</td>
<td>mi-faser decipher city subway microbiome functional fingerprints</td>
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<tr>
<td>12:20 PM</td>
<td>Jolanta Kawulok, Silesian University of Technology, Poland</td>
<td>Environmental Metagenome Classification for construction of a microbiome fingerprint</td>
</tr>
<tr>
<td>12:40 PM</td>
<td>Pawel P Labaj, Austrian Academy of Sciences and Jagiellonian University, Poland</td>
<td>Meta-analysis of the MetaSUB forensics challenge, and Outlook: Follow-on challenges 2019</td>
</tr>
<tr>
<td>2:00 PM</td>
<td>Tyler Grimes, University of Florida, United States</td>
<td>Meta-analysis of Breast Cancer and Neuroblastoma through the integration of RNA-seq network analysis, clinical data, and known signaling pathways</td>
</tr>
<tr>
<td>3:00 PM</td>
<td>Maarten Larmuseau, Ghent University, Belgium</td>
<td>Pair-based Integration of Gene Expression and CNV Data</td>
</tr>
<tr>
<td>3:40 PM</td>
<td>Ben Lengerich, Carnegie Mellon University, United States</td>
<td>Proceedings Presentation: Personalized Regression Enables Sample-Specific Pan-Cancer Analysis</td>
</tr>
<tr>
<td>4:00 PM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
<td>RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL</td>
</tr>
<tr>
<td>4:40 PM</td>
<td>So Yeon Kim, Ajou University, South Korea</td>
<td>Robust Pathway-based Multi-Omics Data Integration using Directed Random Walk and a Denoising Autoencoder for Survival Prediction in Cancer Studies</td>
</tr>
<tr>
<td>5:20 PM</td>
<td>Shraddha Thakkar, NCTR, FDA, United States</td>
<td>FDA Meta-analysis of the CMap Drug Safety Challenge, and Outlook: Follow-on Challenges 2019</td>
</tr>
<tr>
<td>5:40 PM</td>
<td>Wenzhong Xiao, Harvard Medical School &amp; Stanford, United States; David P. Kreil, Boku University Vienna, Austria</td>
<td>Contest voting, awards, and outlook</td>
</tr>
</tbody>
</table>
RNA: Computational RNA Biology

COSI TRACK PRESENTATIONS
SATURDAY, JULY 7 • ROOM: GRAND BALLROOM B

10:15 AM-10:20 AM Introduction

10:20 AM-11:00 AM Invited Talk 1
Michael Seiler, H3 Biomedicine, United States

10:00 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-12:40 PM Vanessa Aguia-Pulido, Cornell University, United States
High-throughput single-cell transcriptomics profiling interneuron specification during brain development

12:40 PM-2:00 PM Lunch (On Own)

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

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**  

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

ROOM: COLUMBUS KL
Critical assessment communities
Leader: Steven E Brenner, University of California Berkeley, United States

You spend so much time in Computational Biology & Bioinformatics making connections.
Don’t forget to make a few of your own.

Education: Computational Biology and Bioinformatics Education and Training

COSI TRACK PRESENTATIONS
SUNDAY, JULY 8 • ROOM: COLUMBUS CD

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


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

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

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

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

10:20 AM-10:30 AM  **Elizabeth White**

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

11:00 AM-11:20 AM  **Bonnie Berger**

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-12:40 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

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 genominc immune variation to deduce role of MHC Class II in cancer susceptibility and evolution

3:40 PM-3:50 PM  **Alex Kaplun**, Variantyx
Detection of pathologic short tandem repeat extensions using Whole Genome Sequencing

4:00 PM-4:40 PM  **Olga Troyanskaya**, Princeton University, United States
Decoding the human genome with deep learning models.

4:40 PM-4:50 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

4:50 PM-5:20 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


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)

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

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

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 Leuven, 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  Kendall 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


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
One 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 Niesel, University of Tübingen, Germany
Closing Remarks
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<th>Time</th>
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<tr>
<td>10:00 AM-10:10 AM</td>
<td>Introduction</td>
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<td>10:10 AM-10:15 AM</td>
<td><strong>Edward L. Braun</strong>, University of Florida, United States</td>
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<td>Proceedings Presentation: An evolutionary model motivated by physico-chemical properties of amino acids reveals variation among proteins</td>
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<td>10:15 AM-10:20 AM</td>
<td><strong>Daniella F Lato</strong>, McMaster University, Canada</td>
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<td>Spatial Patterns of Substitutions in Bacterial Genomes</td>
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<td>10:20 AM-10:25 AM</td>
<td><strong>Huy Nguyen</strong>, Iowa State University, United States</td>
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<td>Tracing the Ancestry of Operons in Bacteria</td>
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<td>10:25 AM-10:30 AM</td>
<td><strong>Ana Maria Rojas</strong>, CSIC-IBIS, Spain</td>
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<td>A novel MMR pathway in prokaryotes</td>
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<td>10:30 AM-10:35 AM</td>
<td><strong>Wataru Iwasaki</strong>, The University of Tokyo, Japan</td>
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<td>Generalist species drive microbial dispersion and evolution.</td>
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<td>10:35 AM-10:40 AM</td>
<td><strong>Itamar Sela</strong>, NCBI/NIH, United States</td>
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<td>Evolution of the pangenome and core genome in prokaryotes</td>
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<td>10:40 AM-10:45 AM</td>
<td><strong>Louxin Zhang</strong>, A package for computing distance metrics for phylogenetic networks</td>
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<td>10:45 AM-10:50 AM</td>
<td><strong>Jesse Eaton</strong>, Carnegie Mellon University, United States</td>
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<td>Proceedings Presentation: Deconvolution and phylogeny inference of structural variations in tumor genomic samples</td>
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<td>10:50 AM-10:55 AM</td>
<td><strong>Mohammed El-Kebir</strong>, University of Illinois at Urbana-Champaign, United States</td>
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<td>Inferring Parsimonious Migration Histories for Metastatic Cancers</td>
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<td>10:55 AM-11:00 AM</td>
<td><strong>Benjamin Siranosian</strong>, Harvard University, United States</td>
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<td>Genetic and transcriptional instability alters cancer cell line drug response</td>
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<td>11:00 AM-11:05 AM</td>
<td><strong>Zena Lapp</strong>, University of Michigan, United States</td>
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<td>Regional transmission and antibiotic resistance evolution of the hospital pathogen Klebsiella pneumoniae</td>
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<td>11:05 AM-11:10 AM</td>
<td><strong>Giltae Song</strong>, Pusan National University, South Korea</td>
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<td>A non-parametric statistical test for determining fine-scale temporal variation patterns in evolving populations</td>
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<td>11:10 AM-11:15 AM</td>
<td><strong>Louxin Zhang</strong></td>
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**LUNCH (ON OWN)**
Available Exhibition / Poster Area —
RIVERSIDE EXHIBIT HALL — EXHIBIT LEVEL
3DSIG: Structural Bioinformatics and Computational Biophysics

COSI TRACK PRESENTATIONS
MONDAY, JULY 9 • ROOM: COLUMBUS AB

10:15 AM-10:20 AM Introduction

10:20 AM-11:00 AM Structural insights into the impacts of genetic variations in splicing and disease
Christine Orengo, University College London, United Kingdom

11:00 AM-11:20 AM scoreD: Deep discriminative ensemble classifiers for protein scoring
Debswapna Bhattacharya, Auburn University, United States

11:20 AM-11:40 AM Network approach integrates 3D structural and sequence data to improve protein structural comparison
Khalique Newaz, University of Notre Dame, United States

11:40 AM-12:00 PM Backbone Brackets and Arginine Tweezers delineate Class I and Class II aminoacyl tRNA synthetases
Khalique Newaz, University of Notre Dame, United States

12:00 PM-12:20 PM Structural Classification of Proteins in the post-Structural Genomics era
John-Marc Chandonia, Berkeley National Lab, United States

12:20 PM-12:40 PM Improved protein contact prediction using two-level deep convolutional neural networks
John-Marc Chandonia, Berkeley National Lab, United States

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

2:00 PM-2:20 PM Proceedings Presentation: Protein threading using residue co-variation and deep learning
Jinbo Xu, Toyota Technological Institute at Chicago, United States

2:20 PM-2:40 PM Where the context-free grammar meets the contact map: a probabilistic model of protein sequences aware of contacts between amino acids
Witold Dyrka, Wroclaw University of Science and Technology, Poland

2:40 PM-3:00 PM Predicting Loop Conformational Ensembles
Charlotte Deane, University of Oxford, United Kingdom

3:00 PM-3:20 PM Systematic Analysis of Symmetry and Pseudo-Symmetry in Membrane Protein Structures
Antoniya Aleksandrova, NINDS – NIH, United States

3:20 PM-3:40 PM Pseudo-Symmetry in 7 Transmembrane Helix (7TMH) Proteins: Intragenic Duplication of Protodomains with Evolutionary Balance of Structural Constraints and Functional Divergence
Philippe Youkharibache, NCI/NIH, United States

3:40 PM-4:00 PM Predicting the assembly order of multimeric heteroprotein complexes
Daisuke Kihara, Purdue University, United States

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

4:40 PM-5:00 PM MAINMAST: De novo Main-chain Modeling for EM maps Using Tree-graph optimization.
Genki Terashi, Purdue University, United States

5:00 PM-5:20 PM Proceedings Presentation: An integration of fast alignment and maximum-likelihood methods for electron subtomogram averaging and classification
Xiangrui Zeng, Carnegie Mellon University, United States

5:20 PM-5:40 PM Metalloproteome landscape from the amino acid covariance perspective
Alexey Porollo, Cincinnati Children’s Hospital Medical Center, United States

5:40 PM-6:00 PM Clustering and classification of active and inactive protein kinase structures
Vivek Modi, Fox Chase Cancer Center, United States
3DSIG: Structural Bioinformatics and Computational Biophysics

COSI TRACK PRESENTATIONS
TUESDAY, JULY 10 • ROOM: COLUMBUS AB

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

COSI TRACK PRESENTATIONS
TUESDAY, JULY 10 • ROOM: COLUMBUS EF

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

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**


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

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Microbiome
COSI TRACK PRESENTATIONS
TUESDAY, JULY 10 • ROOM: COLUMBUS KL

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 Ehsanedin 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


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**


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<tr>
<th>Time</th>
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<td>8:35 AM</td>
<td>Introduction</td>
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<td>8:40 AM</td>
<td><strong>Quaid Morris</strong></td>
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<td>8:40 AM</td>
<td><strong>Keynote: Machine learning in cancer genomics</strong></td>
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<td>9:40 AM</td>
<td><strong>Coffee Break with Exhibitors</strong></td>
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<td>10:40 AM</td>
<td><strong>Ahmet Süreyya Rifaioglu</strong></td>
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<td>10:40 AM</td>
<td><strong>Drug-Target Interaction Prediction with Deep Convolutional Neural</strong></td>
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<td>11:40 AM</td>
<td><strong>Andrew Rouillard</strong>, GSK, United States</td>
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<td>11:40 AM</td>
<td><strong>Can Deep Learned Omic features predict clinically successful</strong></td>
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<td>11:40 AM</td>
<td><strong>therapeutic targets?</strong></td>
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<td>11:40 AM</td>
<td><strong>Samuel Kaski</strong>, Aalto University, Finland</td>
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<td>11:40 AM</td>
<td><strong>Proceedings Presentation: Improving genomics-based predictions</strong></td>
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<td>11:40 AM</td>
<td><strong>for precision medicine through active elicitation of expert knowledge</strong></td>
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<td>11:40 AM</td>
<td><strong>Mehmet Gönen</strong>, Koç University, Turkey</td>
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<td>11:40 AM</td>
<td><strong>Proceedings Presentation: Discriminating early- and late-stage</strong></td>
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<td>11:40 AM</td>
<td><strong>cancers using multiple kernel learning on gene sets</strong></td>
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<td>11:40 AM</td>
<td><strong>Francesca Petralia</strong>, Mount Sinai Medical School, United States</td>
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<td>11:40 AM</td>
<td><strong>Proceedings Presentation: A new method for constructing tumor</strong></td>
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<td><strong>specific gene co-expression networks based on samples with tumor</strong></td>
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<td><strong>heterogeneity</strong></td>
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<td>11:40 AM</td>
<td><strong>Yves Moreau</strong>, Katholieke Universiteit Leuven, Belgium</td>
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<td>11:40 AM</td>
<td><strong>Proceedings Presentation: Gene Prioritization Using Bayesian Matrix</strong></td>
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<td>11:40 AM</td>
<td><strong>Factorization with Genomic and Phenotypic Side Information</strong></td>
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<tr>
<td>11:40 AM</td>
<td><strong>Marinka Zitnik</strong>, Stanford University, United States</td>
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<tr>
<td>11:40 AM</td>
<td><strong>Proceedings Presentation: Modeling Polypharmacy Side Effects</strong></td>
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<tr>
<td>11:40 AM</td>
<td><strong>with Graph Convolutional Networks</strong></td>
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<tr>
<td>12:00 PM</td>
<td><strong>Lunch (on own)</strong></td>
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<tr>
<td>12:00 PM</td>
<td><strong>Alexis Battle</strong></td>
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<tr>
<td>12:00 PM</td>
<td><strong>Keynote: Context-specific and dynamic effects of genetic variation</strong></td>
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<td>12:00 PM</td>
<td><strong>Ana Stanescu</strong>, University of West Georgia, United States</td>
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<tr>
<td>12:00 PM</td>
<td><strong>Integrating heterogeneous predictive models using Reinforcement</strong></td>
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<td>12:00 PM</td>
<td><strong>Learning</strong></td>
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<td>12:00 PM</td>
<td><strong>Tahmid Mehdi</strong>, University of Toronto, Canada</td>
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<tr>
<td>12:00 PM</td>
<td><strong>Applying semi-supervised variational inference to heterogeneous</strong></td>
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<td>12:00 PM</td>
<td><strong>genomic data predicts heart enhancers</strong></td>
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<td>12:00 PM</td>
<td><strong>Yue Wu</strong>, University of California, Los Angeles, United States</td>
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<tr>
<td>12:00 PM</td>
<td><strong>Proceedings Presentation: A scalable estimator of SNP heritability</strong></td>
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<td>12:00 PM</td>
<td><strong>for Biobank-scale data</strong></td>
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<td>12:00 PM</td>
<td><strong>Ruth Johnson</strong>, University of California, Los Angeles, United States</td>
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<tr>
<td>12:00 PM</td>
<td><strong>Proceedings Presentation: A unifying framework for joint trait</strong></td>
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<td>12:00 PM</td>
<td><strong>analysis under a non-infinitesimal model</strong></td>
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<td>Time</td>
<td>Speaker</td>
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<td>10:15-10:20 AM</td>
<td>Julia Zeitlinger</td>
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<tr>
<td>10:20-10:50 AM</td>
<td>Remo Rohs</td>
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<tr>
<td>10:50-11:00 AM</td>
<td>Raluca Gordan</td>
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<tr>
<td>11:00-11:10 AM</td>
<td>Ariel Afek</td>
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<tr>
<td>11:20-11:30 AM</td>
<td>Raluca Gordan</td>
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<tr>
<td>11:30-11:40 AM</td>
<td>Jinfeng Xiao</td>
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<tr>
<td>11:40-11:50 AM</td>
<td>Juri Reimand</td>
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<tr>
<td>11:50-12:00 PM</td>
<td>Dennis Kostka</td>
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<tr>
<td>12:00-12:10 PM</td>
<td>Verena Heinrich</td>
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<tr>
<td>12:10-12:20 PM</td>
<td>Matteo Barberis</td>
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<tr>
<td>12:20-12:30 PM</td>
<td>Joydeep Mitra</td>
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<tr>
<td>12:30-12:40 PM</td>
<td>Atul Deshpande</td>
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<tr>
<td>12:40-12:50 PM</td>
<td>Yungil Kim</td>
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<tr>
<td>12:50-1:00 PM</td>
<td>Konstantine Tchourine</td>
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<tr>
<td>1:00-1:10 PM</td>
<td>Aleksander Jankowski</td>
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<tr>
<td>1:10-1:20 PM</td>
<td>Vivekanandan Ramalingam</td>
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</tbody>
</table>

**MONDAY, JULY 9 continued • ROOM: GRAND BALLROOM B**
RegSys: Regulatory and Systems Genomics
COSI TRACK PRESENTATIONS
MONDAY, JULY 9 continued • ROOM: GRAND BALLROOM B

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  
**Ruoqi 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

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>8:35 AM-8:40 AM</td>
<td>Welcome to RegSys Day 2</td>
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<tr>
<td>8:40 AM-9:10 AM</td>
<td>Yoav Gilad, University of Chicago, United States</td>
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<td></td>
<td>Keynote: What are the big barriers to a complete understanding of gene regulation?</td>
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<tr>
<td>9:10 AM-9:20 AM</td>
<td>Chao-Chung Kuo, RWTH Aachen Medical Faculty, Germany</td>
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<td></td>
<td>Long noncoding RNAs as sequence-specific DNA-binding factors</td>
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<td>9:20 AM-9:40 AM</td>
<td>Siamak Zamani Dadaneh, Texas A&amp;M University, United States</td>
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<td>Proceedings Presentation: Covariate-Dependent Negative Binomial Factor Analysis of RNA Sequencing Data</td>
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<tr>
<td>9:40 AM-10:15 AM</td>
<td>COFFEE BREAK WITH EXHIBITORS</td>
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<tr>
<td>10:15 AM-10:45 AM</td>
<td>Jun Song, University of Illinois at Urbana-Champaign, United States</td>
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<td></td>
<td>Keynote: Predictive local sequence features can distinguish the binding specificity of transcription factor family members</td>
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<tr>
<td>10:45 AM-11:00 AM</td>
<td>Timothy Durham, University of Washington, United States</td>
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<td>PREDICTD: PaRallel Epigenomics Data Imputation with Cloud-based Tensor Decomposition</td>
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<td>11:00 AM-11:20 AM</td>
<td>Akshay Balsubramani, Stanford University, United States</td>
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<td></td>
<td>Systematic evaluation of multimodal approaches to predict in vivo transcription factor binding across cell types</td>
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<td>11:20 AM-11:40 AM</td>
<td>Shaun Mahony, The Pennsylvania State University, United States</td>
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<td></td>
<td>Deep neural networks for characterizing sequence and chromatin pre-determinants of transcription factor binding</td>
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<td>11:40 AM-12:00 PM</td>
<td>Jun Song, University of California, Los Angeles, United States</td>
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<td>Fine Mapping of Chromatin Interactions via Neural Networks</td>
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<td>12:00 PM-12:20 PM</td>
<td>Jun Ding, Carnegie Mellon University, United States</td>
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<td>Reconstructing differentiation networks and their regulation from time series single-cell expression data</td>
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<td>12:20 PM-12:40 PM</td>
<td>Jingyi Jessica Li, University of California, Los Angeles, United States</td>
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<td>Quantitating translational control: mRNA abundance-dependent and independent contributions and the mRNA sequences that specify them</td>
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<td>12:40 PM-2:00 PM</td>
<td>LUNCH (ON OWN)</td>
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<td>2:00 PM-2:30 PM</td>
<td>Manolis Kellis, Massachusetts Institute of Technology, United States</td>
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<td>Keynote: From Genetics To Therapeutics: Uncovering And Manipulating The Circuitry Of Non-coding Disease Variants</td>
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<td>2:40 PM-3:00 PM</td>
<td>Wouter Meuleman, Altius Institute for Biomedical Sciences, United States</td>
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<td>Consensus architectures of regulatory DNA actuation across 420 human cell types and states</td>
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<td>3:00 PM-3:20 PM</td>
<td>Yang Yang, Carnegie Mellon University, United States</td>
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<td>Continuous-trait probabilistic model for comparing multi-species functional genomic data</td>
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<td>3:20 PM-3:40 PM</td>
<td>Deborah Chasman, University of Wisconsin-Madison, United States</td>
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<td></td>
<td>Dynamic Regulatory Module Networks for integrative inference of cell type-specific regulatory programs</td>
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<td>3:40 PM-4:00 PM</td>
<td>Kjong-Van Lehmann, ETH Zurich, Switzerland</td>
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<td>Assessing the Gene Regulatory Landscape in 1,188 Human Tumors</td>
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<td>4:20 PM-4:40 PM</td>
<td>Natalie Sauerwald, Carnegie Mellon University, United States</td>
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<tr>
<td></td>
<td>Proceedings Presentation: Quantifying the similarity of topological domains across normal and cancer human cell types</td>
</tr>
</tbody>
</table>
**Technology Track**

**PRESENTATIONS**


**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

**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

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 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


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 Scholar-One 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.

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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
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.
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.

KEYNOTE SPEAKERS

ANA CONESA, PhD
University of Florida, USA
Department of Biochemistry Lab - DPF

DAVID HOLMES, PhD
Universidad de Santiago, Santiago, Chile

NIKOS KYRPIDES, PhD
US Department of Energy, Joint Genome Institute, USA

ANA TEREZA RIBEIRO DE VASCONCELOS, PhD
The National Laboratory for Scientific Computation (LCC), Minas Gerais

MORTEN Sogaard, PhD
IHES Genome Sciences & Technologies, Paris

JANET THORNTON, PhD
EMBL-FPS Protein, EMBL-EBI

The EMBL Keynote Lecture

http://www.iscb.org/iscb-latinamerica2018

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MIT, USA

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Professor
University of California San Diego, USA

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

Christine Orengo, Ph.D.
Vice President, ISCB
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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 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!
ECCB2018
GREECE - ATHENS
SEP 08, 2018 THROUGH SEP 12, 2018
http://eccb18.org

INCOB2018
INDIA - NEW DELHI
SEP 26, 2018 THROUGH SEP 28, 2018

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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