ISCBNewsletter

SUMMER 2019 ISSUE 02

BASEL
JULY 21–25 2019

ISMB ECCB

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

CONFERENCE PROGRAMME

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COSI SCHEDULES

Featuring the
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LETTER FROM THE PRESIDENT

Dear Colleagues and Friends,

As I enter my second year serving as your Society president, I am encouraged by our progress and proud of what we have accomplished. Over the course of the last year, the ISCB Executive Board and Board of Directors, staff, advisory councils and committees have been working diligently to serve our membership, and the ISCB Student Council continues to amaze me, as they work to develop new programs and implement their existing programs. Through the volunteers of the Society, we were able to develop a Code of Conduct and Safe Place Program; conduct a full analysis of the memberships needs and develop a living strategic map; closely listen to the needs of the community and the feedback of our Equity, Diversity and Inclusion Task Force to pilot a childcare service at our flagship meeting; and continue to cultivate, nurture, and enhance the relationship with the ISCB communities of special interest to ensure we are offering our members the best knowledge exchange and collaboration opportunity possible.

ISCB remains to be a rather young organization when compared to many other scientific organizations, which presents both challenges and opportunities. One of the biggest challenges we have faced was the lack of a professional code of conduct. Over the course of the Fall of 2018, a small task force worked very hard on developing a Society-wide code of ethical and professional conduct. Towards the end of the year a draft of the code of conduct was presented to our membership for inspection and comments. We incorporated the comments received in this process, and in February 2019, the ISCB Board of Directors unanimously approved the adoption of the resulting new Code of Ethics and Professional Conduct. I encourage you to review the code and become familiar with the elements that make up the document — www.iscb.org/codeofconduct. As members of ISCB, we are all responsible for upholding and representing our discipline in the upmost honor.

Along with the Code of Ethics and Professional Conduct, the ISCB Board of Directors implemented the ISCB Safe program (https://www.iscb.org/ismbeccb2019-general/codeofconduct). ISCB works to maintain an environment that allows science and scientific careers to flourish through respectful, inclusive, and equitable treatment of others and is committed to providing a safe place for its members and nonmember participants. Our goal is to foster a culture that creates a safe and open working environment for all who are participating in ISCB activities, conferences, and programs. ISCB has appointed Ombudspersons (wearing ribbon designations) who can be consulted, give advice or help seek out appropriate authorities to further handle any form of harassment or assault.

Another major accomplishment, which presents an opportunity for the Society, was the development and approval of the ISCB Strategic Map. This living document (https://www.iscb.org/strategicmap) presents the strategic direction for ISCB. Started under the leadership of Alfonso Valencia, the core competencies that make up the foundation of the Strategic Map were carefully considered to ensure each enhances or helps to progress our purpose as an organization. Specific milestones, activities, and programs have been identified to support the achievement of the competency goal, all developed to provide great member value, enhance the community experience and promote the value of our profession and discipline. As we work to achieve our goals, I invite you to get involved. We are a Society driven by our members to serve our members and welcome your expertise, support, knowledge and feedback.

To further our collaboration with the Communities of Special Interest (COSIs), we continue to work closely with each of our established communities and work to add new communities. The ISMB/ECCB scientific program remains to be supported and developed with close coordination of the COSIs. I encourage you to join your COSI of choice and engage with the community through our ISCBconnect program (www.connect.iscb.org). We aim to extend the impact of the COSIs throughout the year and continue the conversation that started at and before ISMB/ECCB 2019.

The ISCB Student Council continues to work diligently to serve our student and postdoc membership. I am so impressed and encouraged as I watch our students and postdocs work to enhance the offerings of ISCB. They accomplish so much and impact our community greatly. Watching them thrive solidifies that our future is in good hands. From internships to growing regional student groups and organizing student-managed symposia, no challenge seems to big to achieve.

I am also very excited about this year's ISMB/ECCB conference. We had record-breaking submissions in almost every submission category. The scientific program has an excellent balance of innovative, cutting-edge research and highlights of already published work. We have also introduced CompBio Ignite talks. This un-conference component of the meeting will give members who were not selected for oral presentation the opportunity to give a six-minute lighting style talk during the lunch hour. Much appreciation goes to all of the volunteers who worked selflessly to put together this conference. It is by far one of the best programs offered in our community.

As I come to a close for this edition of the ISCB Summer Newsletter, I would like to take the opportunity to recognize Casey Greene and Lucia Peixoto for assisting on the offering of the ISCB Childcare Services at ISMB/ECCB 2019 in Basel. These two individuals were instrumental on supporting the fundraising efforts to pilot this service at the flagship meeting. I would also like to thank Steven Leard, Pat Rodenberg and Jermey Hennig for their hard work on ISMB/ECCB. Finally, my gratitude also goes to the ISCB staff, Nadine Costello, Bel Hanson, and Diane Kovats. It takes a tremendous amount of work to keep ISCB thriving. Their dedication to our Society and mission enables us to continue to offer the highest level of services and programs to our members.

As we move to continue to make ISCB your Society and community, please do not hesitate to reach out to me and share your ideas, provide your feedback, or give of your time.

Sincerely,

Thomas Lengauer

Thomas Lengauer

2019 ISCB INNOVATOR AWARD
WILLIAM STAFFORD NOBLE

The ISCB Innovator Award honors an ISCB scientist who is within two decades of having completed his or her graduate degree and has made outstanding contributions to the field of computational biology. The 2019 winner is Dr. William Stafford Noble, Professor in the Department of Genome Science, University of Washington.

WILLIAM STAFFORD NOBLE – INTERESTED IN LEARNING STUFF

William Stafford Noble was raised in Naperville, IL, with his brothers and his parents who were both college professors. As a child, he didn't have a specific interest in science, but he remembered, "I was just interested in learning stuff." A simple test gave Noble a peek into his future career path. Noble recalled, "I took a career aptitude test in high school, and the results said I should be a college professor or computer scientist, but at that point I had never touched a computer."

Noble went to Stanford University to complete a bachelor's degree in Symbolic Systems, with a concentration in Philosophy. After graduating in 1991, Noble gained work experience in the field of speech recognition, and he also spent two years in the US Peace Corps in Lesotho, Africa. Noble said, "Both of my brothers went overseas after college, so I picked the Peace Corps. It seemed to be a little better organized than some other options." Noble spent two years teaching math, physics and English literature to secondary students and had to develop teaching skills to explain complex material in a clear and straightforward way, training that has served him well throughout his career. All the while, he kept thinking about computer programming, and he would write down programs on paper in his free time. At the end of his first year in Lesotho, his parents visited him and brought him a laptop, so he could use the brief hours of evening electricity to transfer his programs from paper to a computer. Noble also developed an interest at this time in artificial life, which was a relatively new field. Relatively quickly, he came to feel that this field was too descriptive, so he began to search for a different dissertation subject. His future Ph.D. mentor at the University of California, San Diego, Charles Elkan, emailed him about a funding opportunity that would allow him to study hidden Markov models (HMMs) in protein and DNA sequences. Noble was open to this topic because he was already familiar with HMMs from his work in speech recognition, and he went on to complete his Ph.D. in computer science and cognitive science in 1998. Noble's first bioinformatics publication, which was based on his Ph.D. research, described a web server for motif-based sequence analysis (the MEME Suite) that is still in use today.

Noble went on to David Haussler's lab at the University of California, Santa Cruz as a Sloan/DOE postdoctoral fellow and co-authored the first paper that applied support vector machines to microarray gene expression data. He also developed kernel functions that could be used to represent a variety of data types, and he showed how kernels could be used to perform inference jointly from these heterogenous types of data. This work was ultimately developed into applications in inference of protein-protein interactions and gene function that are used by many researchers.

In 1999, Noble became an Assistant Professor in the Department of Computer Science at Columbia University, with a joint appointment at the Columbia Genome Center. He moved to his current appointment at the University of Washington in 2002 in the newly formed Department of Genome Sciences with adjunct appointments in the Department of Computer Science and Engineering, the Department of Medicine, and the Department of Biomedical Informatics and Medical Education. As an independent investigator, Noble has expanded his research interests including the development of unsupervised machine learning methods for semi-automated genome annotation, and the application of machine learning and statistical methods to analyze proteomic data.

Throughout his career, Noble has grown as a scientist and mentor by learning from those who have mentored him, as well as observing how his collaborators mentor students and run their labs. Noble also credits his wife, Nancy Stafford Noble, for being a valuable sounding board and providing her expertise as an executive coach as he has navigated the many challenges of being a PI. He has trained and advised 15 graduate students and 21 postdoctoral fellows, many of whom now hold faculty appointments, and he was honored with the Postdoc Mentor of the Year Award by the University of Washington Postdoctoral Association.

Outside of the lab, Noble is an active member of the global computational biology community through his service on multiple editorial boards, conference committees, study sections, and roles on the ISCB Board and various committees. Noble has been a part of ISCB since its early years and has always felt at home at ISMB meetings, which he considers one of the few gatherings that brings together computational biologists who bridge the gap between basic computer science and applications in biology. Noble feels deeply honored by his recognition with the 2019 ISCB Innovator Award, particularly as this award is bestowed upon him by colleagues for whom he holds great respect and admiration.

2019 ISCB ACCOMPLISHMENT BY A SENIOR SCIENTIST AWARD

BONNIE BERGER

ISCB honors a leader in the fields of computational biology and bioinformatics each year with the Accomplishments by a Senior Scientist Award. This award is the highest honor conferred by ISCB to a scientist who is recognized for significant research, education, and service contributions. Bonnie Berger, Simons Professor of Mathematics and Professor of Electrical Engineering and Computer Science at the Massachusetts Institute of Technology (MIT) is the 2019 recipient of the Accomplishments by a Senior Scientist Award.

BONNIE BERGER—FROM MATH RIDDLES TO GENOMICS

Bonnier Berger grew up in Miami, Florida with her parents and older brother and has early memories of being curious about mathematics. She recalled, "As a young child, I responded, "I want one too, please," when my father slipped math problems under my brother's door. My father would continue to challenge me with math riddles and chess puzzles. He would also engage me in science projects. Our relationship laid the foundation for my comfort with, and interest in, math and science, even though it was not so common for girls at the time." Berger's early interest in math and science led her to complete her AB in computer science at Brandeis University. In 1990, she completed her PhD in computer science at MIT under the mentorship of Silvio Micali. Berger's dissertation research on randomized and parallel algorithms was recognized by the Machtey Award for a manuscript that she co-published with fellow graduate student John Rompel, as well as the George M. Sprowles Award.

After graduate school, Berger remained at MIT and stumbled upon computational biology quite unexpectedly. She recounted, "My postdoc supervisor Daniel J. Kleitman, who has Erdos #1 and solved dynamic programming for RNA base-pairings with Ruth Nussinov, had just come back from an NSF workshop whose goal was to get mathematicians and biologists together to solve challenges at the interface between the two fields. He was so taken with Michael Levitt's talk that he said, "Proteins, that's what you should do." Well, fortunately, he didn't say, "Plastics," as in "The Graduate," or I might have ended up a material scientist." She appreciates the freedom she had as a postdoc and took to heart the advice Kleitman gave her when he told her, "We are applied mathematicians looking for interesting problems to investigate." Following her postdoc, Berger became an Assistant Professor of Mathematics at MIT, and as a PI, she was one of the pioneers of the use of computer algorithms for analyzing, interpreting, and sharing diverse types of biological data.

Among Berger's scientific contributions, she developed the use of pairwise residue correlations to predict protein structure from sequence through her highly cited Paircoil/Multicoil programs. Her seminal work on the hardness of protein folding was recognized with the 2010 RECOMB Test of Time Award. Berger's interest in genomics included development of the ARACHNE genome assembly tool, which was used by the Human Genome Consortium for whole genome assembly. She also initiated the area of comparative genomics with her cutting-edge work comparing human and mouse genomes. Berger launched the subfield of global network alignment with her Isorank/IsorankN programs and advanced protein structure alignment with her MATT program.

Berger considers her theoretical computer science background to be critical to her success in identifying and studying computational biology problems. She said, "I have realized that with my algorithms background and flexibility, I can easily shift between areas as the research landscape changes. As I gain knowledge across diverse research areas, I can see connections between them and techniques that can be used to address them." Berger has also come to appreciate the many mentors that helped her bridge the gap between computer science and biology, including Peter Shor, Peter S. Kim and Jonathan King. She recalled, "[They] taught me biology on a need-to-know basis. It took many rounds of back-and-forth by, would you believe, fax machine with Peter Kim for me to turn my early Paircoil writeup from definitions and theorems to one accessible to a biology audience."

Berger has trained numerous graduate students and postdocs, using an approach she learned from her NSF Postdoc supervisor. She said, "[Kleitman] gave me a lot of freedom to pursue whatever interested me, and that's how I mentor my students. I ask them what interests them and suggest several research problems, or I encourage them to bring entirely new research areas to us." Many of her trainees have become leaders in the field of computational biology.

Berger has served the computational biology community in many capacities, including her roles as Vice President of ISCB and Head of the RECOMB Steering Committee; as well as her service on multiple editorial boards, and program and conference committees. Her scientific contributions have been recognized by numerous awards, including the NSF Career Award, Biophysical Society Dayhoff Award for Research, inaugural Technology Review Top 100 Innovators, ACM Fellow, ISCB Fellow, AMS Fellow, AIMBE Fellow, NIH Margaret Pittman Award for Outstanding Scientific Achievement & Lectureship, election to the American Academy of Arts & Sciences, and an Honorary Doctorate from EPFL.

Berger is extremely grateful for this recognition by ISCB, especially considering her longtime involvement with the Society. She said, "It's a tremendous honor to join such a distinguished and accomplished group of scientists."

Administrative building of the Novartis Campus in Basel by Frank O. Gehry / Photo by Novartis

2019 OUTSTANDING CONTRIBUTIONS TO ISCB
BARB BRYANT

The Outstanding Contributions to the International Society of Computational Biology (ISCB) Award recognizes outstanding service contributions to the Society by any member through exemplary leadership, education, service, or a combination of these three elements. Barbara (Barb) Bryant, Senior Director at Constellation Pharmaceuticals, is the 2019 ISCB winner of the Outstanding Contributions to ISCB Award.

BARB BRYANT—FINDING COMMUNITY THROUGH SERVICE

Barb Bryant has spent much of her career as a computational biologist working in the pharmaceutical industry, where she has managed and directed a wide array of bioinformatics projects related to cancer diagnostics, clinical biomarker identification, and mechanism of action of small molecule inhibitors. Bryant first became involved with ISCB by attending conferences like ISMB and engaging in leadership opportunities through ISCB. She has continued to be involved with ISCB because she has benefited and genuinely treasured being a part of this unique community. She said, “I have enjoyed working with colleagues to find ways to support other computational biologists, particularly students and postdocs. It was great to have a shared purpose, in contrast to the somewhat competitive nature you can sometimes find in scientific research. It is gratifying to be able to see progress on community projects such as nurturing the Student Council, encouraging open sharing of data and software, putting on conferences, or developing publishing venues. Above all, I value the friendships that I have developed with others on the Board and Committees.”

Bryant has served on the ISCB Board of Directors in several capacities, including ISCB Secretary (2002-2005) and Vice President (2005-2007). She also chaired the Public Affairs Committee during this time and was instrumental in maintaining ISCB’s affiliation with FASEB. Bryant worked on the Editorial Board of PLoS Computational Biology and has been thankful for these diverse service opportunities. She said, “I loved collaborating with Phil Bourne on the Editorial Board of PLoS Computational Biology. It is great to work with colleagues who have a ton of great ideas and an inclusive, forward-looking attitude. Thinking about how to bring positive change on the Board and within the Society has also been a good challenge. I appreciated serving as the representative of ISCB to FASEB in order to have a voice in Washington at a critical time, post-9/11, when it was becoming harder to travel to the USA for scientific conferences and collaboration.”

Bryant sees ISCB playing a critical future role in advancing important initiatives related to computational biology, including advocating for improved research funding and open access to findings from government funded research. She considers one of ISCB’s strengths to be in the exchange of scientific information through conferences and publications, and she hopes the Society can continue to innovate novel approaches to enhance the communication and dissemination of computational biology research.

Bryant hopes trainees and junior faculty members seek out constructive service opportunities with ISCB and other similar organizations. She said, “There are two key aspects of serving that I think matter even more than the particular area of service. The first is to find a way to make a positive difference -- to change how the world operates. The second is to do it with other people who are positive and effective and fun to be with. If it is a toxic environment, leave. If the people are awesome, stick with it and find a way to contribute, no matter how hard the problem!”

Bryant will be recognized for her distinguished service to ISCB at the 2019 Joint ISMB/ECCB conference in Basel, Switzerland alongside this year’s other ISCB award recipients.

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ISCB'S FALL NEWSLETTER!

2019 ISCB OVERTON PRIZE

CHRISTOPHE DESSIMOV

Each year the International Society for Computational Biology (ISCB) honors the achievements of an early- to mid-career scientist with the Overton Prize. This prize was instituted in 2001 to honor the untimely loss of Dr. G. Christian Overton, a respected computational biologist and founding member of the ISCB Board of Directors. The Overton Prize recognizes early or mid-career phase scientists who have made significant contributions to computational biology or bioinformatics through their research, teaching, and service. In 2019, ISCB recognized Dr. Christophe Dessimoz, SNSF Professor at the University of Lausanne, Associate Professor at the University College London, and Group Leader at the Swiss Institute for Bioinformatics.

CHRISTOPHE DESSIMOZ—LEARNING TO STOP RESISTING

Christophe Dessimoz grew up in Switzerland and was deeply drawn to computers from a young age, right around the dawn of the web and widespread internet access. As a teenager, he spent a lot of time programming and developing websites. To avoid spending too much time in front of computers, he decided instead to pursue a first degree in Biology at ETH Zurich, Switzerland. During and after his studies, he traveled and spent several months doing biology research at Northwestern University in the United States, Tsinghua University in China, and Chulalongkorn University in Thailand. Dessimoz recalled his struggles at the bench and feared he was just too clumsy to pursue a career in biology. He was also still drawn to computers, and he said, “I just stopped resisting,” and returned to ETH Zurich to complete a PhD in Computer Science under the mentorship of Gaston Gonnet.

Dessimoz joined Gonnet’s team in 2004 to purse a PhD research project in comparative genomics, right at the time when genomes were starting to become routinely available. There was an obvious need to compare these genomes and identify the corresponding genes in different species—the orthologs. Dessimoz’s first scientific paper introduced the “Orthologous Matrix” (OMA) algorithm. The work provided the foundation for the OMA database.

After completing his PhD and working as a teaching faculty member and senior research associate at ETH Zurich, Dessimoz received a fellowship from the Swiss National Science Foundation to be a visiting scientist at the EMBL-European Bioinformatics Institute (EBI) in Hinxton, UK. He joined Nick Goldman’s group to collaborate on large-scale phylogenetic methods. During his stint at EBI, Dessimoz became increasingly interested in benchmarking and developed an appreciation for this often overlooked but critical methodological process. This interest is exemplified in his leadership role in the Quest for Orthologs Consortium, a community effort to improve orthology methods and their applications. Together with Adrian Altenhoff, his

close associate since their days in Gonnet's lab, Dessimoz developed a more direct approach to benchmarking orthology inference methods based on congruence tests between genes and species trees, which has become a definitive method for orthology benchmarking. He has continued to advocate for the importance of benchmarking and standardization for progress in bioinformatics.

In 2013, Dessimoz moved to University College London as a Lecturer and held a joint appointment between the Department of Genetics, Evolution & Environment and the Department of Computer Science. He was promoted to Reader in 2015, and he also joined the University of Lausanne (UNIL) as SNSF Professor. Dessimoz became a group leader at the Swiss Institute of Bioinformatics in 2015, and he continues to maintain his UCL and UNIL labs. Beyond his contributions to benchmarking, Dessimoz has made critical contributions to phylogenetics tests of sequence alignment accuracy. Despite the decades of work in this area, he said, "We still struggle to assess the correctness of alignments." Dessimoz has also made valuable contributions to methods used for Gene Ontology (GO) annotation, particularly with the development of a technique using historical time series to track the fate of inferred annotations over time. This approach has changed the way the GO consortium tracks annotation quality and has been adapted for other projects. Dessimoz continues to be drawn to research focused on evolutionary biology and orthology inference, and he also fascinated by the challenges of handling huge heterogeneous datasets.

Dessimoz feels deeply honored by his selection as the 2019 Overton Prize winner, and he acknowledges that the support and relative independence that his mentors gave, as well as the productive partnerships with his staff, trainees and collaborators have been instrumental to his success as an independent investigator.

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BASEL
JULY 21–25
2019

ISMB ECCB

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CONFERENCE PROGRAMME

Welcome to Basel!

On behalf of the organizing committee of ISMB/ECCB 2019 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 beautiful city of Basel. The combined ISCB and ECCB Conference promises to be the key meeting for computational biologists in 2019.

We continue to build on the successful launch of a COSI-centric ISMB/ECCB meeting. COSIs are Communities of Special Interest reflecting most of the major research themes and training in computational biology. This year we have 20 COSIs participating at ISMB/ECCB with major computational biology themes ensuring you can connect more easily to researchers sharing common interests and come together and listen to exciting new developments in your field. These communities 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 2019 ISCB award winners, will cover topics as diverse as: Challenges and rewards of benchmarking; Traveling across spaces: the power of embedding genomic and proteomic data into a latent space; Biomedical Data Sharing and Analysis at Scale.

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, BioInfo Core Workshop 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, 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 Basel.

The program includes

- 5 Keynote addresses, including our 3 2019 ISCB Award Winners
- 20 community-led COSI tracks and workshops
- 7 Special Sessions
- 2 Special Tracks by ELIXIR and BD2K
- 19 Technology Track presentations
- The pre-conference Student Council Symposium organized by and for students
- 7 Pre-conference Tutorials

Equally as important, there are more than 1,100 posters on display throughout the conference and presented by their authors in three sessions. Discussions directly with authors can be so much more revealing than just hearing a presentation, so do go along.

We acknowledge all the chairs of the Proceedings, COSIs, Poster, Technology Track, Travel Fellowship, Tutorials, Art in Science, and Student Council Symposium committees. Their dedication and leadership in working with their committees have been invaluable. Over the course of the conference please take a moment to thank them for their efforts and dedication to the success of ISMB/ECCB 2019.

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: Yana Bromberg, Nadia El-Mabrouk, Bruno Gaeta, Janet Kelso, Diane Kovats, Steven Leard, Christine Orengo, Predrag Radivojac, and Thomas Lengauer. We truly appreciate the support and efforts of the conference 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 Basel for its welcoming hospitality and wish you all a great conference!

Yours sincerely,

Nicola Mulder
Conference Co-Chair

Torsten Schwede
Conference Co-Chair

ISMB/ECCB 2019 Scientific Organizing Committee

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Robert Hoehndorf, *King Abdullah University of Science & Technology, Saudi Arabia*
Philippe Rocca-Serra, *University of Oxford, United Kingdom*

BIOVIS: BIOLOGICAL DATA VISUALIZATION
Danielle Albers Szafir, *University of Colorado at Boulder, United States*
Thomas Höllt, *TU Delft, The Netherlands*
Michael Krone, *University of Tübingen, Germany*

BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE
Christopher Fields, *University of Illinois Urbana-Champaign, United States Bastian Greshake Tzovaras, openSNP, United States*
Nomi Harris, *Lawrence Berkeley National Laboratory, United States*
Michael Heuer, *UC Berkeley AMPLab, United States*
Karsten Hokamp, *Trinity College Dublin, Ireland*
Monica Munoz-Torres, *Oregon State University, United States*
Heather Wiencko, *Open Bioinformatics Foundation, Ireland*
Yo Yehudi, *InterMine (University of Cambridge), United Kingdom*

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS
Joaquin Dopazo, *Fundacion Progreso y Salud, Spain*
David Kreil, *Boku University Vienna, Austria*
Paweł Łabaj, *Jagiellonian University, Poland*
Wenzhong Xiao, *mgh/harvard medical school, United States*

COMPMS: COMPUTATIONAL MASS SPECTROMETRY
Oliver Kohlbacher, *University of Tübingen, Germany*
William Noble, *University of Washington, United States*
Olga Vitek, *Northeastern University, United States*

EDUCATION: COMPUTATIONAL BIOLOGY EDUCATION
Terri Attwood, *The University of Manchester, United Kingdom*
Cath Brooksbank, *EMBL-EBI, United Kingdom*
Patricia Palagi, *SIB Swiss Institute of Bioinformatics, Switzerland*
Russell Schwartz, *Carnegie Mellon University, United States*

EVOLUTION AND COMPARATIVE GENOMICS
Lars Arvestad, *Stockholm University, Sweden*
Christophe Dessimoz, *University College London, United Kingdom*
Aida Ouangraoua, *University of Sherbrooke, Canada*

FUNCTION: GENE AND PROTEIN FUNCTION ANNOTATION
Iddo Friedberg, *Iowa State University, United States*
Casey Greene, *University of Pennsylvania, United States*
Kimberly Reynolds, *University of Texas Southwestern Medical Center, United States*
Mark Wass, *University of Kent, United Kingdom*

HITSEQ: HIGH-THROUGHPUT SEQUENCING
Can Alkan, *Bilkent University,Turkey*
Ana Conesa, *Genomics of Gene Expression Lab, Spain*
Francisco M. De La Vega, *Stanford University, United States*
Dirk J. Evers, *Dr. Dirk Evers Consulting, Germany*
Gang Fang, *Mount Sinai School of Medicine, United States*
Kjong Lehmann, *ETH-Zürich, Switzerland*
Layla Oesper, *Carleton College, United States*

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY
Manfred Claassen, *ETH Zurich, Switzerland*
Anna Goldenberg, *SickKids Research Institute, Canada*

MICROBIOME
Aaron Darling, *ithree institute, University of Technology Sydney, Australia*
Alice McHardy, *HZI, Germany*
Alex Sczyrba, *Bielefeld University, Germany*
NIcola Segata, *University of Trento, Italy*

NETBIO: NETWORK BIOLOGY
Martina Kutmon, *Maastricht University, The Netherlands*
Alex Pico, *Gladstone Institutes, United States*

REGSYS: REGULATORY AND SYSTEMS GENOMICS
Anaïs Bardet, *CNRS – University of Strasbourg, France*
Ay Ferhat, *La Jolla Institute, United States*
Raluca Gordan, *Duke University, United States*
Shaun Mahony, *Penn State, United States*
Anthony Mathelier, *Oslo University Hospital, Norway*
Judith Zaugg, *EMBL, Germany*

RNA: COMPUTATIONAL RNA BIOLOGY
Yoseph Barash, *University of Pennsylvania, United States*
Alex Bateman, *EBI, United Kingdom*
Eduardo Eyras, *Universitat Pompeu Fabra, Spain*
Klemens Hertel, *University of California, Irvine, United States*
Michelle Scott, *Université de Sherbrooke, Canada*

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS
Claudine Chaouiya, *Instituto Gulbenkian de Ciência, Portugal*
Andreas Dräger, *University of Tübingen, Germany*
María Rodríguez Martínez, *IBM Research – Zurich, Switzerland*

TEXT MINING FOR BIOLOGY AND HEALTHCARE
Cecilia Arighi, *University of Delaware, United States*
Lars Juhl Jensen, *University of Copenhagen*
Robert Leaman, *NLM, NIH, United States*
Zhiyong Lu, *NLM, NIH, United States*

TRANSMED: TRANSLATIONAL MEDICAL INFORMATICS
Bissan Al-Lazikani, *The Institute of Cancer Research, United Kingdom*
Irina Balaur, *EISBM, France*
Wei Gu, *University of Luxembourg*
Saqi Mansoor, *KCL, United Kingdom*
Venkata Satagopam, *University of Luxembourg*
Maria Secrier, *UCL Genetics Institute, United Kingdom*

VARI: VARIANT INTERPRETATION
Yana Bromberg, *Rutgers, United States*
Emidio Capriotti, *University of Bologna, Italy*
Hannah Carter, *UCSD, United States*
Antonio Rausell, *Imagine Institute, France*

GENERAL COMPUTATIONAL BIOLOGY
Birte Kehr, *Berlin Institute of Health, Germany*

ISMB/ECCB 2019 COSI CONFERENCE LEADS

3D-SIG: STRUCTURAL BIOINFORMATICS AND COMPUTATIONAL BIOPHYSICS

Charlotte Deane, *Oxford University, United Kingdom*

Rafael Najmanovich, *University of Montreal, Canada*

OBF: OPEN BIOINFORMATICS FOUNDATION

Nomi Harris, *Lawrence Berkeley National Laboratory, United States*

Heather Wiencko, *Open Bioinformatics Foundation, Ireland*

Peter Cock, *James Hutton Institute, United Kingdom*

BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Jim Procter, *University of Dundee, United Kingdom*

Michel Westenberg, *Eindhoven University of Technology, The Netherlands*

BIO-ONTOLOGIES

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

Philippe Rocca-Serra, *University of Oxford, United Kingdom*

Michel Dumontier, *Maastricht University, The Netherlands*

Karin Verspoor, *University of Melbourne, Australia*

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

Joaquin Dopazo, *University Hospital Virgen del Rocío Spain*

David P Kreil Boku, *University Vienna, Austria*

Paweł Łabaj, *Jagiellonian University, Poland*

COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Oliver Kohlbacker, *University of Tübingen, Germany*

William Noble, *University of Washington, United States*

Olga Vitek, *Northeastern University ,United States*

EDUCATION: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS EDUCATION AND TRAINING

Russell Schwartz, *Carnegie Mellon University, United States*

Annette McGrath, *Australian Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia*

EvolCompGen: Evolution & Comparative Genomics

Christophe Dessimoz, *University of Lausanne, Switzerland*

Louxin Zhang, *National University of Singapore*

FUNCTION: GENE AND PROTEIN FUNCTION ANNOTATION

Iddo Friedberg, *Iowa State University, United States*

Mark Wass, *University of Kent, United Kingdom*

Kimberly Reynolds, *University of Texas Southwestern Medical Center, United States*

HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

Francisco M. De La Vega, *Stanford University, United States*

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

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Manfred Claassen, *ETH Zurich ,Switzerland*

Anna Goldenberg, *SickKids Research Institute, Canada*

MICROBIOME

Alice McHardy, *Helmholtz Centre for Infection Research, Germany*

Alexander Sczyrba, *Bielefeld University, Germany*

NETBIO: NETWORK BIOLOGY

Alexander Pico, *Gladstone Institutes, United States*

Natasa Przulj, *University College London, United Kingdom*

REGSYS: REGULATORY AND SYSTEMS GENOMICS

Anthony Mathelier, *Centre for Molecular Medicine, Norway*

Judith Zaugg, *EMBL, Germany*

IRB: INTEGRATIVE RNA BIOLOGY

Yoseph Barash, *University of Pennsylvania, United States*

Eduardo Eyras, *Universitat Pompeu Fabra, Spain*

Klemens Hertel, *University of California, Irvine, United States*

Michelle Scott, *Université de Sherbrooke, Canada*

Mihaela Zavolan, *UNIBAS, Switzerland*

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Claudine Chaouiya, *Instituto Gulbenkian de Ciência, Portugal*

María Martínez, *IBM Research – Zurich, Switzerland*

Andreas Dräger, *University of Tübingen, Germany*

TRANSMED: TRANSLATIONAL MEDICINE INFORMATICS & APPLICATIONS

Wei Gu, *University of Luxembourg*

Venkata Satagopam, *University of Luxembourg*

VARI: VARIANT INTERPRETATION

Hannah Carter, *University of California, San Diego, United States*

TECHNOLOGY TRACK COMMITTEE

Chair: Hagit Shatkay, *University of Delaware, United States*

Co-chair: Dominic Clark, *Pistoia Alliance, Inc, United Kingdom*

TRAVEL FELLOWSHIP COMMITTEE

Chair: Lucia Peixoto, *Washington State University, United States*

Co-chair: Dimitri Perrin, *Queensland University of Technology, Australia*

POSTERS COMMITTEE

Chair: Arjun Krishnan, *Michigan State University, United States*

Co-chair: Casey Greene, *University of Pennsylvania, United States*

Co-chair: Virginie Uhlmann, *European Bioinformatics Institute (EMBL-EBI), United Kingdom*

TUTORIALS COMMITTEE

Chair: Michelle D. Brazas, *Ontario Institute for Cancer Research, Canada*

Co-chair: Patricia M. Palagi, *SIB Swiss Institute of Bioinformatics, Switzerland*

Committee Meetings and Special Events Schedule

ALL EVENTS AT CONGRESS CENTER BASEL UNLESS NOTED

SUNDAY, JULY 21

9:00 AM – 5:30 PM	ISCB Board of Directors Meeting**	HYPERION HOTEL BASEL, GENEVA 4
6:15 PM – 7:30 PM	ISMB/ECCB 2019 Welcome & Opening Keynote (RAJEWSKY)	SAN FRANCISCO ROOM (3RD FLOOR)
7:30 PM – 8:30 PM	ISMB/ECCB 2019 Welcome Reception	2ND FLOOR FOYER

MONDAY, JULY 22

8:15 AM – 10:00 AM	Introduction of the Class of 2019 Fellows & ISCB 2019 Innovator Award Keynote (NOBLE)	SAN FRANCISCO ROOM (3RD FLOOR)
12:45 PM – 1:45 PM	ISCB Town Hall (Open to all!)	SINGAPORE ROOM (2ND FLOOR)
12:45 PM – 1:55 PM	Committee Meeting: ECCB Steering**	MEXICO ROOM (2ND FLOOR)
6:30 PM – 7:30 PM	Committee Meeting: Affiliated Groups**	MEXICO ROOM (2ND FLOOR)
	Committee Meeting: Publications++	HONGKONG (2ND FLOOR)
8:00 PM – 10:00 PM	President's Reception**	VOLKSHAUS BASEL

TUESDAY, JULY 23

8:15 AM – 10:00 AM	Presentation of ISCB 2019 Outstanding Service Award & Keynote (BATTLE)	SAN FRANCISCO ROOM (3RD FLOOR)
12:45 PM – 1:55 PM	Committee Meeting: ISCB COSI**	SINGAPORE (2ND FLOOR)
6:30 PM – 7:30 PM	Committee Meeting: Public Affairs Committee++	HONG KONG (2ND FLOOR)
	Committee Meeting: Education Committee++	MEXICO ROOM (2ND FLOOR)
8:00 PM – 11:00 PM	ISMB/ECCB 2019 Social Event	BASEL MARKTHALLE

WEDNESDAY, JULY 24

8:15 AM – 10:00 AM	ISCB 2019 Overton Prize Keynote (DESSIMOZ)	SAN FRANCISCO ROOM (3RD FLOOR)
12:40 PM – 2:00 PM	Committee Meeting: ISCB Fellows**	MEXICO ROOM (2ND FLOOR)

THURSDAY, JULY 25

12:40 PM – 2:00 PM	Career Fair	EXHIBITION AREA, 2ND FLOOR FOYER
5:00 PM – 6:00 PM	ISCB 2019 Outstanding Accomplishments by a Senior Scientist Keynote (BERGER)	SAN FRANCISCO ROOM (3RD FLOOR)
6:00 PM – 6:30 PM	Closing Ceremony and Awards	SAN FRANCISCO ROOM (3RD FLOOR)

** *By invitation only* ++ *All active ISCB members are welcome to attend if interested in engaging in committee activities*

Posters on Display

PRESENTATION SCHEDULE 6:00 PM – 8:00 PM

HALL 4.1, 1ST FLOOR

SET UP

SESSION A POSTERS
Monday, *July 22 7:30 am – 10:00 am*

SESSION B POSTERS
Wednesday, *July 24 7:30 am – 10:00 am*

REMOVAL

SESSION A POSTERS
Tuesday, *July 23, 8:00 pm*

SESSION B POSTERS
Thursday, *July 25, 2:00 pm*

SESSION A: (JULY 22 AND JULY 23)

JULY 22
- A) 3DSIG
- B) BioVis
- C) Function
- D) HitSeq
- E) RegSys
- F) SysMod
- G) TransMed
- H) SST01: Text Mining for Biology and Healthcare

JULY 23
- I) Bio-Ontologies
- J) CompMS
- K) EvolCompGe
- L) Microbiome
- M) NetBio

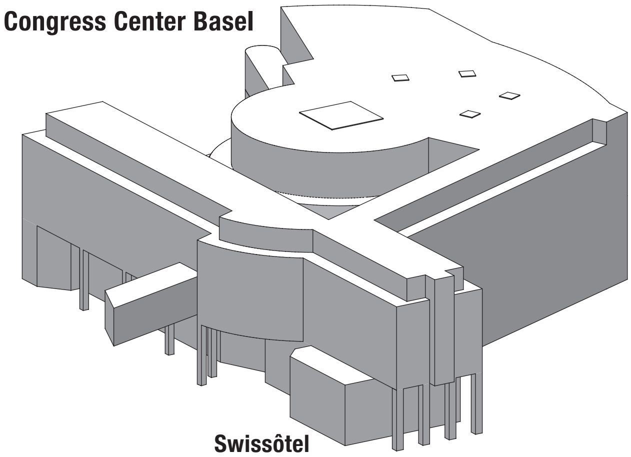
SESSION B: (JULY 24 AND JULY 25)

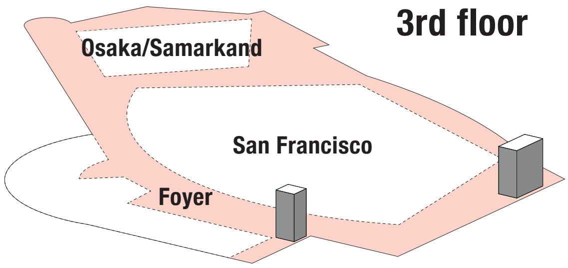
JULY 24
- P) BOSC
- Q) CAMDA
- R) Education
- S) MLCSB
- T) RNA
- U) VarI
- V) General Computational Biology

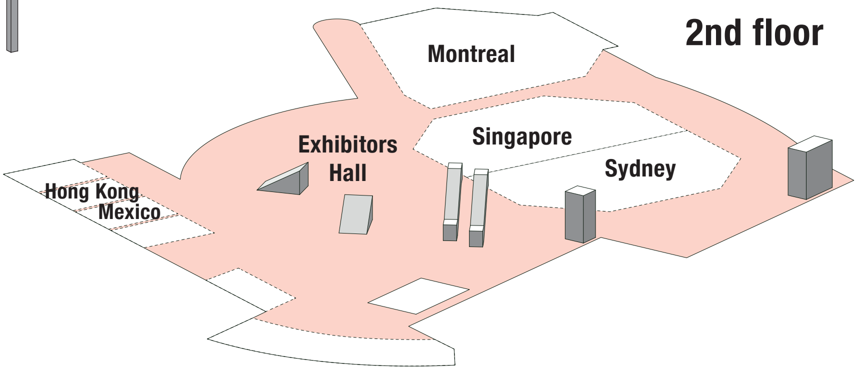
Posters not removed at outlined times will be taken down and placed on side tables. ISCB will not be responsible for damaged or missing posters.

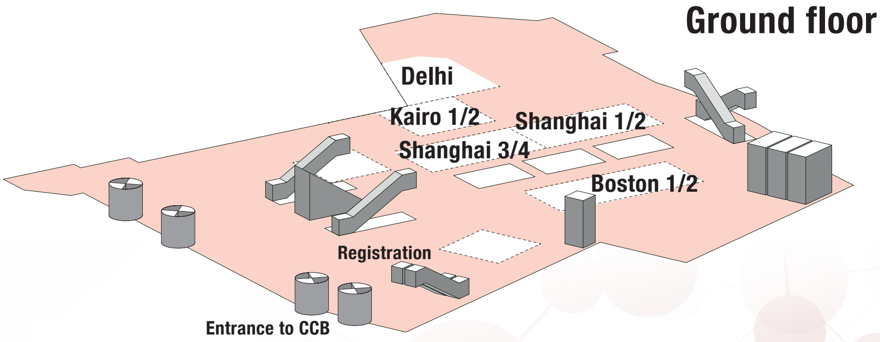
Congress Center Basel

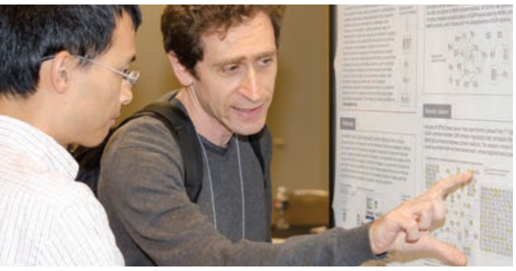
MCH MESSE BASEL, MESSEPLATZ 21, 4058 BASEL







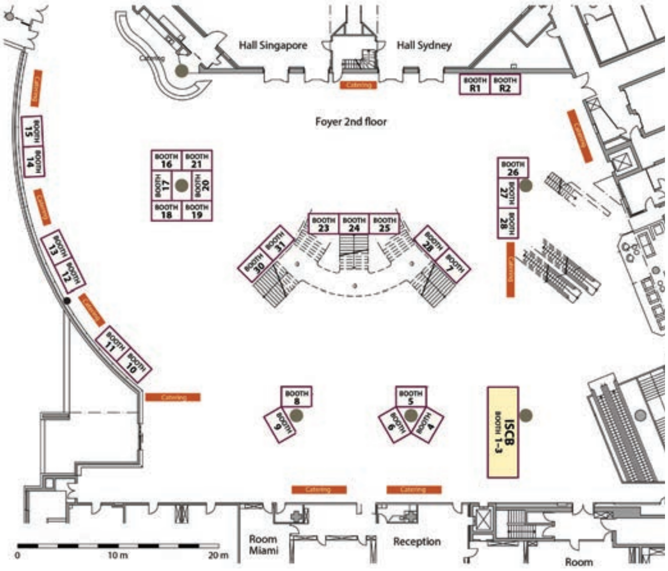





MIT
Structural finger
Protein doma
Pfam

Recruiters & Exhibitors

CONGRESS CENTER BASEL FOYER 2ND FLOOR



RECRUITERS

R1	St. Jude Children's Research Hospital
R2	Novo Nordisk A/S

EXHIBITORS

1/2	International Society for Computational Biology
3	ISCB Student Council
4	WEKA.IO
5	Overleaf
6	eLife
7	Public Library of Science (PLOS)
8	National Cancer Institute (NCI), Informatics Technology for Cancer Research (ITCR) Program
9	The MIT Press
10	Harvard Medical School Department of Biomedical Informatics
11	Cambridge University Press
12	The Hyve
13	BD2K CCC
14	Tech Data (Schweiz) GmbH
15	ACQUIFER
16	Genomics, Proteomics & Bioinformatics (GPB)
17	ECCB 2020
18	Jalview and the Dundee Resource for Sequence analysis and Structure Prediction
19	Springer Nature
20	Royal Society Publishing
21	F1000 Research
22	The European Bioinformatics Institute
23/24	ELIXIR
25	GOBLET
26	GeneXplain
27	Oxford University Press
28	BioLizard
30	IBM - Zurich Research Laboratory
31	SIB Swiss Institute of Bioinformatics

Distinguished Keynote Presentations

ROOM: SAN FRANCISCO (3RD FLOOR)

SUNDAY, JULY 21 • 6:30 PM – 7:30 PM

NIKOLAUS RAJEWSKY

Max-Delbrück-Centrum for Molecular Medicine in the Helmholtz Association, Berlin-Buch, Germany

Principles of gene regulation in space and time by single-cell analyses
Introduction by: Thomas Lengauer, ISCB President

MONDAY, JULY 22 • 8:30 AM – 9:30 AM

ISCB 2019 Innovator Award Keynote

WILLIAM STAFFORD NOBLE

Department of Genome Sciences; Department of Computer Science and Engineering, University of Washington, Seattle, United States

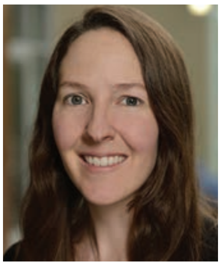
Traveling across spaces: The power of embedding genomic and proteomic data into a latent space
Introduction by: Ron Shamir, Chair, ISCB Awards Committee

TUESDAY, JULY 23 • 8:30 AM – 9:30 AM

ALEXIS BATTLE

Biomedical Engineering and Computer Science, John Hopkins University, Baltimore, United States

Modeling the complex impact of common and rare genetic variation on gene expression
Introduction by: Nicola Mulder, ISMB/ECCB 2019 Conference Co-chair



WEDNESDAY, JULY 24 • 8:30 AM – 9:30 AM

ISCB 2019 Overton Prize Keynote

CHRISTOPHE DESSIMOZ

SNSF Professor, University of Lausanne, Switzerland, Associate Professor, University College London, United Kingdom,
Group leader, SIB Swiss Institute of Bioinformatics, Switzerland

Challenges and rewards of benchmarking – how to cope with a biased, incomplete, or even entirely missing ground truth
Introduction by: Torsten Schwede, ISMB/ECCB 2019 Conference Co-chair

THURSDAY, JULY 25 • 5:00 PM – 6:00 PM

ISCB 2019 Accomplishments by a Senior Scientist Award Keynote

BONNIE BERGER

Simons Professor of Mathematics at MIT; Electrical Engineering and Computer Science,
Massachusetts Institute of Technology, Cambridge, United States

Biomedical Data Sharing and Analysis at Scale
Introduction by: Thomas Lengauer, ISCB President

Schedule-at-a-Glance • Sunday

CONGRESS CENTER BASEL

SUNDAY, JULY 21

ROOM	MONTREAL (2ND FLOOR)	SYDNEY (2ND FLOOR)	KAIRO 1/2 (GROUND FLOOR)	SHANGHAI 1/2 (GROUND FLOOR)	DELHI (GROUND FLOOR)
8:00 AM – 10:30 AM REGISTRATION: MORNING TUTORIALS AND STUDENT COUNCIL SYMPOSIUM ONLY					GROUND FLOOR
9:00 AM	TUTORIAL FD1: Interpretability for deep learning models in computational biology	TUTORIAL AM2: Recent Advances in Statistical Methods and Computational Algorithms for Single-Cell Omics Analysis	TUTORIAL AM3: Building a Distributed Knowledge Graph to Assist with Computational Drug Discovery	TUTORIAL AM4: A Practical Introduction to Reproducible Computational Workflows	Student Council Symposium
11:30 AM	COFFEE BREAK – TUTORIALS				
11:45 PM	TUTORIAL FD1: Interpretability for deep learning models in computational biology *continues*	TUTORIAL AM2 *continues*	TUTORIAL AM3: Building a Distributed Knowledge Graph to Assist with Computational Drug Discovery *continues*	TUTORIAL AM4: A Practical Introduction to Reproducible Computational Workflows *continues*	Student Council Symposium: *continues*
1:00 PM	LUNCH BREAK – TUTORIALS				
1:30 PM – 2:15 PM REGISTRATION: AFTERNOON TUTORIALS ONLY					GROUND FLOOR
2:00 PM	TUTORIAL FD1: Interpretability for deep learning models in computational biology *continues*	TUTORIAL PM6: Visualization of Large Biological Data	TUTORIAL PM5: Biomarker discovery and machine learning in large pharmacogenomics datasets	TUTORIAL PM7 Tools for reproducible research	Student Council Symposium: *continues*
3:00 PM – 7:00 PM CONFERENCE REGISTRATION					GROUND FLOOR
4:00 PM	COFFEE BREAK – TUTORIALS				
4:15 PM	TUTORIAL FD1: Interpretability for deep learning models in computational biology *continues*	TUTORIAL PM6: Visualization of Large Biological Data *continues*	TUTORIAL PM5: Biomarker discovery and machine learning in large pharmacogenomics datasets *continues*	TUTORIAL PM7 Tools for reproducible research *continues*	Student Council Symposium: *continues*
6:00 PM	TUTORIALS AND STUDENT COUNCIL SYMPOSIUM END				
6:15 PM	**WELCOME AND OPENING KEYNOTE** *Principles of gene regulation in space and time by single-cell analyses* **Nikolaus Rajewsky,** *Max-Delbrück-Centrum for Molecular Medicine in the Helmholtz Association, Berlin-Buch, Germany*				ROOM: SAN FRANCISCO (3RD FLOOR)
7:30 PM	OPENING RECEPTION WITH EXHIBITORS				FOYER 2ND /3RD FLOOR

Schedule-at-a-Glance • Monday

CONGRESS CENTER BASEL

MONDAY, JULY 22

7:30 AM – 6:30 PM CONFERENCE REGISTRATION GROUND FLOOR

8:15 AM **MORNING WELCOME AND INTRODUCTION OF ISCB 2019 DISTINGUISHED FELLOWS** ROOM: SAN FRANCISCO (3RD FLOOR)

8:30 AM **ISCB INNOVATOR AWARD KEYNOTE** ROOM: SAN FRANCISCO (3RD FLOOR)

Traveling across spaces: the power of embedding genomic and proteomic data into a latent space
William Stafford Noble, *University of Washington, Seattle, United States*

9:30 AM COFFEE BREAK WITH EXHIBITORS 2ND FLOOR FOYER

ROOM	SAN FRANCISCO (3RD FLOOR)	DELHI (GROUND FLOOR)	SINGAPORE (2ND FLOOR)	OSAKA/SAMARKAND (3RD FLOOR)	BOSTON 1/2 (GROUND FLOOR)
10:15 AM	HiTSeq COSI	TransMed COSI	RegSys: Regulatory and Systems Genomics COSI	ELIXIR Special Track	BioVis COSI
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA				ROOM: HALL 4.1 (1ST FLOOR)
12:45 PM - 1:45 PM			ISCB Town Hall Meeting		
2:00 PM	HiTSeq COSI *continues*	TransMed COSI *continues*	RegSys COSI *continues*	ELIXIR Special Track *continues*	BioVis COSI *continues*
4:00 PM	COFFEE BREAK WITH EXHIBITORS				FOYER (2ND FLOOR)
4:40 PM	HiTSeq COSI *continues*	TransMed COSI *continues*	RegSys COSI *continues*	ELIXIR Special Track *continues*	BioVis COSI *continues*
6:00 PM – 8:00 PM	POSTER SESSION A				HALL 4.1 (1ST FLOOR)

MONDAY, JULY 22

	7:30 AM – 6:30 PM CONFERENCE REGISTRATION				GROUND FLOOR
8:15 AM	**MORNING WELCOME AND INTRODUCTION OF ISCB 2019 DISTINGUISHED FELLOWS**				ROOM: SAN FRANCISCO (3RD FLOOR)
8:30 AM	**ISCB INNOVATOR AWARD KEYNOTE** *Traveling across spaces: the power of embedding genomic and proteomic data into a latent space* **William Stafford Noble,** *University of Washington, Seattle, United States*				ROOM: SAN FRANCISCO (3RD FLOOR)
9:30 AM	COFFEE BREAK WITH EXHIBITORS				2ND FLOOR FOYER
ROOM	SHANGHAI 1/2 (GROUND FLOOR)	SHANGHAI 3/4 (GROUND FLOOR)	SYDNEY (2ND FLOOR)	MONTREAL (2ND FLOOR)	KAIRO 1/2 (GROUND FLOOR)
10:15 AM	BioInfo Core Workshop	Function COSI	3DSIG COSI	SysMod COSI	Special Session SST01: Text Mining for Biology and Healthcare
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA				ROOM: HALL 4.1 (1ST FLOOR)

		*continues*	*continues*	*continues*	Text Mining for Biology and Healthcare *continues*
4:00 PM	COFFEE BREAK WITH EXHIBITORS				2ND FLOOR FOYER
4:40 PM		Function COSI *continues*	3DSIG COSI *continues*	SysMod COSI *continues*	Special Session SST01: Text Mining for Biology and Healthcare *continues*
6:00 PM – 8:00 PM		POSTER SESSION A			HALL 4.1 (1ST FLOOR)

Schedule-at-a-Glance • Tuesday

CONGRESS CENTER BASEL

TUESDAY, JULY 23

7:30 AM – 6:30 PM CONFERENCE REGISTRATION — GROUND FLOOR

8:15 AM **MORNING WELCOME AND ISCB OUTSTANDING CONTRIBUTIONS AWARD PRESENTATION to Barb Bryant by Scott Markel, ISCB Executive Secretary** — ROOM: SAN FRANCISCO (3RD FLOOR)

8:30 AM *Keynote: Modeling the complex impact of common and rare genetic variation on gene expression*
Alexis Battle, *John Hopkins University, Baltimore, United States*

9:30 AM COFFEE BREAK WITH EXHIBITORS — FOYER 2ND FLOOR

ROOM	SAN FRANCISCO (3RD FLOOR)	DELHI (GROUND FLOOR)	SINGAPORE (2ND FLOOR)	OSAKA/SAMARKAND (3RD FLOOR)	BOSTON 1/2 (GROUND FLOOR)
10:15 AM	HiTSeq COSI	Microbiome COSI	RegSys COSI	BD2K CCC Special Track	EvolCompGen: Evolution & Comparative Genomics COSI
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA — ROOM: HALL 4.1 (1ST FLOOR)				
12:45 – 1:45 PM		12:50 PM – 1:50 PM CompBio Ignite — POSTER HALL (HALL 4.1, FIRST FLOOR)			BoF: The ISCB code of conduct, *Organizers: Lucia Peixoto and Casey Greene*
2:00 PM	HiTSeq COSI *continues*	Microbiome COSI *continues*	RegSys COSI *continues*	BD2K CCC Special Track *continues*	EvolCompGen COSI *continues*
4:00 PM	COFFEE BREAK WITH EXHIBITORS — FOYER 2ND FLOOR				
4:40 PM	HiTSeq COSI *continues*	Microbiome COSI *continues*	RegSys COSI *continues*	BD2K CCC Special Track *continues*	EvolCompGen COSI *continues*
6:00 PM – 8:00 PM		POSTER SESSION A — HALL 4.1 (1ST FLOOR)			
8:00 PM – 11:00 PM		ISMB/ECCB 2019 Social Event (See page 61 for details) — BASEL MARKTHALLE			

TUESDAY, JULY 23

7:30 AM – 6:30 PM CONFERENCE REGISTRATION GROUND FLOOR

8:15 AM **MORNING WELCOME AND ISCB OUTSTANDING CONTRIBUTIONS AWARD PRESENTATION to Barb Bryant by Scott Markel, ISCB Executive Secretary** ROOM: SAN FRANCISCO (3RD FLOOR)

8:30 AM *Keynote: Modeling the complex impact of common and rare genetic variation on gene expression*
Alexis Battle, *John Hopkins University, Baltimore, United States*

9:30 AM COFFEE BREAK WITH EXHIBITORS FOYER 2ND FLOOR

ROOM	SHANGHAI 1/2 (GROUND FLOOR)	SHANGHAI 3/4 (GROUND FLOOR)	SYDNEY (2ND FLOOR)	MONTREAL (2ND FLOOR)	KAIRO 1/2 (GROUND FLOOR)
10:15 AM	Bio-ontologies COSI	CompMS COSI	3DSIG COSI	NetBio COSI	**TECHN TRACK TALKS**
10:20 AM					EMBL-EBI Tools as a Service, *Fabio Madeira*
10:40 AM					EBI Search API – Looking for more, *Young mi Park*
11:00 AM					RNAcentral: a hub of information for non-coding RNA sequences, *Blake Sweeney*
11:20 AM					Protein services, tools and visual components enabling integration and interpretation of the UniProt Knowledgebase (UniProtKB), *Andrew Nightingale*
11:40 AM					IT Infrastructure for AI and Analytics in medicine and research, *Ulrich Walter*
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA 				ROOM: HALL 4.1 (1ST FLOOR)
2:00 PM	Bio-ontologies COSI *continues*	CompMS COSI *continues*	3DSIG COSI *continues*	NetBio COSI *continues*	**TECH TRACK TALKS** Storage Systems that Support Tomorrow's Life Science Applications Today, *David Hiatt*
2:20 PM					The CPTAC Data Browser: A New Generation of Data Visualization Tools from the Clinical Proteomic Tumor Analysis Consortium, *Anna Calinawan*
2:40 PM					BioThings API: Promoting Best-practices via a Biomedical API Development Ecosystem, *Chunlei Wu*
3:00 PM					Big Data Meets Drug Target Discovery, *Robert Gentleman*
4:00 PM	COFFEE BREAK WITH EXHIBITORS				FOYER 2ND FLOOR
4:40 PM	Bio-ontologies COSI *continues*	CompMS COSI *continues*	3DSIG COSI *continues*	NetBio COSI *continues*	TECHNOLOGY TRACK TALKS Towards a production-ready solution for reproducible articles, *Emmy Tsang*
6:00 PM – 8:00 PM	POSTER SESSION A				HALL 4.1 (1ST FLOOR)
8:00 PM – 11:00 PM	ISMB/ECCB 2019 Social Event (See page 61 for details)				BASEL MARKTHALLE

Schedule-at-a-Glance • Wednesday

CONGRESS CENTER BASEL

*schedule as of July 3 and subject to change

WEDNESDAY, JULY 24

7:30 AM – 6:30 PM CONFERENCE REGISTRATION GROUND FLOOR

8:15 AM **MORNING WELCOME AND CONFERENCE UPDATES** ROOM: SAN FRANCISCO (3RD FLOOR)

8:30 AM **ISCB OVERTON PRIZE AWARD KEYNOTE** ROOM: SAN FRANCISCO (3RD FLOOR)

Challenges and rewards of benchmarking – how to cope with a biased, incomplete, or even entirely missing ground truth
Christophe Dessimoz, *University of Lausanne, Switzerland*

9:30 AM COFFEE BREAK WITH EXHIBITORS FOYER 2ND FLOOR

ROOM	SAN FRANCISCO (3RD FLOOR)	DELHI (GROUND FLOOR)	SINGAPORE (2ND FLOOR)	OSAKA/SAMARKAND (3RD FLOOR)	BOSTON 1/2 (GROUND FLOOR)
10:15 AM	MLCSB - Machine Learning in Computational and Systems Biology COSI	OBF: BOSC COSI	RNA COSI	Education COSI	CAMDA COSI
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA ROOM: HALL 4.1 (1ST FLOOR)				
12:45 PM – 1:45 PM BIRDS OF A FEATHER		BoF: Welcome to BOSC (the Bioinformatics Open Source Conference), *Organizer: Monica Munoz-Torres*		BoF: Bioinformaticians in Aging & Senescence Research, *Organizer: Georg Fuellen*	BoF: Actionable ways to increase diversity in our community: Next steps for ISCB EDI TaskForce, *Organizer: Malvika Sharan*
2:00 PM	MLCSB COSI *continues*	OBF: BOSC COSI *continues*	RNA COSI *continues*	Education COSI *continues*	CAMDA COSI *continues*
4:00 PM	COFFEE BREAK WITH EXHIBITORS FOYER 2ND FLOOR				
4:40 PM	MLCSB COSI *continues*	OBF: BOSC COSI *continues*	RNA COSI *continues*	Education COSI *continues*	CAMDA COSI *continues*
6:00 PM – 8:00 PM		POSTER SESSION B HALL 4.1 (1ST FLOOR)			
8:00 PM –10:00 PM			RNA COSI DINNER (TICKETED EVENT)		CAMDA COSI DINNER (TICKETED EVENT)

WEDNESDAY, JULY 24

	7:30 AM – 6:30 PM CONFERENCE REGISTRATION	GROUND FLOOR
8:15 AM	**MORNING WELCOME AND CONFERENCE UPDATES**	ROOM: SAN FRANCISCO (3RD FLOOR)
8:30 AM	**ISCB OVERTON PRIZE AWARD KEYNOTE** *Challenges and rewards of benchmarking – how to cope with a biased, incomplete, or even entirely missing ground truth* **Christophe Dessimoz,** *University of Lausanne, Switzerland*	ROOM: SAN FRANCISCO (3RD FLOOR)
9:30 AM	COFFEE BREAK WITH EXHIBITORS	FOYER 2ND FLOOR

ROOM	SHANGHAI 1/2 (GROUND FLOOR)	SHANGHAI 3/4 (GROUND FLOOR)	SYDNEY (2ND FLOOR)	MONTREAL (2ND FLOOR)	KAIRO 1/2 (GROUND FLOOR)
10:15 AM	Bio-ontologies COSI	Special Session SST02: Scalable Plant-Research in Cloud Environments	General Computational Biology Talks	VarI: Variant Interpretation COSI	**TECHNOLOGY TRACK TALKS**
10:20 AM					PDFigCapX and FigSplit — a Pipeline for Extracting Figures, SubFigures and Captions from Biomedical Publications: Supporting Bio-Curation and Discovery, *Pengyuan Li*
10:40 AM					Phyre, PhyreRisk and Missense3D: Modelling protein structure and the impact of missense variants, *Michael Sternberg*
11:00 AM					Isabl — An open-source patient-centric framework for scalable bioinformatics operations, *Juan S Medina*
11:20 AM					MISO LIMS: managing information for sequencing operations, *Morgan Taschuk*
11:40 AM					Bioinformatics and Exploratory Data Analysis in Pharmaceutical Industry. Applications to drug research and development, *Fabian Birzele, Daniel Marbach, Jitao David Zhang*
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA				ROOM: HALL 4.1 (1ST FLOOR)
12:45 PM – 1:45 PM	BoF: Dos and Don'ts' checklist for computational training, *Organizer: Sara El-Gebali*	BoF: Integrative queryable genomics with InterMine, *Organizer: Yo Yehudi*	12:50 PM – 1:50 PM CompBio Ignite POSTER HALL (HALL 4.1, FIRST FLOOR)		BoF: Portable data analysis workflows with the CWL standards, *Organizer: Michael R. Crusoe, ELIXIR-NL & ELIXIR Interoperability Platform*
2:00 PM	Special Session SST03: Social media mining for drug discovery research: challenges and opportunities of Real World Text	Special Session SST02: Scalable Plant-Research in Cloud Environments *continues*	General Computational Biology Talks *continues*	VarI COSI *continues*	**TECHNOLOGY TRACK**
2:00 PM					The geneXplain platform for bioinformatic and systems biology analysis, *Philip Stegmaier*
3:00 PM					Fairspace, *Kees van Bochove*
4:00 PM	COFFEE BREAK WITH EXHIBITORS				FOYER 2ND FLOOR
4:40 PM	Special Session SST03: Social media mining for drug discovery research: challenges and opportunities of Real World Text *continues*	Special Session SST02: Scalable Plant-Research in Cloud Environments *continues*	General Computational Biology Talks *continues*	VarI COSI *continues*	**TECHNOLOGY TRACK**
					SWISS-MODEL: homology modelling of protein structures and complexes, *Gerardo Tauriello*
5:00 PM					GeneWeaver.org: A RESTful service for multi-species data integration in functional genomics, *Erich Baker*
5:30 PM					CATH: tools and datasets to analyse protein structure, *sequence and function, Ian Sillitoe*
6:00 PM – 8:00 PM	POSTER SESSION B				HALL 4.1 (1ST FLOOR)

Schedule-at-a-Glance • Thursday

CONGRESS CENTER BASEL

THURSDAY, JULY 25

ROOM	SAN FRANCISCO (3RD FLOOR)	DELHI (GROUND FLOOR)	SINGAPORE (2ND FLOOR)	OSAKA / SAMARKAND (3RD FLOOR)	BOSTON 1/2 (GROUND FLOOR)	SHANGHAI 1/2 (GROUND FLOOR)	SHANGHAI 3/4 (GROUND FLOOR)
	7:30 AM – 12:00 PM CONFERENCE REGISTRATION						GROUND FLOOR
8:30 AM	MLCSB: Machine Learning in Computational and Systems Biology COSI	OBF: BOSC COSI	RNA COSI	Workshop on Education in Bioinformatics (WEB)	CAMDA COSI	Special Session SST04: Computational Oncology – Heterogeneity and Immune Defence	Special Session SST05: Omics Data Formats, *Compression and Storage: Present and Future*
9:40 AM	COFFEE BREAK WITH EXHIBITORS						FOYER 2ND FLOOR
10:15 AM	MLCSB COSI *continues*	OBF: BOSC COSI *continues*	RNA COSI *continues*	Workshop on Education in Bioinformatics (WEB)	CAMDA COSI *continues*	Special Session SST04: Computational Oncology – Heterogeneity and Immune Defence *continues*	Special Session SST05: Omics Data Formats, *Compression and Storage: Present and Future continues*
12:40 PM	LUNCH (AVAILABLE FOR PURCHASE) IN POSTER AREA ISCB CAREER FAIR – EXHIBITION AREA						ROOM: HALL 4.1 (1ST FLOOR) 2ND FLOOR FOYER
12:45 – 1:45 PM		BoF: Open Bioinformatics Foundation Board Meeting, *Organizer: Heather Wiencko,*					BoF: Cytoscape Roadmap and Feedback, *Organizer: Scooter Morris*
2:00PM	MLCSB COSI *continues*	OBF: BOSC COSI *continues*	RNA COSI *continues*	Special Session SST06: CAID: The Critical Assessment of Intrinsic protein Disorder	CAMDA COSI *continues*	Special Session SST07: Reproducibility of findings from big data: From vision to reality	Special Session SST05: Omics Data Formats, *Compression and Storage: Present and Future continues*
4:40 PM	GRAB AND GO REFRESHMENT BREAK						FOYER 2ND FLOOR
5:00 PM	**ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD KEYNOTE** *Biomedical Data Sharing and Analysis at Scale* **Bonnie Berger,** *Massachusetts Institute of Technology, United States*						ROOM: SAN FRANCISCO (3RD FLOOR)
6:00 PM	**AWARDS PRESENTATIONS**						ROOM: SAN FRANCISCO (3RD FLOOR)

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MONDAY, JULY 22, 10:15 AM – 6:00 PM

ROOM: KAIRO 1/2 (GROUND FLOOR)

SST01: Text Mining for Biology and Healthcare

WEBSITE: HTTP://COSI.ISCB.ORG/WIKI/TEXTMINING:HOME

Organizers: Robert Leaman, ***National Library of Medicine, National Center for Biotechnology Information, United States***
Lars Juhl Jensen, ***University of Copenhagen, Novo Nordisk Foundation Center for Protein Research, Denmark***
Cecilia Arighi, ***University of Delaware, Computer and Information Sciences Department, United States***
Zhiyong Lu, ***National Library of Medicine, National Center for Biotechnology Information, United States***

10:15 AM **Welcome**

10:20 AM **MORNING KEYNOTE: Sophia Ananiadou,** *University of Manchester, United Kingdom*

11:00 AM **Ruth Dannenfelser,** *Princeton University, United States*
Tissue-aware framework for unraveling rare and complex diseases using biomedical literature

11:20 AM **Minh Pham,** *Baylor College of Medicine, United States*
Discovery of disease- and drug-specific pathways through community structures of a literature network

11:40 AM **Jennifer R. Smith,** *Rat Genome Database, Medical College of Wisconsin, United States*
OntoMate: a text-mining tool to facilitate curation at the Rat Genome Database

11:50 AM **Peipei Ping,** *BD2K Center of Excellence @ UCLA, United States*
Cloud-based Phrase Mining Reveals Critical Molecular Insights of Major Cardiovascular Diseases

12:00 PM **Wei Wang,** *University of California, Los Angeles, United States*
Learning Structured Knowledge from Clinical Case Reports

12:20 PM **Debarati Roychowdhury,** *University of Delaware, United States*
A text-mined integrated knowledge map for MicroRNAs

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **KEYNOTE: Larry Hunter,** *University of Colorado School of Medicine, United States*

2:40 PM **Gonzalez-Hernandez Graciela,** *University of Pennsylvania, United States*
Deep Neural Networks Ensemble for Detecting Medication Mentions in Tweets

3:00 PM **Jiawei Han,** *BD2K Center of Excellence @ UIUC, United States*
ClaimMiner: Query-guided Claim Mining in Biomedical Literature

3:20 PM **Shanfeng Zhu,** *Fudan University, China*
FullMeSH: Improving Large-Scale MeSH Indexing with Full Text

3:30 PM **Xiangying Jiang,** *University of Delaware, United States*
An Effective Biomedical Document Classification Scheme in Support of Biocuration: Addressing Class Imbalance

3:40 PM **Aravind Venkatesan,** *EMBL-EBI, United Kingdom*
Using the power of text-mining for biological discovery with Europe PMC Annotations platform

3:50 PM **Raul Rodriguez-Esteban,** *Roche, Switzerland*
A new approach and gold standard toward author disambiguation in MEDLINE

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Poster lightning talks**

5:00 PM **Graciela Gonzalez-Hernandez,** *University of Pennsylvania, United States*
Martin Krallinger, *CNIO – Spanish National Cancer Research Centre, Spain*
Hongfang Liu, *Mayo Clinic, United States*
Raul Rodriguez-Esteban, *Roche, Switzerland*
PANEL DISCUSSION: New challenges and opportunities in biomedical text mining and beyond

Special Sessions

MONDAY, JULY 22 • WEDNESDAY, JULY 24 • THURSDAY, JULY 25

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WEDNESDAY, JULY 24 • 10:15 AM – 6:00 PM

ROOM: SHANGHAI 3/4 (GROUND FLOOR)

SST02: Scalable Plant-Research in Cloud Environments

Organizer: **Frederik Coppens, *VIB, Belgium***

10:30 AM **Frederik Coppens,** *VIB, Belgium*
Introduction to the ELIXIR plant community

11:00 AM **Cyril Pommier,** *INRA, France*
Plant Phenotyping infrastructure: Breeding API & MIAPPE

11:30 AM **Erin Haskell,** *EMBL-EBI, United Kingdom*
(Plant) Data Resources at Ensembl

12:00 PM **Alexander Kanitz,** *University of Basel, Switzerland*
ELIXIR Cloud Computing and Authentication

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Jason Williams,** *CyVerse, United States*
Overview of CyVerse tools and services: Introduction to data/metadata management and sharing with CyVerse

2:30 PM **Anika Erxleben,** *University of Freiburg, Germany*
Introduction to Galaxy and the European Galaxy community

3:00 PM **Kristian Peters,** *Leibniz Institute of Plant Biochemistry, Germany*
A PhenoMeNal Workflow to Study the Metabolites Variation in Bryophytes across Seasons

3:30 PM **Helena Rasche,** *University of Freiburg, Germany*
Apollo and Galaxy: Scaling Genome Annotation for the Masses

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:30 **Hervé Ménager,** *Institut Pasteur, Paris, France*
Overview of tools and container infrastructure

5:00 **Björn Grüning,** *University of Freiburg, Germany*
FAIRly maintain and publish research data with e!DAL (electronic Data Archive Library)

WEDNESDAY, JULY 24 • 2:00 PM – 6:00 PM

ROOM: SHANGHAI 1/2 (GROUND FLOOR)

SST03: Social media mining for drug discovery research: challenges and opportunities of Real World Text

Organizers: **Raul Rodriguez-Esteban, *Roche, Switzerland***
Mathias Leddin, *Roche, Switzerland*
Juergen Gottowik, *Roche, Switzerland*

2:00 PM **Graciela Gonzalez-Hernandez,** *University of Pennsylvania, United States*
Myths and Misconceptions: Social Media Mining for Health Research

3:00 PM **Nigel Collier,** *University of Cambridge, United Kingdom*
Pushing natural language processing and social media: towards automated understanding of layman's language

3:20 PM **Elena Tutubalina,** *Kazan University, Russia*
Towards the Semantic Interpretation of User-Generated Texts about Drug Therapy

3:40 PM **Fabio Rinaldi,** *University of Zurich, Switzerland*
Tilia Ellendorff, *University of Zurich, Switzerland*
Literature and Social Media Mining in OntoGene

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Albert Weichselbraun,** *University of Applied Sciences Chur, Switzerland*
Capturing, analyzing and visualizing user generated content from social media

5:00 PM **Tom Willgoss,** *Roche, United Kingdom*
Unlocking the value of social media data to identify patient-relevant measurement concepts for clinical trials

5:20 PM **Florian Gutzwiller,** *Novartis, Switzerland*
Generating patient insights in chronic obstructive pulmonary disease (COPD) with social media listening study

5:40 PM **Ben Collins,** *Boehringer Ingelheim, Germany*
Understanding patient-perceived symptoms in a rare disease using semantic analysis

Special Sessions

MONDAY, JULY 22 • WEDNESDAY, JULY 24 • THURSDAY, JULY 25

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THURSDAY, JULY 25 • 8:30 AM – 12:40 PM

ROOM: SHANGHAI 1/2 (GROUND FLOOR)

SST04: Computational Oncology – Heterogeneity and Immune Defence

Organizers: Niko Beerenwinkel, ***ETH Zurich, Switzerland***
Francesca D. Ciccarelli, ***King's College London, United Kingdom***
Jens Lagergren, ***Royal Institute of Technology & SciLifeLab, Sweden***

8:30 AM **Maria Secrier,** *University College London, United Kingdom*
Reconstructing the mutational histories and cellular context of oesophageal cancer development

9:15 AM **Valentina Boeva,** *ETH Zurich, Switzerland*
Deciphering intra-tumor heterogeneity and cell plasticity in neuroblastoma

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

10:15 AM **Nicholas McGranahan,** *University College London, United Kingdom*
Cancer Evolution and Mechanisms of Immune Escape

11:00 AM **Gryte Satas,** *Princeton University, United States*
Single-cell tumor phylogeny inference with supported mutation losses

11:25 AM **Giovanni Ciriello,** *University of Lausanne (UNIL), Swizterland*
Cancer evolutionary templates: from statistical to functional relevance

12:00 PM **Mireia Crispin Ortuzar,** *Univeristy of Cambridge, United Kingdom*
Unraveling cancer heterogeneity using multi-scale data integration

12:20 PM **Matteo Cereda,** *Italian Institute for Genomic Medicine, Italy*
Discretization of transcriptional heterogeneity unravel the altered biological processes in cancer

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

THURSDAY, JULY 25 • 8:30 AM – 4:40 PM

ROOM: SHANGHAI 3/4 (GROUND FLOOR)

SST05: Omics Data Formats, Compression and Storage: Present and Future

Organizers: Mikel Hernaez, ***University of Illinois at Urbana-Champaign, United States***
James Bonfield, ***Wellcome Sanger Institute, United Kingdom***

Part 1: New technologies on Variant Calling Files

8:30 AM **Bonnie Berger,** *Massachusetts Institute of Technology, United States*

9:00 AM **Marcus Klarqvist,** *University of Cambridge, United Kingdom*

9:20 AM **Chris Vittal,** *Broad Institute of MIT and Harvard, United States*

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

Part 2: Compression of omics data

10:15 AM **Idoia Ochoa,** *University of Illinois at Urbana-Champaign, United States*

10:40 AM **Diogo Pratas,** *University of Aveiro, Portugal*

11:05 AM **Josh Moore,** *University of Dundee, United Kingdom*

11:30 AM **Shubham Chandak,** *Stanford University, United States*

11:55 AM **Anthony Cox,** *Illumina Inc., Cambridge, United Kingdom*

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

Part 3: Current and future trends in compressed formats for sequencing data

2:00 PM **Mikel Hernaez,** *University of Illinois at Urbana-Champaign, United States*
James Bonfield, *Wellcome Sanger Institute, United Kingdom*
Welcome remarks

2:10 PM **James Bonfield,** *Wellcome Sanger Institute, United Kingdom*
Updates on the CRAM format

2:40 PM **Mikel Hernaez,** *University of Illinois at Urbana-Champaign, United States*
Updates on the MPEG-G format

3:10 PM **Rishi Nag,** *European Bioinformatics Institute (EMBL-EBI), United Kingdom*
Updates on the ISO/GA4GH joint initiatives

Lightning talks and Panel: Patents, royalties and open source on future omics data formats

3:30 PM **Thomas Keane,** *EMBL-EBI, United Kingdom*
Jaime Delgado, *Polytechnic University of Catalonia, Spain*
Mark Effingham, *UK Biobank, United Kingdom*
Steven Hart, *Mayo Clinic, United States*
Rishi Nag, *EMBL-EBI, United Kingdom*

4:40 PM GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

Special Sessions

MONDAY, JULY 22 • WEDNESDAY, JULY 24 • THURSDAY, JULY 25

https://www.iscb.org/ismbeccb2019-program/special-sessions

THURSDAY, JULY 25 • 2:00 PM – 4:40 PM

ROOM: OSAKA / SAMARKAND (3RD FLOOR)

SST06: CAID: The Critical Assessment of Intrinsic protein Disorder

Organizers:
Silvio Tosatto, ***University of Padua, Italy***
Zsuzsanna Dosztanyi, ***Eötvös Loránd University, Hungary***
Norman Davey, ***University College Dublin, Ireland***
Damiano Piovesan, ***University of Padua, Italy***

2:00 PM **Silvio Tosatto,** *University of Padua, Italy*
CAID Introduction

2:10 PM **Damiano Piovesan,** *University of Padua, Italy*
Benchmarking dataset

2:30 PM **Marco Necci,** *University of Padua, Italy*
Assessment of disorder and binding regions

3:00 PM **Tom Liftin,** *Griffith University, Australia*
Spot Disorder 2

3:15 PM **Claudio Mirabello,** *Linköping University, Sweden*
RawMSA

3:30 PM **Gabriele Orlando,** *Katholieke Universiteit Leuven, Belgium*
DisoMine

3:45 PM **Zsuzsanna Dosztanyi,** *Eotvos Lorand University, Hungary*
ANCHOR 2

4:00 PM *Round table discussion*

4:40 PM GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

THURSDAY, JULY 25 • 2:00 PM – 4:40 PM

ROOM: SHANGHAI 1/2 (GROUND FLOOR)

SST07: Reproducibility of findings from big data. From vision to reality

Organizer:
Stéphanie Boué, ***Philip Morris Products S.A., Switzerland***

2:00 PM **William Hayes,** *BioDati, United States*
From literature to computable knowledge: BEL and BioDati

2:25 PM **Anze Zupanic,** *EAWAG, Switzerland*
Zebrafish: A model organism to model adverse outcome pathways

2:45 PM **Vincenzo Belcastro,** *PMI, Switzerland*
GladiaTOX: Developed by industry and packaged for the scientific community to analyze high content screening data

3:00 PM **Alex Sczyrba,** *Helmholtz Centre for Infection Research, Germany*
Methods benchmarking in metagenomics – CAMI & sbv IMPROVER challenges

3:20 PM **Stéphanie Boué,** *PMI, Switzerland*
INTERVALS – a platform for data transparency, a mine of data

3:35 PM **Sucheendra Kumar Palaniappan,** *SBX Corporation, Japan*
Towards creating an engine of scientific discovery

3:55 PM *Panel discussion – Transparency, crowdsourcing… stronger together*

4:40 PM GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

BIOINFO-CORE

COSI TRACK SCHEDULE

MONDAY, JULY 22 • ROOM: SHANGHAI 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/bioinfocore.php

10:15 AM **Welcome**

10:20 AM **Yang Fann,** *National Institute of Health, United States*
Transitioning bioinformatics core to support biomedical AI/ML research – lessons learned

10:30 AM **Shannan Ho Sui,** *Harvard School of Public Health, United States*
Supporting single cell RNA-seq analysis: A core's perspective

10:40 AM **Devon Ryan,** *Max Planck Institute of Immunobiology and Epigenetics (MPI-IE), Germany*
Conda and Bioconda, the best thing since sliced bread

10:50 AM **Sara Brin Rosenthal,** *University of California, San Diego, United States*
Improving project management and tracking with Asana and Toggl

11:00 AM **Radhika Khetani,** *Harvard School of Public Health, United States*
Bioinformatics training (in the context of a core)

11:10 AM **Alberto Riva,** *University of Florida, United States*
Development of bioinformatics workshop by a core facility

11:20 AM *Small Group Discussions*

11:55 AM *Small Group Reports*

12:20 PM **Harshil Patel,** *The Francis Crick Institute, United Kingdom*
nf-core — A community effort to collect a curated set of pipelines built using Nextflow

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

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COSI TRACK PRESENTATIONS

MONDAY, JULY 22 • ROOM: BOSTON 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/biovis.php

10:15 AM *BioVis General Opening*

10:20 AM **KEYNOTE: Lindsay Edwards,** *GSK, United Kingdom*
Visualisation as a partner to AI and machine learning in drug discovery

11:20 AM **Wouter Meuleman,** *Altius Institute for Biomedical Sciences, United States*
Epilogos: information-theoretic navigation of multi-tissue functional genomic annotations

11:40 AM **Xiao Wang,** *Technical University of Denmark*
GeneDMRs: an R package for Gene-based Differentially Methylated Regions analysis

11:50 AM **Joshua Orvis,** *University of Maryland School of Medicine - Institute for Genome Sciences, United States*
The gene Expression and Analysis Resource (gEAR) Portal

12:00 PM **Jayaram Kancherla,** *University of Maryland, United States*
Proactive Visual and Statistical Analysis of Genomic Data in Epiviz

12:10 PM **Zeynep H. Gümüş,** *Icahn School of Medicine at Mount Sinai, United States*
ImmuneRegulation: A web based tool for identifying human immune regulatory elements

12:20 PM *Poster lightning talks 1*

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **KEYNOTE: Petra Isenberg,** *INRIA, France*
Physical, Contextual, and Full of Value? What do novel directions in Visualization teach us about judging the value of visualization?

3:00 PM **Jaime Huerta-Cepas,** *Centro de Biotecnología y Genómica de Plantas, (CBGP UPM-INIA), Spain*
Combining programmatic visualization and interactive exploration of large phylogenetic trees using ETE toolkit

3:20 PM **Aditya Bharadwaj,** *Virginia Tech, United States*
Flud: a hybrid crowd-algorithm approach for visualizing biological networks

3:30 PM **Mathias Witte Paz,** *University of Tübingen, Center for Bioinformatics, Germany*
Evidente – A visual analytics tool for data enrichment in SNP-based phylogenetic trees

3:40 PM **John Alexis Guerra-Gomez,** *Northeastern University Silicon Valley, United States*
BioCicle: A Tool for Summarizing and Comparing Taxonomic Profiles out of Biological Sequence Alignments

3:50 PM **Tiago Lubiana,** *School of Pharmaceutical Sciences, University of São Paulo, Brazil*
PubScore: quantifying and visualizing the literature relevance of a gene set about any topic

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Mehmet Gönen,** *Koç University, Turkey*
Fast and curious: Efficient exploratory visualization of cross-domain interaction networks

5:00 PM **Ashwin Narayan,** *Massachusetts Institute of Technology, United States*
Density-Preserving Visualization of Single Cells

5:10 PM **Mehmet Volkan Atalay,** *Middle East Technical University, Turkey*
iBioProVis: Interactive Visualization and Analysis of Compound Bioactivity Space

5:20 PM *BioVis Challenges session @VIS*

5:30 PM *Poster lightning talks 2*

5:50 PM *BioVis@VIS and Closing Remarks*

6:00 PM *BioVis poster session*

Function SIG: Gene and Protein Function Annotation

COSI TRACK PRESENTATIONS

MONDAY, JULY 22 • ROOM: SHANGHAI 3/4 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/function.php

10:15 AM *Introduction*

10:20 AM **KEYNOTE: Lucy Colwell,** *Cambridge University and Google AI, United Kingdom*
Using evolutionary sequence variation to build predictive models of protein structure and function

11:00 AM **Lukasz Kurgan,** *Virginia Commonwealth University, United States*
PROCEEDINGS PRESENTATION: SCRIBER: accurate and partner type-specific prediction of protein-binding residues from proteins sequences

11:20 AM **Chelsea J.-T. Ju,** *University of California, Los Angeles, United States*
PROCEEDINGS PRESENTATION: Multifaceted Protein-Protein Interaction PredictionBased on Siamese Residual RCNN

11:40 AM **Aditya Pratapa,** *Virginia Tech, United States*
PROCEEDINGS PRESENTATION: Reconstructing Signaling Pathways Using Regular-Language Constrained Paths

12:00 PM **Riccardo Vicedomini,** *Sorbonne Univesité, France*
ProfileView: a pipeline based on multiple probabilistic models resolving the functional organization of the cryptochrome/photolyase protein family

12:20 PM **Martin Weigt,** *Sorbonne Université, France*
Towards evolution-guided protein design

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Megan Crow,** *Cold Spring Harbor Laboratory, United States*
Predictability of Human Differential Gene Expression

2:20 PM **Vladimir Gligorijević,** *Center for Computational Biology, Flatiron Institute, Simons Foundation, United States*
Geometric Deep Learning Methods for Large-Scale Structure-Based Protein Function Prediction

2:40 PM **Diego Zea,** *Sorbonne Université, France*
Deciphering Protein Functional Complexity With Alternative Splicing Evolution

3:00 PM **Vedrana Vidulin,** *Jožef Stefan Institute, Slovenia*
The evolutionary signal in metagenome phyletic profiles predicts many gene functions

3:20 PM **Meet Barot,** *New York University, United States*
Graph-Regularized Autoencoders for Protein Feature Learning

3:30 PM **Tair Shauli,** *The Hebrew University of Jerusalem, Israel*
Not all protein modification sites are created equal: Insights from a human-specific substitution matrix

3:40 PM **T. M. Murali,** *Virginia Tech, United States*
Data integration through heterogeneous ensembles

3:50 PM **Iddo Friedberg,** *Iowa State University, United States*
Updates on the Critical Assessment of Function Annotation Challenge Series

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Stavros Makrodimitris,** *Delft University of Technology, The Netherlands*
Metric Learning on Expression Data for Gene Function Prediction

5:00 PM **Castrense Savojardo,** *Biocomputing Group, University of Bologna, Italy*
BUSCA for the annotation of protein subcellular localization

5:20 PM **Olivier Lichtarge,** *Baylor College of Medicine, United States*
An Evolutionary Calculus for Identifying Genes under Selection in Mutational Landscapes

5:40 PM **Julien Roux,** *University of Basel, Switzerland*
Choosing the best annotation for functional enrichment testing

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

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HTTPS://WWW.ISCB.ORG/AFFILIATED-GROUPS

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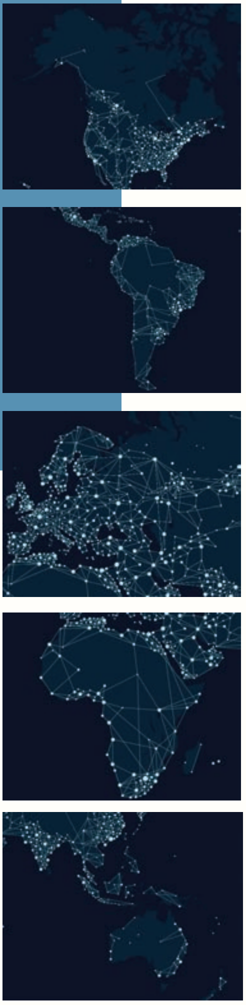

AFRICAN SOCIETY FOR BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (ASBCB)

ASIA PACIFIC BIOINFORMATICS NETWORK (APBIONET)

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VANCOUVER BIOINFORMATICS USER GROUP (VANBUG)

SysMod: Computational Modeling of Biological Systems

COSI TRACK PRESENTATIONS

MONDAY, JULY 22 • ROOM: MONTREAL (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/sysmod.php

10:15 AM **Andreas Dräger,** *University of Tübingen, Germany*
Introduction to SysMod 2019

10:20 AM **Douglas Lauffenburger,** *Massachusetts Institute of Technology, United States*
Cross-Species Translation of Biological Information via Statistical and Machine Learning Computational Frameworks

11:00 AM **Jonas Béal,** *Institut Curie, France*
Personalization of logical models using multi-omics data and its use in the study of clinical stratification and drug response

11:20 AM **Fabian Fröhlich,** *Harvard University, United States*
Making Sense of Large Kinetic Models

11:40 AM **Davide Maspero,** *Biotechnology and Biosciences, University Milano-Bicocca, Italy*
Constraint-based modeling of human single cells to investigate metabolic heterogeneity in cancer subpopulations

12:00 PM **Gregory Smith,** *Icahn School of Medicine at Mount Sinai Hospital, United States*
Modeling the propagation of the innate immune response to control influenza virus infection

12:20 PM **Beatriz García-Jiménez,** *Universidad Politecnica de Madrid, Spain*
Modeling recovery of Crohn’s disease, by simulating microbial community dynamics under perturbations

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12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Edda Klipp,** *Humboldt-Universität zu Berlin, Germany*
Systematic integration of models and data for yeast growth, division and stress response

2:40 PM **Martin Hoffmann,** *Fraunhofer ITEM, Division of Personalized Tumor Therapy, Germany*
Stochastic system identification without an a priori *chosen kinetic model — exploring feasible cell regulation with piecewise linear functions*

3:00 PM **Rodrigo Santibáñez,** *Universidad Mayor, Chile*
Pleiades Toolkit: Automatic rule-based modeling of bacterial gene regulation enables simulation, prediction, and perturbation of gene responses

3:20 PM **Marco Pagni,** *SIB Swiss Institute of Bioinformatics, Switzerland*
Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis

3:40 PM **Florian Centler,** *Helmholtz Centre for Environmental Research - UFZ, Germany*
µbialSim: Simulating complex microbial communities at their natural diversity

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Philip Pearce,** *Massachusetts Institute of Technology, United States*
Learning dynamical information from static protein and sequencing data

5:00 PM **Paulo Eduardo Pinto Burke,** *University of São Paulo, Brazil*
Towards Homogeneous Modeling and Simulation of Whole-Cells

5:05 PM **Christoph Leberecht,** *Hochschule Mittweida, Germany*
The regulation of aquaporin 2 vesicle transport by localized cyclic AMP pools.

5:10 PM **Eugenio Azpeitia,** *University of Zurich, Switzerland*
Optimal information acquisition of the molecular systems in living organisms require a non-minimal level of noise

5:15 PM **Cristina Santini,** *Celgene, Spain*
An in silico mechanistic representation of an in vitro *neutropenia assay to explore dose and schedules*

5:20 PM **Jörg Stelling,** *ETH Zürich, and SIB Swiss Institute of Bioinformatics, Switzerland*
Systems Analysis of Cell-to-Cell Variability

6:00 PM **Claudine Chaouiya,** *Instituto Gulbenkian de Ciência, Portugal; Aix Marseille University, CNRS, France*
Closing remarks and poster award of SysMod 2019

TransMed: Translational Medical Informatics

COSI TRACK PRESENTATIONS

MONDAY, JULY 22 • ROOM: DELHI (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/transmed.php

10:15 AM	*Welcome from the committee*
10:20 AM	**Isaac Kohane,** *Harvard University, United States* *Five ways computational biologists can accelerate medicine*
11:10 AM	**Francesco Iorio,** *Wellcome Sanger Institute, United Kingdom* *Prioritising cancer therapeutic targets through CRISPR-Cas9 screens and multi-omics data integration*
11:20 AM	**Michio Iwata,** *Kyushu Institute of Technology, Japan* *PROCEEDINGS PRESENTATION: Predicting drug-induced transcriptome responses of a wide range of human cell lines by a novel tensor-train decomposition algorithm*
11:40 AM	**Sumit Mukherjee,** *Sage Bionetworks, United States* *PROCEEDINGS PRESENTATION: Identifying and ranking potential driver genes of Alzheimer's Disease using multi-view evidence aggregation*
12:00 PM	**Mengyun Yang,** *Central South University, China* *PROCEEDINGS PRESENTATION: Drug repositioning based on bounded nuclear norm regularization*
12:20 PM	**Caroline Labelle,** *University of Montreal, Canada* *PROCEEDINGS PRESENTATION: Enhancing the Drug Discovery Process: Bayesian Inference for the Analysis and Comparison of Dose-Response Experiments*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**KEYNOTE: Burkhard Rost,** *Technical University of Munich, Germany* *SNAP variation between people + Deep Learning – lessons for protein structure prediction*
2:40 PM	**Antti Honkela,** *University of Helsinki, Finland* *PROCEEDINGS PRESENTATION: Representation Transfer for Differentially Private Drug Sensitivity Prediction*
3:00 PM	**Olivier Gevaert,** *Stanford University, United States* *PROCEEDINGS PRESENTATION: Deep Learning with Multimodal Representation for Pancancer Prognosis Prediction*
3:20 PM	**Vg Saipradeep,** *TCS Research, India* *Rare Disease Gene Prioritization Using MEDLINE Derived Association Network*
3:30 PM	**Arvind Singh Mer,** *University of Toronto, Canada* *Identifying Biomarkers for Precision Cancer Medicine using Patient-Derived Xenografts*
3:40 PM	**Joo Sang Lee,** *NCI/NIH, United States* *Harnessing genetic interactions to advance precision cancer medicine*
3:50 PM	**Benedict Anchang,** *Stanford University, United States* *Combining Machine Learning with Single-cell Analysis for Individualized Precision Medicine*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Bissan Al-Lazikani,** *The Institute of Cancer Research, United Kingdom* *Harnessing Big, Multidisciplinary Data to Inform Cancer Medicine*
5:10 PM	**Martin Hoffmann,** *Fraunhofer Institute for Toxicology and Experimental Medicine, Germany* *Genetic alterations driving metastatic colony formation are acquired outside of the primary tumour in melanoma*
5:20 PM	**Handan Melike Donertas,** *EMBL-EBI, United Kingdom* *Using genetic similarities among ageing-related diseases to understand and intervene ageing*
5:30 PM	**Johann de Jong,** *UCB Biosciences, Germany* *Clustering multivariate longitudinal clinical patient data using variational deep embedding with recurrence*
5:40 PM	**Kees van Bochove,** *The Hyve, The Netherlands* *From question to publication in five days – How OHDSI is changing medical evidence generation through open science*
5:50 PM	**Dominic Clark,** *Pistoia Alliance, Inc., United Kingdom* *CDx/NGS & Regulation: 5 perspectives from the Pistoia Alliance*
6:00 PM	*Closing Remarks*

3DSIG: Structural Bioinformatics & Computational Biophysics

COSI TRACK SCHEDULE

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SYDNEY (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/3dsig.php

MONDAY, JULY 22

10:15 AM **3DSiG KEYNOTE: Torsten Schwede,** *SIB Swiss Institute of Bioinformatics & University of Basel, Switzerland*
Lessons learned from twenty-five years of automated protein structure modelling with SWISS-MODEL

11:00 AM **Anne Lopes,** *Université Paris-Sud, France*
The interaction propensity of protein surfaces is shaped by functional but also non-functional partners

11:20 AM **Emine Sıla Özdemir,** *Koç University (Current Affiliation: OHSU, CEDAR), Turkey*
Unraveling the molecular mechanism of interactions of the Rho GTPases Cdc42 and Rac1 with the scaffolding protein IQGAP2

11:40 AM **Jan Kosinski,** *European Molecular Biology Laboratory, Germany*
An automated pipeline for integrative structural modelling of molecular complexes

12:00 PM **Yang Shen,** *Texas A&M University, United States*
Bayesian active learning for optimization and uncertainty quantification in protein docking

12:20 PM **Simon Kelow,** *University of Pennsylvania, United States*
A New Antibody CDR Structural Database

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Fergus Imrie,** *University of Oxford, United Kingdom*
Deep generative models for 3D compound design from fragment screens

2:20 PM **Mohammad Elgamacy,** *Friedrich Miescher Laboratory of The Max Planck Society, Germany*
De novo protein design of potent hematopoietic agents

2:40 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 (III)

3:00 PM **Ravi Abrol,** *California State University Northridge, United States*
Chiral Graphs as Reduced Representations of Ligand Scaffolds for Stereoselective Drug Discovery and Enhanced Exploration of Chemical Scaffolds Space

3:20 PM **Susan Leung,** *University of Oxford, United Kingdom*
SuCOS: a pharmacophoric-shape overlap metric for comparing binding modes

3:40 PM **Melissa F. Adasme,** *Biotechnology Center TU Dresden, Germany*
Structure-based drug repositioning uncovers a well-known cancer drug as B-cells inactivator

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Philip Kim,** *University of Toronto, Canada*
Method to generate highly stable D-amino acid analogs of bioactive helical peptides using a mirror image of the entire PDB

5:00 PM **Fergus Boyles,** *University of Oxford, United Kingdom*
Improving Scoring Functions for Protein-Ligand Binding Affinity Using Small Molecule Descriptors

5:20 PM **Avner Schlessinger,** *Icahn School of Medicine, United States*
Strategies to design conformation-specific kinase inhibitors

5:40 PM **Jiansheng Wu,** *Nanjing University of Posts and Telecommunications, China*
PROCEEDINGS PRESENTATION: Precise Modelling and Interpretation of Bioactivities of Ligands Targeting G Protein-coupled Receptors

3DSIG: Structural Bioinformatics & Computational Biophysics

COSI TRACK SCHEDULE

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SYDNEY (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/3dsig.php

TUESDAY, JULY 23

10:15 AM	**Jinbo Xu,** *Toyota Technological Institute at Chicago, United States* *Progress on protein structure prediction by deep learning*
11:00 AM	**Joe Greener,** *University College London, United Kingdom* *DMPfold: fast de novo protein modelling using iterative deep learning-based prediction of structural constraints*
11:20 AM	**Badri Adhikari,** *University of Missouri – St. Louis, United States* *DEEPCON: Protein Contact Prediction using Dilated Convolutional Neural Networks with Dropout*
11:40 AM	**Juergen Haas,** *SIB Swiss Institute of Bioinformatics, & University of Basel, Switzerland* *Supporting Structure Prediction Method Development with Continuous Automated Model EvaluatiOn (CAMEO)*
12:00 PM	**Clare E. West,** *University of Oxford, United Kingdom* *RFQAmodel: Random Forest Quality Assessment to identify a predicted protein structure in the correct fold*
12:20 PM	**William McLaughlin,** *Geisinger Commonwealth School of Medicine, United States* *ResiRole: Residue-Level Functional Site Predictions to Gauge the Average Accuracies of Protein Structure Prediction Techniques*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Rafael Najmanovich,** *Sherbrooke University, Canada* *Beyond ISMB: 3DSIG (and other COSIs)@Home*
2:40 PM	**Jaume Bonet,** *École Polytechnique Fédérale de Lausanne, Switzerland* *TopoBuilder: Expanding and Functionalizing the Protein Fold Space*
3:00 PM	**Jörn Schmiedel,** *Centre for Genomic Regulation (CRG), Spain* *Determining protein structures using deep mutational scanning*
3:20 PM	**Pablo Gainza,** *Ecole Polytechnique Federale de Lausanne and SIB Swiss Institute of Bioinformatics, Switzerland* *Deciphering interaction fingerprints from protein molecular surfaces*
3:40 PM	**Franca Fraternali,** *King's College London; Francis Crick Institute London, United Kingdom* *Detection of Conformational States and Allosteric Hub Residues in Molecular Simulations*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Ozlem Tastan Bishop,** *Rhodes University, South Africa* *An Integrated Molecular Modeling and Dynamic Residue Network Analysis Strategy to Identify Allosteric Modulators of Human Heat Shock Proteins*
5:00 PM	**R. Gonzalo Parra,** *European Molecular Biology Laboratory, Germany* *Energetic conflicts in catalytic sites of protein enzymes*
5:20 PM	**Georgi Kanev,** *Vrije Universiteit – University Medical Center Amsterdam, The Netherlands* *The landscape of atypical and eukaryotic protein kinases*
5:40 PM	**Renmin Han,** *King Abdullah University of Science and Technology, Saudi Arabia* *PROCEEDINGS PRESENTATION: A joint method for marker-free alignment of tilt series in electron tomography*

RegSys: Regulatory and Systems Genomics

COSI TRACK PRESENTATIONS

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SINGAPORE (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/regsys.php

MONDAY, JULY 22

10:15 AM	**Judith Zaugg,** *EMBL Heidelberg, Germany* **Anthony Mathelier,** *University of Oslo, Norway* *Welcome to RegSys COSI*
10:20 AM	**Eileen Furlong,** *EMBL Heidelberg, Germany* *Understanding enhancer usage during embryonic development at a single cell level*
11:00 AM	**Jeoren de Ridder,** *University Medical Center Utrecht, The Netherlands* *Mapping multi-way chromatin contacts of individual alleles using PromethION long-read sequencing*
11:20 AM	**Da-Inn Lee,** *University of Wisconsin-Madison, United States* *Discovering Structural Units of Chromosomal Organization with Matrix Factorization and Graph Regularization*
11:40 AM	**Sebastian Kurscheid,** *The Australian National University, Australia* *TAD cliques shape the 4-dimensional genome during terminal differentiation*
12:00 PM	**Ferhat Ay,** *La Jolla Institute for Allergy and Immunology, United States* *PROCEEDINGS PRESENTATION: Selfish: Discovery of Differential Chromatin Interactions via a Self-Similarity Measure*
12:20 PM	**Ignacio Ibarra Del Río,** *EMBL Heidelberg, Germany* *Inference of transcription factor cooperativity and its impact on protein-phenotype interactions*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Bart Deplancke,** *EPFL, École Polytechnique Fédérale de Lausanne, Spain* *On the impact of genetic variation on molecular and organismal phenotypes*
2:40 PM	**Roza Berhanu Lemma,** *University of Oslo, Norway* *Pan-cancer identification of transcription factors associated with aberrant DNA methylation patterns*
3:00 PM	**Wouter Meuleman,** *Altius Institute for Biomedical Sciences, United States* *Index and vocabulary of accessible DNA elements in the human genome*
3:20 PM	**Swann Floc’Hlay,** *Institut de Biologie de l’Ecole normale supérieure, France* *Allele-specific analysis of epigenomic and transcriptomic data to study Drosophila developmental cis-regulatory architecture.*
3:40 PM	**Surag Nair,** *Stanford University, United States* *PROCEEDINGS PRESENTATION: Integrating regulatory DNA sequence and gene expression to predict genome-wide chromatin accessibility across cellular contexts*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Robin Andersson,** *University of Copenhagen, Denmark* *Insights into gene regulatory elements from transcription start site sequencing*
5:20 PM	**Susanne Bornelöv,** *University of Cambridge, United Kingdom* *Gene regulation through optimization of codon usage in embryonic stem cells*
5:40 PM	**Max Schubach,** *Berlin Institute of Health (BIH), Germany* *Saturation mutagenesis of disease-associated regulatory elements*

RegSys: Regulatory and Systems Genomics

COSI TRACK PRESENTATIONS

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SINGAPORE (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/regsys.php

TUESDAY, JULY 23

10:15 AM **Judith Zaugg,** *EMBL Heidelberg, Germany*
Anthony Mathelier, *University of Oslo, Norway*
Welcome to RegSys COSI

10:20 AM **Barbara Treutlein,** *ETH Zurich, Switzerland*
TBA

11:00 AM **Joshua Welch,** *University of Michigan, United States*
Single-cell multi-omic integration compares and contrasts features of brain cell identity

11:20 AM **Matthew Stone,** *University of Wisconsin-Madison, United States*
Identifying strengths and weaknesses of computational network inference methods on single cell RNA-seq data

11:40 AM **Wei Vivian Li,** *University of California, Los Angeles, United States*
PROCEEDINGS PRESENTATION: A statistical simulator scDesign for rational scRNA-seq experimental design

12:00 PM **Shaun Mahony,** *The Pennsylvania State University, United States*
Characterizing the spatial organization of protein-DNA complexes in a comprehensive epigenome

12:20 PM **Harshit Sahay,** *Duke University, United States*
Transcription factor binding to mismatched DNA and its potential role in mutagenesis

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12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Stein Aerts,** *KU Leuven, The Netherlands*
Deciphering gene regulatory programs in the era of single-cell genomics

2:40 PM **Jaime A Castro-Mondragon,** *Centre for Molecular Medicine, Norway*
Combining transcriptional and post-transcriptional regulation to predict mutations altering the gene regulatory program in cancer cells

3:00 PM **Markus List,** *Technical University of Munich, Germany*
PROCEEDINGS PRESENTATION: Large-scale inference of competing endogeneous RNA networks with sparse partial correlation

3:20 PM **Emily R. Miraldi,** *Cincinnati Children's Hospital Medical Center, United States*
Benchmarked strategies to improve accuracy of gene regulatory networks from scRNA-seq

3:40 PM **Ewa Szczurek,** *University of Warsaw, Poland*
PROCEEDINGS PRESENTATION: Learning signaling networks from combinatorial perturbations by exploiting siRNA off-target effects

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Julia Zeitlinger,** *Stowers Institute for Medical Research, United States*
BPNet: base-resolution deep learning of transcription factor binding reveals nuanced organizational features of the cis-regulatory code in mouse ES cells

5:20 PM **Avanti Shrikumar,** *Stanford University, United States*
PROCEEDINGS PRESENTATION: GkmExplain: Fast and Accurate Interpretation of Nonlinear Gapped k-mer SVMs

5:40 PM **Asa Ben-Hur,** *Colorado State University, United States*
PROCEEDINGS PRESENTATION: Comprehensive Evaluation of Deep Learning Architectures for Prediction of DNA/RNA Sequence Binding Specificities

HiTSeq: High-Throughput Sequencing

COSI TRACK SCHEDULE

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SAN FRANCISCO (3RD FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/hitseq.php

MONDAY, JULY 22

10:15 AM **Welcome**

10:20 AM **KEYNOTE: Christina Curtis,** *Stanford University, United States*
Quantifying the rates and routes of metastasis

11:20 AM **Xiao Yang,** *Grail, Inc, United States*
PROCEEDINGS PRESENTATION: Alignment-free Filtering for cfNA Fusion Fragments

11:40 AM **Gryte Satas,** *Princeton University, United States*
Descendant Cell Fraction: Copy-aware Inference of Clonal Composition and Evolution in Cancer

12:00 PM **Teresa Przytycka,** *National Center of Biotechnology Information, NLM, NIH, United States*
Subpopulation detection and their comparative analysis across single cell ex-periments with PopCorn

12:20 PM **Hirak Sarkar,** *Stony Brook University, United States*
PROCEEDINGS PRESENTATION: Minnow: A principled framework for rapid simulation of dscRNA-seq data at the read level

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Ali Ghaffaari,** *Max Planck Institute for Informatics, Germany*
PROCEEDINGS PRESENTATION: Fully-sensitive Seed Finding in Sequence Graphs Using a Hybrid Index

2:20 PM **Martin Muggli,** *Colorado State University, United States*
PROCEEDINGS PRESENTATION: Building Large Updatable Colored de Bruijn Graphs via Merging

2:40 PM **Aranka Steyaert,** *Ghent University, Belgium*
Accurate determination of node and arc multiplicities in de Bruijn graphs using conditional random fields

3:00 PM **Mikko Rautiainen,** *Max Planck Institute for Informatics, Germany*
GraphAligner: Rapid and Versatile Sequence-to-Graph Alignment

3:20 PM **Ivan Tolstoganov,** *St. Petersburg State University, Russia*
PROCEEDINGS PRESENTATION: cloudSPAdes: Assembly of Synthetic Long Reads Using de Bruijn graphs

3:40 PM **Guillaume Marçais,** *Carnegie Mellon University, United States*
PROCEEDINGS PRESENTATION: Locality sensitive hashing for the edit distance

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Yan Gao,** *Harbin Institute of Technology, China*
PROCEEDINGS PRESENTATION: TideHunter: efficient and sensitive tandem repeat detection from noisy long-reads using seed-and-chain

5:00 PM **KEYNOTE: Zam Iqbal,** *European Bioinformatics Institute, United Kingdom*
Bacterial pangenome graphs — an approximate solution to the correct problem

HiTSeq: High-Throughput Sequencing

COSI TRACK SCHEDULE

MONDAY, JULY 22 AND TUESDAY, JULY 23

ROOM: SAN FRANCISCO (3RD FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/hitseq.php

TUESDAY, JULY 23

10:15 AM **KEYNOTE: Andrew Adey,** *Oregon Health and Sciences University, United States*
Advances in single-cell epigenomics using combinatorial indexing

11:20 AM **Qiao Liu,** *Tsinghua University, China*
PROCEEDINGS PRESENTATION: hicGAN infers super resolution Hi-C data with generative adversarial networks

11:40 AM **Mariano Gabitto,** *Flatiron Institute, United States*
Characterizing chromatin landscape from aggregate and single-cell genomic assays using flexible duration modeling.

12:00 PM **Vikas Bansal,** *University of California San Diego, United States*
PROCEEDINGS PRESENTATION: Integrating read-based and population-based phasing for dense and accurate haplotyping of individual genomes

12:20 PM **Sven Schrinner,** *Heinrich Heine University Düsseldorf, Germany*
Haplotype Threading: Accurate Polyploid Phasing from Long Reads

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Can Alkan,** *Bilkent University, Turkey*
Characterization of large-scale structural variants using Linked-Reads

2:20 PM **Iman Hajirasouliha,** *Cornell University, United States*
Detection and assembly of novel sequence insertions using Linked-Reads

2:40 PM **Lolita Lecompte,** *INRIA, France*
Genotyping structural variations using long reads data

3:00 PM **Hyun-Hwan Jeong,** *Baylor College of Medicine, United States*
Beta-binomial modeling of CRISPR pooled screen data identifies target genes with greater sensitivity and fewer false negatives

3:20 PM **Jonas Fischer,** *Max Planck Institute for Informatics, Germany*
Fast and accurate bisulfite alignment and methylation calling for mammalian genomes

3:40 PM **Pavlo Lutsik,** *German Cancer Research Center (DKFZ), germany*
PipelineOlympics: Benchmarking of processing workflows for bisulfite sequencing data

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:25 PM **Angus McAllister,** *Amazon Web Services, United Kingdom*
SPONSOR INDUSTRY TALK: AWS for Genomics in the Public Sector

4:40 PM **Yingying Wei,** *The Chinese University of Hong Kong*
Flexible Experimental Designs for Valid Single-cell RNA-sequencing Experiments Allowing Batch Effects Correction

5:00 PM **Yuanhua Huang,** *EMBL-European Bioinformatics Institute, United Kingdom*
Bayesian deconvolution of somatic clones and pooled individuals with expressed variants in single-cell RNA-seq data

5:20 PM **Andre Kahles,** *ETH Zurich, Switzerland*
ImmunoPepper: Generating Neoepitopes from RNA-Seq data

5:40 PM **Simone Tiberi,** *University of Zurich, Switzerland*
BANDITS: A Bayesian hierarchical model for differential splicing accounting for sample-to-sample variability and mapping uncertainty

RSG WITH DREAM 2019

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

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

NOVEMBER 4-6, 2019 NEW YORK, NY

DETAILS

WHEN

NOVEMBER 4-6, 2019

WHERE

MSKCC

430 E 67TH St.
NEW YORK, NY 10065

COST*

ISCB

Professional $375
Post Doc $275
Student $250

Non-Members

Professional $575
Post Doc $475
Student $450

*Reflects Earlybird rates.
Rates increase on Oct 29

MORE INFO

www.iscb.org/recomb-regsysgen2019

SUBMIT TODAY!

SUBMISSION DEADLINE

Oral Abstract & Posters
September 9, 2019

TOPICS:

- Network visualization and analysis
- Regulatory motifs and modules
- Epigenomics and chromatin state
- Non-coding RNAs
- Regulatory networks
- Co-transcriptional, post-transcriptional, and translational regulation
- Signal transduction networks
- Genetic, molecular, and phenotypic variation and human disease
- Cellular signatures of biological responses and disease states
- Mathematical modeling and simulation of biological systems
- Methods for systematic validation of high-throughput biological predictions
- Single-cell transcriptomics
- Single-cell proteomics
- Metabolomics
- Microbiome
- Machine learning methods for systems biology
- Translational systems biology

Featuring a Special Session on Single Cell Analysis

We welcome submissions on computational and experimental advances in single cell analysis at the transcriptomic, epigenomic and proteomic levels as well as emerging technologies that can resolve the spatial organization of cells in complex tissues while providing molecular data at the single cell level. Applications of single cell methods to important biomedical questions – for example in cancer biology, immunology, or development – are also encouraged.

This special session is sponsored by the Research Center for Cancer Systems Immunology at Memorial Sloan Kettering Cancer Center, an NCI-funded Cancer Systems Biology Consortium (CSBC) Center.

CompMS: Computational Mass Spectrometry

COSI TRACK PRESENTATIONS

TUESDAY, JULY 23 • ROOM: SHANGHAI 3/4 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/compms.php

10:15 AM **Oliver Kohlbacher,** *Universität Tübingen, Germany*
William Noble, *University of Washington, United States*
Olga Vitek, *Northeastern University, United States*
Welcome

10:20 AM **Hannes Roest,** *University of Toronto, Canada*
Mobi-DIK: A novel algorithm for analysis of data-independent acquisition (DIA) data coupled to ion mobility

11:00 AM **Hao Chi,** *Chinese Academy of Sciences, China*
PROCEEDINGS PRESENTATION: pNovo 3: precise de novo peptide sequencing using a learning-to-rank framework

11:20 AM **Alexey Gurevich,** *St. Petersburg State University, Russia*
PROCEEDINGS PRESENTATION: NPS: scoring and evaluating the statistical significance of peptidic natural product–spectrum matches

11:40 AM **Manfred Claassen,** *ETH Zurich, Switzerland*
Anything to gain from single-cell measurements?

12:20 PM **Yannick Cogne,** *Laboratory «Innovative technologies for Detection and Diagnostics» CEA-Marcoule, DRF-Li2D, France*
Proteomics & bioinformatics to evaluate the quality of transcriptome assembly and to measure the extent of animal intrapopulation variability

2:00 PM **Isabell Bludau,** *ETH Zurich, Switzerland*
Complex-centric proteome profiling by SEC- SWATH-MS

2:40 PM **Dai Hai Nguyen,** *Kyoto University, Japan*
PROCEEDINGS PRESENTATION: ADAPTIVE: leArning DAta-dePendenT, conclse molecular VEctors for fast, accurate metabolite identification from tandem mass spectra

3:00 PM **Dan Guo,** *Northeastern University, United States*
PROCEEDINGS PRESENTATION: Unsupervised segmentation of mass spectrometric ion images characterizes morphology of tissues

3:20 PM **Markus Fleischauer,** *Friedrich Schiller University Jena, Germany*
SIRIUS 4: a rapid tool for turning tandem mass spectra into metabolite structure information

3:40 PM **Oliver Kohlbacher,** *Universität Tübingen, Germany*
William Noble, *University of Washington, United States*
Olga Vitek, *Northeastern University, United States*
CompMS COSI business meeting

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM *Poster lightning talks*

JPI: Junior Principal Investigators

COSI TRACK PRESENTATIONS

TUESDAY, JULY 23 • ROOM: BOSTON 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/jpi.php

12:45 PM **Lucia Peixoto,** *Washington State University, United States*
Casey Greene, *University of Pennsylvania, United States*
The ISCB code of conduct

Transitioning from a post-doc to a junior PI can be a challenging process requiring careful planning. Once running a group, junior PIs are faced with many new tasks, some of which are learnt on the job. The Junior Principal Investigators group (JPI) aims to provide support during this process via a community of peers.

EvolCompGen: Evolution and Comparative Genomics

COSI TRACK PRESENTATIONS

TUESDAY, JULY 23 • ROOM: BOSTON 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/evolution.php

10:20 AM **Pavel Skums,** *Georgia State University, United States*
PROCEEDINGS PRESENTATION: Inference of clonal selection in cancer populations using single-cell sequencing data

10:40 AM **Robert Noble,** *ETH Zurich, Switzerland*
Spatial structure governs the mode of tumour evolution

10:50 AM **Leonidas Salichos,** *Yale University, United States*
Growth patterns and driver effects from individual samples provide insights in tumor evolution

11:00 AM **Krister Swenson,** *CNRS, Université de Montpellier, France*
PROCEEDINGS PRESENTATION: Large-Scale Mammalian Genome Rearrangements Coincide with Chromatin Interactions

11:20 AM **David Sankoff,** *University of Ottawa, Canada*
Distinguishing successive ancient polyploidy levels based on genome-internal syntenic alignments

11:30 AM **Stephane Guindon,** *CNRS, France*
Accounting for calibration uncertainty: Bayesian molecular dating as a "doubly intractable" problem

11:40 AM **Nuraini Aguse,** *University of Illinois at Urbana-Champaign, United States*
PROCEEDINGS PRESENTATION: Summarizing the Solution Space in Tumor Phylogeny Inference by Multiple Consensus Trees

12:00 PM **Jeff Wintersinger,** *University of Toronto, Canada*
Pairtree: fast cancer phylogeny reconstruction using multiple samples

12:10 PM **Yuval Tabach,** *The Hebrew University of Jerusalem, Israel*
Mapping global and local coevolution across 600 species to identify novel homologous recombination repair genes

12:20 PM **Maureen Stolzer,** *Carnegie Mellon University, United States*
Evolution of the Metazoan Protein Domain Toolkit

12:30 PM **Safa Jammali,** *Université de Sherbrooke, Canada*
Spliced alignment for the reconstruction of gene and transcript evolution

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Erin Molloy,** *University of Illinois at Urbana-Champaign, United States*
PROCEEDINGS PRESENTATION: TreeMerge: A new method for improving the scalability of species tree estimation methods

2:20 PM **Yufeng Wu,** *University of Connecticut, United States*
Accurate and Efficient Cell Lineage Tree Inference from Noisy Single Cell Data: The Maximum Likelihood Perfect Phylogeny Approach

2:30 PM **Blerina Sinaimeri,** *INRIA, France*
AmoCoala: Towards a more realistic model for cophylogeny reconstruction via an approximate Bayesian computation

2:40 PM **Dinithi Sumanaweera,** *Monash University, Australia*
PROCEEDINGS PRESENTATION: Statistical Compression of Protein Sequences and Inference of Marginal Probability Landscapes over Competing Alignments using Finite State Models and Dirichlet Priors

3:00 PM **Lars Arvestad,** *Stockholm University, Sweden*
Choosing amino-acid replacement models

3:10 PM **Edward Braun,** *Univeristy of Florida, United States*
Amino acid exchangeability parameters in models of protein evolution are strongly structure dependent and non-stationary across the tree of life

3:20 PM **Sayed-Rzgar Hosseini,** *Cancer Research UK, Cambridge Institute, United Kingdom*
PROCEEDINGS PRESENTATION: Estimating the predictability of cancer evolution

3:40 PM **Gatis Melkus,** *lUniversity of Latvia*
Graph-based network analysis of transcriptional regulation pattern divergence in duplicated yeast gene pairs

3:50 PM **Louxin Zhang,** *National University of Singapore*
Enumerating Galled Networks

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Luay Nakhleh,** *Rice University, United States*
PROCEEDINGS PRESENTATION: A Divide-and-Conquer Method for Scalable Phylogenetic Network Inference from Multi-locus Data

5:00 PM **Moses Stamboulian,** *Indiana University Bloomington, United States*
The Ortholog Conjecture Revisited: the Value of Orthologs and Paralogs in Function Prediction

5:10 PM **Salvatore Cosentino,** *The University of Tokyo, Japan*
SonicParanoid: Fast, accurate and easy orthology inference

5:20 PM **André Hennig,** *University of Tübingen, Germany*
PROCEEDINGS PRESENTATION: Efficient Merging of Genome Profile Alignments

5:40 PM **Fabio Pardi,** *LIRMM, France*
Improving classification of novel genes into known gene families via the phylo-kmers

5:50 PM **Giltae Song,** *Pusan National University, South Korea*
IMAP: Chromosome-level genome assembler combining multiple de novo assemblies

NetBio: Network Biology

COSI TRACK PRESENTATIONS

TUESDAY, JULY 23 • ROOM: MONTREAL (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/netbio.php

10:20 AM **Torsten Gross,** *Humboldt University, Germany*
PROCEEDINGS PRESENTATION: Robust network inference using response logic

10:40 AM **Marinka Zitnik,** *Stanford University, United States*
Evolution of resilience in protein interactomes across the tree of life

11:00 AM **Marjan Farahbod,** *The University of British Columbia, Canada*
Coexpression and regulation: The expectation, the observation and the reality

11:20 AM **Shawn Gu,** *University of Notre Dame, United States*
Next-generation biological network alignment

11:40 AM **Mathias Cardner,** *ETH Zurich, Switzerland*
PROCEEDINGS PRESENTATION: Inferring signalling dynamics by integrating interventional with observational data

12:00 PM **KEYNOTE: Christian von Mering,** *University of Zurich, Switzerland*
Protein-protein association networks and their use in complementing functional pathway enrichment analysis

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Joris Cadow,** *IBM, Switzerland*
PIMKL: Pathway Induced Multiple Kernel Learning

2:20 PM **Noel Malod-Dognin,** *Barcelona Supercomputing Center, Spain*
Towards a data-integrated cell

2:40 PM **Roberta Marino,** *University of Turin, Italy*
Integrative network-based approach identifies gene communities in COPD

3:00 PM **Marieke Kuijjer,** *Centre for Molecular Medicine Norway, University of Oslo, Norway*
Single-sample network modeling identifies regulation of PD1 signaling associated with glioblastoma survival

3:20 PM **Scooter Morris,** *University of California, San Francisco, United States*
scNetViz: A Cytoscape App for the Network Analysis and Visualization of scRNA-Seq Data

3:30 PM **Marc Legeay,** *Novo Nordisk Foundation Center for Protein Research, Denmark*
Omics Visualizer: a Cytoscape App to visualize omics data

3:40 PM **Daniel Marbach,** *Roche Innovation Center Basel, Switzerland*
Community challenge assesses network module identification methods across complex diseases

3:50 PM **Joaquim Aguirre-Plans,** *GRIB (IMIM-UPF), Spain*
GUILDify v2.0: A tool to identify molecular networks underlying human diseases, their comorbidities and their druggable targets

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Samson Fong,** *University of California San Diego, United States*
DiseaseScope: Automatic Construction and Interpretation of Hierarchical Disease Models

5:00 PM **Yoo-Ah Kim,** *National Institue of Health, United States*
Identifying Drug Sensitivity Subnetworks with NETPHIX

5:20 PM **KEYNOTE: Laura I. Furlong,** *GRIB (IMIM-UPF), Spain*
Connecting genomics and network properties of genes relevant for disease and drug response

MICROBIOME

COSI TRACK PRESENTATION

TUESDAY, JULY 23 • ROOM: DELHI (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/microbiome.php

10:20 AM **Peer Bork,** *EMBL Heidelberg, Germany*
The human gut microbiome and its clinical relevance

11:00 AM **Richard Bonneau,** *Simons Foundation, United States*
Learning accurate representations of microbe-metabolite interactions

11:10 AM **Benjamin Albrecht,** *University of Tübingen, Germany*
Efficient mobile taxonomic classification for nanopore data using a multilevel approach

11:20 AM **Siavash Mirarab,** *University of California San Diego, United States*
PROCEEDINGS PRESENTATION: TADA: Phylogenetic augmentation of microbiome samples enhances phenotype classification

11:40 AM **Fabio Cumbo,** *University of Trento, Italy*
MetaRefSGB: a scalable framework to organize genomes from metagenomes and their annotations into species-level genome bins

12:00 PM **Shibu Yooseph,** *University of Central Florida, United States*
PROCEEDINGS PRESENTATION: Learning a Mixture of Microbial Networks Using Minorization-Maximization

12:20 PM **Tommi Mäklin,** *University of Helsinki, Finland*
Bacterial lineage identification from multi-strain sequencing data

12:30 PM **Wataru Iwasaki,** *The University of Tokyo, Japan*
Metaepigenomic analysis reveals the unexplored diversity of DNA methylation in an environmental prokaryotic community.

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Ami Bhatt,** *Stanford Medical School and Stanford University, United States*
From precision microbial genomics to precision medicine

2:40 PM **Camilo Valdes,** *Florida International University, United States*
PROCEEDINGS PRESENTATION: Large Scale Microbiome Profiling in the Cloud

3:00 PM **Johannes Soeding,** *Max Planck Institute for Biophysical Chemistry, Germany*
Protein-level assembly increases protein sequence recovery from metagenomic samples manyfold

3:20 PM **Tomasz Kosciolek,** *Małopolska Centre of Biotechnology, Poland*
Massive-scale structure and function predictions of human gut microbiome proteins for metagenomic applications

3:30 PM **Tatyana Zamkovaya,** *University of Florida, United States*
Unraveling the Role of Microbial Dark Matter in Extreme Environmental Networks

3:40 PM **Dileep Kishore,** *Boston University, United States*
Inferring microbial co-occurrence networks from 16S data: A systematic evaluation

3:50 PM **Kangjin Kim,** *Seoul National University, South Korea*
Phylogenetic Tree-based Microbiome Association Test

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Alexander Sczyrba,** *Bielefeld University, Germany*
Update on the CAMI 2 Challenge

5:00 PM **Alexander Sczyrba,** *Bielefeld University, Germany*
CAMI future challenges

5:20 PM **Fernando Meyer,** *Helmholtz Centre for Infection Research, Germany*
Assessing taxonomic metagenome profilers with OPAL

5:30 PM **Ziye Wang,** *Fudan University, China*
Assessment of metagenomic assemblers based on hybrid reads of real and simulated metagenomic sequences

5:40 PM **Eli Levy Karin,** *Max-Planck Institute for Biophysical Chemistry, Germany*
MetaEuk – Sensitive, high-throughput gene discovery and annotation for large-scale eukaryotic metagenomics

5:50 PM **Christopher Woelk,** *Merck Exploratory Science Center, United States*
DeepBGC: Applying deep learning algorithms to biosynthetic gene cluster identification

Bio-Ontologies

COSI TRACK PRESENTATIONS

TUESDAY, JULY 23 AND WEDNESDAY, JULY 24

ROOM: SHANGHAI 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/bioontologies.php

TUESDAY, JULY 23

10:15 AM **Michel Dumontier,** *Maastricht University, The Netherlands*
Welcome

10:20 AM **KEYNOTE: Helena Deus,** *Elsevier, The Netherlands*
A Knowledge Graph for Health: Can graphs really save lives?

11:20 AM **Mona Alshahrani,** *King Abdullah University of Science and Technology, Saudi Arabia*
Knowledge graph representation learning: Approaches and applications to bio-medicine

11:40 AM **Francesco Taglino,** *National Research Council of Italy*
Combining knowledge-based approach with logic data mining techniques to improve data querying and analysis on Alzheimer's Disease data

12:00 PM **Andreea Grigoriu,** *Maastricht University, The Netherlands*
SIENA: Semi-automatic Semantic Enhancement of Datasets using Concept Recognition

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12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **KEYNOTE: Ioannis Xenarios,** *Université de Lausanne, Switzerland*
Knowledge graph and computable models

3:00 PM **Hao Chen,** *University of California, Riverside, United States*
PROCEEDINGS PRESENTATION: DIFFUSE: Predicting isoform functions from sequences and expression profiles via deep learning

3:20 PM **Hande Küçük McGinty,** *Collaborative Drug Discovery, United States*
Extending Machine Learning Capabilities of BioAssay Express

3:40 PM **Raul Rodriguez-Esteban,** *Roche, Switzerland*
Semantic persistence of ambiguous biomedical names in the citation network

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Ahmed Youssef,** *Boston University, United States*
A multi-class decision tree for identifying cell cluster marker genes in single-cell RNAseq analysis

5:00 PM **András Hatos,** *University of Padua, Italy*
Standardising intrinsic disorder description

5:20 PM **Zoë May Pendlington,** *EMBL-EBI, United Kingdom*
Mapping UK Biobank to the Experimental Factor Ontology

5:40 PM *Flash Presentations*

WEDNESDAY, JULY 24

10:15 AM **Michel Dumontier,** *Maastricht University, The Netherlands*
Welcome

10:20 AM **Thodoris Koutsandreas,** *National Hellenic Reasearch Foundation, Greece*
Proposing a unified framework of topological factors in order to refine semantic network analysis on biomedical ontologies

10:40 AM **Chris Mungall,** *Lawrence Berkeley National Laboratory, United States*
Managing ontology releases with the Ontology Development Kit

11:00 AM **Peter Karp,** *SRI International, United States*
Ontology-driven Omics Data Visualization and Database Update Notifications

11:20 AM **Hande Küçük McGinty,** *Collaborative Drug Discovery, United States*
OntoloBridge – A FAIR Semi-Automated Ontology Update Request System

11:40 AM **Tunca Dogan,** *European Bioinformatics Institute, Turkey*
CROssBAR: Comprehensive Resource of Biomedical Relations with Network Representations and Deep Learning

12:00 PM **Michel Dumontier,** *Maastricht University, The Netherlands*
Closing session

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

General Computational Biology

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 • ROOM: SYDNEY (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/general.php

10:20 AM **Cui Su,** *University of Luxembourg*
PROCEEDINGS PRESENTATION: Controlling Large Boolean Networks with Single-Step Perturbations

10:40 AM **Seyed Reza Miraskarshahi,** *Simon Fraser University, Canada*
PROCEEDINGS PRESENTATION: MCS^2 : Minimal coordinated supports for fast enumeration of minimal cut sets in metabolic networks

11:00 AM **Markus Heinonen,** *Aalto University, Finland*
PROCEEDINGS PRESENTATION: Bayesian Metabolic Flux Analysis reveals intracellular flux couplings

11:20 AM **Natalie Twine,** *CSIRO, Australia*
Novel software 'tribes' enables distant relationship and disease variant discovery in amyotrophic lateral sclerosis

11:40 AM **Brian Browning,** *University of Washington, United States*
Rapid genotype imputation from large-scale sequence data

12:00 PM **Shubham Chandak,** *Stanford University, United States*
Large blocklength LDPC codes for Illumina sequencing-based DNA storage

12:20 PM **Xuegong Zhang,** *Tsinghua University, China*
A New D2 Statistic and Algorithm for Efficient Detection of Repetitive Sequences in Whole Genomes and in Short Sequencing Reads

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12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Carles Boix,** *Massachusetts Institute of Technology, United States*
Leveraging single-cell RNA-seq to infer cell type-specific somatic mutations and mosaicism in Alzheimer's disease.

2:20 PM **Kavya Vaddadi,** *TCS Research, India*
Read Mapping on Genome Variation Graphs

2:40 PM **Judith Somekh,** *University of Haifa, Israel*
Batch correction evaluation framework using a-priori gene-gene associations: applied to the GTEx dataset

3:00 PM **Boris Reva,** *Icahn School of Medicine at Mount Sinai, United States*
Inferring pathway activation/suppression to rank tumors by sensitivity to immune checkpoint therapy

3:20 PM **Nishanth Ulhas Nair,** *National Institutes of Health (NIH), United States*
Contribution of synthetic lethality to cancer risk and onset time across human tissues

3:40 PM **Marthe Solleder,** *University of Lausanne, SIB Swiss Institute of Bioinformatics, Switzerland*
Deciphering the landscape of phosphorylated HLA-I ligands

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Huaiyu Mi,** *University of Southern California, United States*
PANTHER Classification System – An integrated platform for genome-wide gene function analysis

5:00 PM **Rajeev Azad,** *University of North Texas, United States*
CAFE: Compositional Anomaly and Feature Enrichment Assessment for Delineation of Genomic Islands

5:20 PM **Gabriel Sturm,** *Columbia University, United States*
Human Aging DNA Methylation Signatures are Conserved but Accelerated in Cultured Fibroblasts

5:40 PM **Nobuto Takeuchi,** *University of Auckland, New Zealand*
The origin of the central dogma through conflicting multilevel selection

VarI: Variant Interpretation

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 • ROOM: MONTREAL (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/vari.php

10:15 AM	*Welcome from the committee*
10:20 AM	**Laura Furlong,** *Hospital del Mar Medical Research Institute, Spain* *The DisGeNET platform of disease genomics to support variant interpretation*
11:00 AM	**James Stephenson,** *EMBL-EBI, United Kingdom* *Enrichment and Clustering of Rare Genetic Variants using Shared Protein Structure Domains*
11:20 AM	**Lambert Moyon,** *PSL Université, France* *Annotation and prioritization of non-coding variants in the context of human diseases*
11:40 PM	**Alexander Gress,** *Helmholtz Centre for Infection Research (HZI), Germany* *The importance of being unbiased: why protein structure and training setup are important for predicting novel pathogenic genetic variants*
12:00 PM	**Alexandre Renaux,** *Universite Libre de Bruxelles, Belgium* *Towards oligogenic disease prediction with ORVAL: a web-platform to uncover pathogenic variant combinations.*
12:20 PM	**Jun Cheng,** *Technical University of Munich / QBM Graduate School, Germany* *MMSplice: modular modeling improves the predictions of genetic variant effects on splicing*
12:30 PM	**Saikat Banerjee,** *Max Planck Institute for Biophysical Chemistry, Germany* *Bayesian multiple logistic regression for case-control GWAS*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	*Vari-COSI afternoon session*
2:05 PM	**Janet Kelso,** *Max Planck Institute for Evolutionary Anthropology, Germany* *What ancient humans can teach us about modern genetic variation*
2:45 PM	**Shaojie Zhang,** *University of Central Florida, United States* *PROCEEDINGS PRESENTATION: Efficient haplotype matching between a query and a panel for genealogical search*
3:05 PM	**Daniel Carlin,** *University of California San Diego, United States* *A fast and flexible framework for network assisted genomic association*
3:25 PM	**Erwin Frise,** *Fabric Genomics, United States* *An Artificial Intelligence Engine for High-Throughput ACMG/AMP Classification of Genetic Variants for Inherited Disease Clinical Gene Panels*
3:45 PM	**Alexander Kaplun,** *Variantyx Inc., United States* *Company presentation: Variantyx – Whole Genome Sequencing (WGS) as a first-line diagnostic test: Its success is in the details*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Iuliana Ionita-Laza,** *Columbia University, United States* *Integrative statistical approaches for predicting functional effects of variants in noncoding regions of the genome*
5:20 PM	**Alexander Schoenhuth,** *Centrum Wiskunde en Informatica/Utrecht University, The Netherlands* *PROCEEDINGS PRESENTATION: Using the structure of genome data in the design of deep neural networks for predicting amyotrophic lateral sclerosis from genotype*
5:40 PM	**Andrea Castro,** *University of California San Diego, United States* *Elevated neoantigen levels in tumors with somatic mutations in the HLA-A, HLA-B, HLA-C and B2M genes*
5:50 PM	**Michal Sadowski,** *Centre of New Technologies, University of Warsaw, Poland* *Spatial Chromatin Architecture Alteration by Structural Variations in Human Genomes at Population Scale*
6:00 PM	*Closing remarks from the committee*

BOSC: Bioinformatics Open Source Conference

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: DELHI (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/bosc.php

WEDNESDAY, JULY 24

10:15 AM **Nomi Harris,** *Lawrence Berkeley National Laboratory, United States*
Opening remarks

10:25 AM **Heather Wiencko,** *Hosted Graphite, Ireland*
The Open Bioinformatics Foundation

10:33 AM **Kai Blin,** *Technical University of Denmark*
Google Summer of Code 2018

10:40 AM **Charlotte Herzeel,** *Imec, Belgium*
elPrep 4: A multi-threaded tool for sequence analysis

11:00 AM **Andrew Moschetti,** *Google Cloud, United States*
Variant Transforms and BigQuery: Large scale data analytics in the cloud

11:05 AM **Michael Bouzinier,** *Division of Genetics, Brigham and Women's Hospital, United States*
Forome Anfisa – an Open Source Variant Interpretation Tool

11:10 AM **Patrick Kunzmann,** *Technical University Darmstadt, Germany*
Biotite: A comprehensive and efficient computational molecular biology library in Python

11:15 AM *Q&A for lightning talks*

11:20 AM **Andrey Kokorev,** *Forome Association, Russia*
Portable Pipeline for Whole Exome and Genome Sequencing

11:25 AM **Jayaram Kancherla,** *University of Maryland, United States*
Epiviz File Server – Query, Compute and Interactive Exploration of data from Indexed Genomic Files

11:30 AM **Morgan Taschuk,** *Ontario Institute for Cancer Research, Canada*
What does 1.0 take? MISO LIMS after 9 years of development

11:35 AM *Q&A for lightning talks*

11:40 AM **Deepak Unni,** *Lawrence Berkeley National Laboratory, United States*
BioLink Model – Standardizing knowledge graphs and making them interoperable

12:00 PM **Saket Choudhary,** *University of Southern California, United States*
pysradb: A Python package to query next-generation sequencing metadata and data from NCBI Sequence Read Archive

12:05 PM **Michael Heuer,** *University of California Berkeley, United States*
Disq, a library for manipulating bioinformatics sequencing formats in Apache Spark

12:10 PM **Dominique Batista,** *University of Oxford e-Research Centre, United Kingdom*
A toolkit for semantic markup, exploration, comparison and merging of metadata models expressed as JSON-Schemas

12:15 PM **Stian Soiland-Reyes,** *The University of Manchester, United Kingdom*
A lightweight approach to research object data packaging

12:20 PM *Q&A for lightning talks*

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **BOSC KEYNOTE: Nicola Mulder,** *University of Cape Town, South Africa*
Building infrastructure for responsible open science in Africa

3:00 PM **Seth Carbon,** *Lawrence Berkeley National Laboratory (LBNL), United States*
The (Re)usable Data Project

3:20 PM **Sergio Contrino,** *University of Cambridge, United Kingdom*
The FAIR data principles and their practical implementation in InterMine

3:40 PM **Rishi Nag,** *Global Alliance for Genomics and Health (GA4GH), United Kingdom*
GA4GH: Developing Open Standards for Responsible Data Sharing

3:45 PM **Brian O'Connor,** *University of California, Santa Cruz, United States*
The Commons Alliance: Building cloud-based infrastructure to support biomedical research in Data STAGE and AnVIL

3:50 PM **Adelaide Rhodes,** *Harvard University, United States*
Fake it 'til You Make It: Open Source Tool for Synthetic Data Generation to Support Reproducible Genomic Analyses

3:55 PM *Q&A for lightning talks*

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM *BOSC extra BoFs (http://bit.ly/BOSC2019-bofs)*

6:00 PM POSTER SESSION B, HALL 4.1 (1ST FLOOR)

BOSC: Bioinformatics Open Source Conference

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: DELHI (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/bosc.php

THURSDAY, JULY 25

8:30 AM	*BOSC announcements*
8:40 AM	**Christian Zmasek,** *J. Craig Venter Institute, United States* *Archaeopteryx.js: Web-based Visualization and Exploration of Annotated Phylogenetic Trees (JavaScript)*
8:45 AM	**Anurag Priyam,** *Queen Mary University of London, United Kingdom* *Sequenceserver: a modern graphical user interface for custom BLAST databases*
8:50 AM	**Ryan Williams,** *Mount Sinai School of Medicine, United States* *Parallel, Scalable Single-cell Data Analysis*
8:55 AM	*Q&A for late-breaking lightning talks*
9:00 AM	**Zeyu Yang,** *Imperial College London, United Kingdom* *RAWG: RNA-Seq Analysis Workflow Generator*
9:05 AM	**Tazro Ohta,** *Database Center for Life Science, Japan* *SAPPORO: workflow management system that supports continuous testing of workflows*
9:10 AM	**Qian Liu,** *Roswell Park Comprehensive Cancer Center, United States* *Lazy representation and analysis of very large genomic data resources in R / Bioconductor*
9:15 AM	*Q&A for late-breaking lightning talks*
9:20 AM	**Monica C Munoz-Torres,** *Oregon State University, United States* *The Monarch Initiative: Closing the knowledge gap with semantics-based tools*
9:25 AM	**Pinar Alper,** *University of Luxembourg* *DAISY: a tool for the accountability of Biomedical Research Data under the GDPR.*
9:30 AM	*Q&A for late-breaking lightning talks*
9:40 AM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
10:20 AM	**Louise Cabansay,** *University of California Santa Cruz Genomics Institute, United States* *Dockstore: Enhancing a community platform for sharing cloud-agnostic research tools*
10:40 AM	**Nitesh Turaga,** *Bioconductor / Roswell Park Comprehensive Cancer Center, United States* *Bioconductor with Containers: Past, Present, and Future*
11:00 AM	*Mini-Break*
11:15 AM	**Salvador Capella-Gutiérrez,** *Barcelona Supercomputing Center (BSC), Spain* *OpenEBench. The ELIXIR platform for benchmarking.*
11:35 AM	**Mateusz Kuzak,** *Dutch Techcentre for Life Sciences, ELIXIR-Netherlands* *ELIXIR Europe on the Road to Sustainable Research Software*
11:55 AM	**Julien Gagneur,** *Technical University of Munich, Germany* *The Kipoi repository: accelerating the community exchange and reuse of predictive models for genomics*
12:15 PM	**Anamaria Crisan,** *The University of British Columbia, Canada* *A method for systematically generating explorable visualization design spaces*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Devon Ryan,** *Max Planck Institute of Immunobiology and Epigenetics (MPI-IE), Germany* *snakePipes enable flexible, scalable and integrative epigenomic analysis*
2:20 PM	**Alexander Peltzer,** *Quantitative Biology Center (QBiC) Tübingen, Germany* *nf-core: Community built bioinformatics pipelines*
2:40 PM	**Luis Pedro Coelho,** *Fudan University, China* *NGLess: a domain-specific language for NGS analysis (the NG-meta-profiler case study)*
3:00 PM	**Kaushik Ghose,** *Seven Bridges Genomics, United States* *Benten: An experimental language server for the Common Workflow Language*
3:05 PM	**Richard Lupat,** *Peter MacCallum Cancer Centre, Australia* *Janis: An open source tool to machine generate type-safe CWL and WDL workflows*
3:10 PM	**Tazro Ohta,** *Database Center for Life Science, Japan* *Collecting runtime metrics of genome analysis workflows by CWL-metrics*
3:15 PM	*Q&A for lightning talks*
3:30 PM	**Malvika Sharan,** *EMBL Heidelberg, Germany* *Inclusiveness in Open Science Communities*
3:50 PM	**Aziz Khan,** *University of Oslo, Norway* *ECRcentral: An open source platform to bring early career researchers and funding together*
4:10 PM	**Jason Williams,** *Cold Spring Harbor Laboratory, United States* *The Data Carpentry Genomics Curriculum: Overview and Impact*
4:15 PM	**Victoria Nembaware,** *University of Cape Town, South Africa* *Impact of The African Genomic Medicine Training Initiative: a Community-Driven Genomic Medicine Competency-Based Training Model for Nurses in Africa*
4:20 PM	**Peter Cock,** *The James Hutton Institute, United Kingdom* *Biopython Project Update 2019*
4:25 PM	*Q&A for lightning talks*
4:30 PM	**Alexander Peltzer,** *University of Tübingen, Denmark* **Michael Heuer,** *University of California Berkeley, United States* **Peter Cock,** *The James Hutton Institute, United Kingdom* *Introducing CoFest 2019 – The post-BOSC Collaboration Festival*
4:35 PM	**Nomi Harris,** *Lawrence Berkeley National Laboratory, United States* *Closing Remarks*
4:40 PM	GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

CAMDA: Critical Assessment of Massive Data Analysis

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: BOSTON 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/camda.php

WEDNESDAY, JULY 24

10:15 AM	**David P. Kreil,** *Boku University Vienna, Austria* *CAMDA Welcome*
10:20 AM	**Christine Moissl-Eichinger,** *Medical University of Graz, Austria* *International Space Station and hospital environments: Composition and function of microbiomes in confined built environments*
11:20 AM	**Wenzhong Xiao,** *Stanford and Harvard Medical School, United States* *Data Analysis Challenges of the CAMDA Contest 2019*
11:40 AM	**Lihong Huang,** *Xiamen University, China* *A Machine Learning Framework to Determine Geolocations from Metagenomics Profiling*
12:00 PM	**Jolanta Kawulok,** *Silesian University of Technology, Poland* *Metagenomic sequence classification to search for the origin of samples*
12:20 PM	**Carlos Loucera,** *Fundacion Progreso y Salud, Spain* *Comparison between functional profiles derived from whole genome sequencing and inferred from 16S sequencing*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Julie Chih-Yu Chen,** *Public Health Agency of Canada – National Microbiology Laboratory, Canada* *Systematic evaluation of microbial abundance from amplicon and shotgun sequencing for machine learning prediction of sample origin*
2:40 PM	**David Danko,** *Weill Cornell Graduate School of Medical Sciences, United States* *MetaSUB: A Global Atlas of the Urban Microbiome*
3:00 PM	**Witold R. Rudnicki,** *University of Białystok and ICM University of Warsaw, Poland* *Integration of human cell lines gene expression and chemical properties of drugs for Drug Induced Liver Injury prediction*
3:40 PM	**Joaquim Aguirre-Plans,** *GRIB (IMIM-UPF), Spain* *An ensemble learning approach for modeling the systems biology of drug-induced injury in human liver*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Anika Liu,** *University of Cambridge, United Kingdom* *Steps towards predictive models for DILI based on chemical structure and gene expression signatures and their interpretation*
5:00 PM	**Thin Nguyen,** *Deakin University, Australia* *Prediction of human clinical drug-induced liver injury: cell-line responses versus chemical structures*
5:10 PM	**Nuriye Özlem Özcan Şimşek,** *Boğaziçi Unversity, Turkey* *A Novel Gene Selection Method for Gene Expression Data for the Task of Cancer Type Classification*
5:20 PM	**Maximilian Miller,** *Rutgers University, United States* *mi-faser based partition of the CAMDA 2019 mystery samples in the Metagenomic Forensics Challenge*
5:30 PM	**Scott Lewis,** *Saint Louis University, United States* *CAMDA Forensics Challenge: An Evaluation of Mass-Transit, Microbiome Profiles*
5:40 PM	**Susmita Datta,** *University of Florida, United States* *Constructing microbial fingerprint for unraveling city-specific signature and identifying sample origin locations*
8:00 PM	*Kohlmann's, CAMDA dinner*

CAMDA: Critical Assessment of Massive Data Analysis

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: BOSTON 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/camda.php

THURSDAY, JULY 25

8:30 AM **Joaquin Dopazo,** *Fundación Progreso y Salud, Spain*
CAMDA Welcome

8:40 AM **Gunnar Rätsch,** *ETH Zurich, Switzerland*
Transcriptome Alterations in Cancer:Challenges and Opportunities

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

10:15 AM **Paweł P. Łabaj,** *Jagiellonian University, Poland*
Data Analysis Challenges of the CAMDA Contest 2019 (II)

10:20 AM **Marta R. Hidalgo,** *Centro de Investigación Príncipe Felipe, Spain*
Analyzing cancer through Hipathia: a new insight on cancer signaling pathways

10:40 AM **Maciej Kańduła,** *Boku University Vienna, Austria*
A systematic analysis of multiple cancer studies within a novel enhanced framework for semantic data integration

11:00 AM **Susmita Datta,** *University of Florida, United States*
A sparse Bayesian factor model for the construction of gene co-expression networks from single-cell RNA sequencing count data

11:40 AM **Xianing Zheng,** *University of Michigan, United States*
Benchmarking scRNA-seq clustering methods using multi-parameter ensembles of simulated data and workflows

12:00 PM **Gregor Sturm,** *Technical University of Munich, Germany*
PROCEEDINGS PRESENTATION: Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology

12:20 PM **Soufiane Mourragui,** *Delft University of Technology and the Netherlands Cancer Institute, The Netherlands*
PROCEEDINGS PRESENTATION: PRECISE: A domain adaptation approach to transfer predictors of drug response from pre-clinical models to tumors

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Nathaniel Lim,** *The University of British Columbia, Canada*
Evaluation of Connectivity Map shows limited reproducibility in drug repositioning

2:40 PM *Contest voting and summary*

2:50 PM **Paweł P. Łabaj,** *Jagiellonian University, Poland*
Retrospective and Outlook: Metagenomic Forensic Challenge

3:20 PM **Andre Kahles,** *ETH Zurich, Switzerland*
Retrospective and Discussion: Read-level Data Anonymization

4:00 PM **Wenzhong Xiao,** *Stanford and Harvard Medical School, United States*
Discussion & outlook

4:20 PM **Julia E. Vogt,** *ETH Zurich, Switzerland*
& David P. Kreil, *Boku University Vienna, Austria*
Awards and Closing

4:40 PM GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

Education: Computational Biology Education

COSI TRACK PRESENTATIONS AND WORKSHOP ON EDUCATION IN BIOINFORMATICS (WEB)

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: OSAKA/SAMARKAND (3RD FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/education.php

WEDNESDAY, JULY 24

10:15 AM **Russell Schwartz,** *Carnegie Mellon University, United States*
Welcome and Introduction

10:20 AM **KEYNOTE: Jason Williams,** *Cold Spring Harbor Laboratory, United States*
Training, Teaching, Technology, Togetherness – Promoting Knowledge Exchange in Life Sciences Through Communities of Practice

11:20 AM **Angela Davies,** *University of Manchester, United Kingdom*
Clinical Bioinformatics education to the masses: enabling change in healthcare

11:40 AM **Mateusz Kuzak,** *Dutch Techcentre for Life Sciences, ELIXIR-Netherlands*
FAIR Training in ELIXIR Europe

12:00 PM **Celia van Gelder,** *Dutch Techcentre for Life Sciences, The Netherlands*
Towards a community-endorsed data steward description for life science research

12:20 PM **Martin Stražar,** *University of Ljubljana, Slovenia*
PROCEEDINGS PRESENTATION: scOrange – A Tool for Hands-On Training of Concepts from Single Cell Data Analytics

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **KEYNOTE: Daniel Barker,** *The University of Edinburgh, United Kingdom*
4273pi: Bringing practical bioinformatics to schools in Scotland

3:00 PM **David Martin,** *University of Dundee, United Kingdom*
Scaffolding undergraduate student learning with video instruction — a case study

3:20 PM **Ozlem Tastan Bishop,** *Rhodes University, South Africa*
Challenges and solutions to teach structural bioinformatics to biochemistry undergraduate students in short university modules

3:40 PM **Elodie Laine,** *Sorbonne Université, France*
Meet-U: Educating through Research Immersion

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Suzanne Duce,** *University of Dundee, United Kingdom*
Crossing continents, experience of using video sharing services to deliver biological sequence analysis and visualisation training around the world

5:00 PM **KEYNOTE: Victoria Nembaware,** *University of Cape Town, South Africa*
Overview of The African Genomic Medicine Training Initiative: a Community-Driven Genomic Medicine Competency-Based Training Model for Nurses in Africa (Travel Fellowship funded by GOBLET)

THURSDAY, JULY 25

Workshop on Education in Bioinformatics (WEB)

8:35 AM **Cath Brooksbank,** *EMBL-European Bioinformatics Institute, United Kingdom*
WEB Introduction

8:40 AM **KEYNOTE: Nicola Mulder,** *University of Cape Town, South Africa*
Developing guidelines and resources for bioinformatics trainers and educators

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

10:20 AM **Jessica M. Lindvall,** *NBIS, Sweden*
The Mastery Rubric for Bioinformatics: A tool to support curriculum design and evaluation

10:40 AM **Cath Brooksbank,** *EMBL-European Bioinformatics Institute, United Kingdom*
WEB Workshop Session

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

MLCSB: Machine Learning in Computational and Systems Biology

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: SAN FRANCISCO (3RD FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/mlcsb.php

WEDNESDAY, JULY 24

10:15 AM *Welcome and Start*

10:20 AM **KEYNOTE: Gunnar Ratsch,** *ETH Zurich, Switzerland*
Representation Learning of Patient Health States

11:20 AM **Lisa Handl,** *University of Tübingen, Germany*
PROCEEDINGS PRESENTATION: Weighted Elastic Net for Unsupervised Domain Adaptation with Application to Age Prediction from DNA Methylation Data

11:40 AM **Jakob Richter,** *TU Dortmund, Germany*
PROCEEDINGS PRESENTATION: Model-Based Optimization of Subgroup Weights for Survival Analysis

12:00 PM **Héctor Climente-González,** *Institut Curie, France*
PROCEEDINGS PRESENTATION: Block HSIC Lasso: model-free biomarker detection for ultra-high dimensional data

Spotlight Session 1

12:20 PM **Jisoo Park,** *University of California San Diego, United States*
DrugCell: A visible neural network to guide precision medicine

Andrew Guy, *RMIT University, Australia*
Identifying glycan motifs using a novel tree representation that considers terminal connections

Murat Can Cobanoglu, *UT Southwestern Medical Center, United States*
Generative classification of cell types in scRNA-seq data

Rakesh Kaundal, *Utah State University, United States*
Comparative machine learning framework for efficient prediction of host-pathogen protein-protein interactions using sequence-based features

Savvas Kinalis, *University of Copenhagen, Denmark*
Deconvolution of autoencoders to learn biological modules from single cell mRNA sequencing data

Andreas Kopf, *ETH Zürich, Switzerland*
CellGen: A mixture of expert autoencoder to cluster single cell data

An-Phi Nguyen, *IBM Research Zurich, Switzerland*
Interpretability for computational biology

Angela Lopez-Del Rio, *Polytechnic University of Catalonia, Spain*
Bijective Encoding of Proteins In a Scalable Distributed Deep Learning Framework

Matteo Manica, *IBM, Switzerland*
Towards Explainable Anticancer Compound Sensitivity Prediction via Multimodal Attention-based Convolutional Encoders

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12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Benjamin Chidester,** *Carnegie Mellon University, United States*
PROCEEDINGS PRESENTATION: Rotation equivariant and invariant neural networks for microscopy image analysis

2:20 PM **Lei Du,** *Northwestern Polytechnical University, China*
PROCEEDINGS PRESENTATION: Identifying progressive imaging genetic patterns via multi-task sparse canonical correlation analysis: a longitudinal study of the ADNI cohort

Spotlight Session 2

2:40 PM **Hakime Öztürk,** *Boğaziçi University, Turkey*
WideDTA: prediction of drug-target binding affinity

Xiaobo Zhou, *Tongji University, China*
RLFimpute: Using reinforcement learning framework for imputation of scRNA-seq data

Arjun Baghela, *The University of British Columbia, Canada*
Using Gene Expression and Clinical Data Profiles to Predict Sepsis at ER Admission

Da-Bin Lee, *Soongsil University, South Korea*
Applying deep neural networks with feature extraction to target-gene expression prediction from landmark genes

Jitao David Zhang, *F. Hoffmann-La-Roche AG, Switzerland*
Deep neural networks predict drug-induced histopathology based on gene expression

Dongpin Oh, *Pusan National University, South Korea*
CNN-Peaks: ChIP-seq peak detector using convolution neural networks

3:00 PM **KEYNOTE: Barbara Engelhardt,** *Princeton University, United States*
Sequential decision-making for biomedical data: challenges and opportunities

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4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Dohoon Lee,** *Seoul National University, South Korea*
PROCEEDINGS PRESENTATION: PRISM: Methylation Pattern-based, Reference-free Inference of Subclonal Makeup

5:00 PM **Martin Ester,** *Simon Fraser University, Canada*
PROCEEDINGS PRESENTATION: Collaborative Intra-Tumor Heterogeneity Detection

5:20 PM **Judith Abécassis,** *Institut Curie, France*
Clonesig: Joint Inference of intra-tumor heterogeneity and signature deconvolution in tumor bulk sequencing data

5:40 PM **Aline Marguet,** *University Grenoble Alpes, France*
PROCEEDINGS PRESENTATION: Inheritance and variability of kinetic gene expression parameters in microbial cells: Modelling and inference from lineage tree data

6:00 PM *Posters*

MLCSB: Machine Learning in Computational and Systems Biology

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: SAN FRANCISCO (3RD FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/mlcsb.php

THURSDAY, JULY 25

8:35 AM *Welcome and Start*

8:40 AM **Brandon Carter,** *Massachusetts Institute of Technology, United States*
PROCEEDINGS PRESENTATION: DeepLigand: accurate prediction of MHC class I ligands using peptide embedding

9:00 AM **Xiangrui Zeng,** *Carnegie Mellon University, United States*
PROCEEDINGS PRESENTATION: Adversarial domain adaptation for cross data source macromolecule in situ structural classification in cellular electron cryo-tomograms

9:20 AM **Anvita Gupta,** *Stanford University, United States*
Targeted Genetic Optimization of TF Binding with Neural Editing Architectures

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

10:15 AM **KEYNOTE: William Noble,** *University of Washington, United States*
NOT all the things: submodular representative set selection for when big data is too big

11:15 AM **Hossein Sharifi-Noghabi,** *Simon Fraser University, Canada*
PROCEEDINGS PRESENTATION: MOLI: Multi-Omics Late Integration with deep neural networks for drug response prediction

11:35 AM **Danila Bredikhin,** *EMBL, Germany*
Multi-group factor analysis framework for structured single-cell omics data

11:55 AM **Welles Robinson,** *University of Maryland, United States*
PROCEEDINGS PRESENTATION: Modeling Clinical and Molecular Covariates of Mutational Process Activity in Cancer

12:15 PM **Gurnit Atwal,** *University of Toronto, Canada*
A deep learning system can accurately classify primary and metastatic cancers based on patterns of passenger mutations

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **KEYNOTE: Marinka Zitnik,** *Stanford University, United States*
Relational Representation Learning as a New Approach in Computational Biology

3:00 PM **Dhouha Grissa,** *University of Copenhagen, Denmark*
Data Mining of Alcoholic Liver Disease Progression from Health Registry Data

3:20 PM **Jacob Schreiber,** *University of Washington, United States*
A pitfall for machine learning methods aiming to predict across cell types

3:40 PM **Anupama Jha,** *University of Pennsylvania, United States*
Interpretation of deep learning models in genomics: splicing codes as a case study

4:00 PM **Jose Juan Almagro Armenteros,** *Technical University of Denmark*
Learning the language of life

4:20 PM *Concluding Remarks*

ISCB TOWN HALL
MONDAY JULY 22

12:45 PM – 1:45 PM

ROOM: Singapore

Learn more about ISCB

Shape the future of ISCB by providing feedback and suggestions.

RNA (IRB): Computational RNA Biology

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: SINGAPORE (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/rna.php

WEDNESDAY, JULY 24

10:15 AM	**Yoseph Barash,** *University of Pennsylvania, United States* **Klemens Hertel,** *University of California, Irvine, United States* **Michelle Scott,** *University of Sherbrooke, Canada* *Opening Remarks*
10:20 AM	**Ana Claudia Marques,** *Université de Lausanne, Switzerland* *Translation is required to initiate miRNA-dependent decay of endogenous transcripts*
11:00 AM	**Kritika Karri,** *Boston University, United States* *Single cell transcriptomics of liver-expressed long non-coding RNAs*
11:20 AM	**Xin Lai,** *University Hospital Erlangen, Germany* *MiR-205-5p and miR-342-3p cooperate in the repression of the E2F1 transcription factor in the context of anticancer chemotherapy resistance*
11:30 AM	**Maina Bitar,** *QIMR Berghofer Medical Research Institute, Australia* *Transcriptional Landscape of Human Progenitor Cell Populations*
11:40 AM	**Florian Erhard,** *Julius-Maximilians-Universität Würzburg, Germany* *scSLAM-seq and GRAND-SLAM reveal core features of CMV-induced regulation in single cells*
12:00 PM	**Reut Shalgi,** *Technion, Israel* *Cellular proteostasis collapse and decoupling between transcription and translation regulation in mammalian senescence*
12:20 PM	**Song-Yao Zhang,** *Northwestern Polytechnical University, China* *PROCEEDINGS PRESENTATION: FunDMDeep-m6A: Identification and prioritization of functional differential m6A methylation genes.*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Peter White,** *The Institute for Genomic Medicine at Nationwide Children's Hospital, United States* *Global analysis of human mRNA folding demonstrates significant population constraint of disruptive synonymous variants*
2:20 PM	**David S.M. Lee,** *University of Pennsylvania, United States* *Integrative analysis of untranslated regions in human messenger RNAs uncovers G-quadruplexes as constrained regulatory features*
2:40 PM	**Russell Hamilton,** *University of Cambridge, United Kingdom* *RNA 2D/3D structure prediction with a consensus of contact methods*
3:00 PM	**Liang Huang,** *Oregon State University and Baidu Research USA, United States* *PROCEEDINGS PRESENTATION: LinearFold: Linear-Time Approximate RNA Folding by 5'-to-3' Dynamic Programming and Beam Search*
3:20 PM	**Michael Peeri,** *Tel-Aviv University, Israel* *High resolution analysis of functional regions of mRNA folding in protein-coding sequences across the tree of life*
3:30 PM	**Guilia Corsi,** *University of Copenhagen, Denmark* *Feature reduction of CRISPR-Cas9 on-target efficiency prediction improves the accuracy*
3:40 PM	**Mikel Heranez,** *University of Illinois at Urbana-Champaign, United States* *ShiRIOc: A robust computational approach to analyze Polysome Profiling RNA-Seq Data*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Rolf Backofen,** *Albert-Ludwigs-University Freiburg, Germany* *What can we do with RNA-protein interaction?*
5:00 PM	**Gabrielle Deschamps-Francoeur,** *Université de Sherbrooke, Canada* *Predicting canonical and non-canonical box C/D snoRNA interactions using machine learning*
5:20 PM	**Xinan Yang,** *The University of Chicago, United States* *Chromatin-enriched RNAs mark both active and repressive cis-regulation: a computational analysis of nuclear RNA-seq*
5:40 PM	**Gulden Olgun,** *Bilkent University, Turkey* *miRCoop: Identifying Cooperating Pairwise miRNAs \\ via Kernel Based Interaction Test*
5:50 PM	**Liang Huang,** *Oregon State University and Baidu Research USA, United States* *LinearCoFold: Two-Strand RNA Folding in Linear Time*
8:00 PM	*RNA COSI Dinner, Hotel Sorell Merian*

RNA (IRB): Computational RNA Biology

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 24 AND THURSDAY, JULY 25

ROOM: SINGAPORE (2ND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/rna.php

THURSDAY, JULY 25

8:30 AM **Chen Yang,** *BC Cancer Genome Sciences Centre, Canada*
Is this the "end"? Termin(A)ntor: Transcriptome annotation with deep learning

8:50 AM **Joël Simoneau,** *Université de Sherbrooke, Canada*
RNA-seq methodological landscape: the ignored importance of the choice of genome annotations

9:00 AM **Jasleen Grewal,** *Canada's Michael Smith Genome Sciences Centre, Canada*
Learning biologically meaningful representations of cancer transcriptomes with hierarchical Variational Bayes

9:10 AM **Svetlana Shabalina,** *NCBI/NLM/NIH, United States*
Complexity and evolution of the mammalian transcriptome: the architecture of alternative transcription and processing

9:30 AM **Ka Ming Nip,** *University of British Columbia, Canada*
Reference-free transcriptome assembly of nanopore RNA-seq data

9:40 AM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

10:15 AM **Yoseph Barash,** *University of Pennsylvania, United States*
Klemens Hertel, *University of California, Irvine, United States*
Michelle Scott, *University of Sherbrooke, Canada*
Introduction to Computational RNA COSI

10:20 AM **Uwe Ohler,** *Max Delbrück Center for Molecular Medicine, Germany*
Computational approaches to dissect post-transcriptional gene regulation

11:00 AM **Runxuan Zhang,** *The James Hutton Institute, United Kingdom*
Innovative advanced computational solutions for improved gene and transcript level analysis using RNA-seq

11:20 AM **Stefan Mautner,** *Albert-Ludwigs-University Freiburg, Germany*
PROCEEDINGS PRESENTATION: ShaKer: RNA SHAPE prediction using graph kernel

11:40 PM **Zichao Yan,** *McGill University, Canada*
PROCEEDINGS PRESENTATION: Prediction of mRNA subcellular localization using deep recurrent neural networks

12:00 PM **Francisco Pardo Palacios,** *Centro de Investigación Príncipe Felipe (CIPF), Spain*
Novel bioinformatics tools to assess the functional impact of alternative isoform usage

12:10 PM **Barry Slaff,** *University of Pennsylvania, United States*
Adjusting for known and unknown confounding factors in RNASeq based splicing analysis

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Mihaela Zavolan,** *Biozentrum – Universität Basel, Switzerland*
Regulation of translation in relation to cell fate

2:40 PM **Rukeia El-Athman,** *Humboldt University of Berlin and Charité – University Medicine Berlin, Germany*
A landscape of circadian and ultradian alternative splicing in mammalian tissues

3:00 PM **Hagen Tilgner,** *Cornell University, United States*
Isoforms across single cells and brain cell types.

3:20 PM **Ángeles Arzalluz-Luque,** *Polytechnic University of Valencia, Spain*
Measuring isoform co-expression in single-cell RNAseq successfully decodes splicing coordination as a key determinant of neural cell-type identity

3:40 PM **Shalom Hillel Roth,** *Bar-Ilan University, Israel*
Genome wide quantification of ADAR A-to-I RNA editing activity

4:00 PM **Zhandong Liu,** *Baylor College of Medicine, United States0PolyA-miner: Accurate Estimation of Alternative Poly-Adenylation from 3'Seq data using Non-negative matrix factorization and Vector algebra*

4:20 PM **Yoseph Barash,** *University of Pennsylvania, United States*
Klemens Hertel, *University of California, Irvine, United States*
Michelle Scott, *University of Sherbrooke, Canada*
Wrap-up and Poster Prizes

4:40 PM GRAB AND GO REFRESHMENT BREAK, FOYER 2ND FLOOR

ELIXIR

SPECIAL PRESENTATIONS

MONDAY, JULY 22

ROOM: OSAKA/SAMARKAND (3RD FLOOR)

www.iscb.org/cms_addon/conferences/ismbeccb2019/elixir.php

MONDAY, JULY 22

10:15 AM	**Gary Saunders,** *ELIXIR Hub, United Kingdom* **Jonathan Tedds,** *ELIXIR Hub, United Kingdom* *The ELIXIR::GA4GH Strategic Partnership*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Gary Saunders,** *ELIXIR Hub, United Kingdom* **Frederic Haziza,** *ELIXIR-ES, CRG, Spain* *ELIXIR Beacons: Federating Data Discoverability*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Kenneth McLeod,** *ELIXIR, United Kingdom* **Mateusz Kuzak,** *Dutch Techcentre for Life Sciences, The Netherlands* **Leyla Garcia,** *ELIXIR Hub, United Kingdom* *Bioschemas and 4OSS: recommendations on metadata for tools*

BD2K

SPECIAL PRESENTATIONS

TUESDAY, JULY 23

ROOM: OSAKA/SAMARKAND (3RD FLOOR)

www.iscb.org/cms_addon/conferences/ismbeccb2019/bd2k.php

TUESDAY, JULY 23

10:15 AM	**Susan Gregurick,** *NIH/NIGMS, United States* *Introduction to the BD2K Special Sessions*
10:20 AM	**Susan Gregurick,** *NIH/NIGMS, United States*
10:40 AM	**Phil Bourne,** *University of Virginia, PLoS, United States*
11:00 AM	**Neil Sarkar,** *Brown University, JAMIA Open, United States*
11:20 AM	**Elisa De Ranieri,** *Nature Publishing, United Kingdom*
11:40 AM	**Kim Pruitt,** *NIH/NLM/NCBI, United States*
12:00 PM	*BD2K Session 1 Panel Discussion*
12:40 PM	LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)
2:00 PM	**Jennie Larkin,** *NIH/NIDDK, United States*
2:20 PM	**Henning Hermjakob,** *EMBL-EBI, United Kingdom*
2:40 PM	**Ian Fore,** *NIH/NCI, United States*
3:00 PM	**Avi Ma'ayan,** *Mount Sinai, United States*
3:20 PM	*BD2K Session 2 Panel Discussion*
4:00 PM	COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR
4:40 PM	**Hongfang Liu,** *Mayo Clinic, United States*
5:00 PM	**Zhiyong Lu,** *NIH/NLM/NCBI, United States*
5:20 PM	**Lars Juhl Jensen,** *University of Copenhagen, Denmark*
5:40 PM	*BD2K Session 3 Panel Discussion*

Markthalle Networking and Social

TUESDAY JULY 23, 8:00 PM – 10:00 PM

Join delegates on Tuesday, July 23 for an evening of informal networking and fun.

Over 20 vendors will be available offering a variety of food styles and beverage options.

The venue will have areas identified by COSI groups where delegates can look for colleagues to network with that have similar scientific interests.

Travel to Markthalle by tram using your Basel card.

MARKTHALLE, STEINENTORBERG 20 CH-4051 BASEL

No participation fee is required!
You are responsible for your own food and beverages purchases.
While most vendors accept credit cards not all do.
There is an ATM located at the venue for your convenience.

Technology Track Presentations

TUESDAY, JULY 23 AND WEDNESDAY, JULY 24

ROOM: KAIRO 1/2 (GROUND FLOOR)

https://www.iscb.org/cms_addon/conferences/ismbeccb2019/technologytrack.php

Session Chairs:

Hagit Shatkay, *University of Delaware, United States*
Dominic Clark, *Pistoia Alliance, Inc., United Kingdom*

TUESDAY, JULY 23

10:20 AM **Fabio Madeira,** *EMBL-EBI, United Kingdom*
EMBL-EBI Tools as a service

10:40 AM **Young mi Park,** *EMBL-EBI, United Kingdom*
EBI Search API – Looking for more

11:00 AM **Blake Sweeney,** *European Molecular Biology Laboratory, United Kingdom*
RNAcentral: A hub of information for non-coding RNA sequences

11:20 AM **Andrew Nightingale,** *EMBL-EBI, United Kingdom*
Protein services, tools and visual components enabling integration and interpretation of the UniProt Knowledgebase (UniProtKB)

11:40 AM **Ulrich Walter,** *IBM Deutschland GmbH, Germany*
IT Infrastructure for AI and Analytics in medicine and research

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **David Hiatt,** *WekaIO, United States*
Storage Systems that Support Tomorrow's Life Science Applications Today

2:20 PM **Anna Calinawan,** *Icahn School of Medicine at Mount Sinai, United States*
The CPTAC Data Browser: A new generation of data visualization tools from the clinical proteomic tumor analysis consortium

2:40 PM **Chunlei Wu,** *The Scripps Research Institute, United States*
BioThings API: Promoting best-practices via a biomedical API development ecosystem

3:00 PM **Robert Gentleman,** *23andMe, United States*
Big Data Meets Drug Target Discovery

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Emmy Tsang,** *eLife, United Kingdom*
Towards a production-ready solution for reproducible articles

WEDNESDAY, JULY 24

10:20 AM **Pengyuan Li,** *University of Delaware, United States*
PDFigCapX and FigSplit – A Pipeline for Extracting Figures, SubFigures and Captions from Biomedical Publications: Supporting bio-curation and discovery

10:40 AM **Michael Sternberg,** *Imperial College London, United Kingdom*
Phyre, PhyreRisk and Missense3D: Modelling protein structure and the impact of missense variants

11:00 AM **Juan S Medina,** *Memorial Sloan Kettering Cancer Center, United States*
Isabl – An open-source patient-centric framework for scalable bioinformatics operations

11:20 AM **Morgan Taschuk,** *Ontario Institute for Cancer Research, Canada*
MISO LIMS : Managing information for sequencing operations

11:40 AM **Daniel Marbach,** *Roche Innovation Center Basel, Switzerland*
Jitao David Zhang, *Roche Innovation Center Basel, Switzerland*
Fabian Birzele, *F. Hoffmann-La Roche Ltd., Switzerland*
Bioinformatics and Exploratory Data Analysis in Pharmaceutical Industry: Applications to drug research and development.

12:40 PM LUNCH (FOR PURCHASE), HALL 4.1 (1ST FLOOR)

2:00 PM **Philip Stegmaier,** *geneXplain GmbH, Germany*
The geneXplain platform for bioinformatic and systems biology analysis

3:00 PM **Kees van Bochove,** *The Hyve, The Netherlands*
Fairspace

4:00 PM COFFEE BREAK WITH EXHIBITORS, FOYER 2ND FLOOR

4:40 PM **Gerardo Tauriello,** *SIB Swiss Institute of Bioinformatics & University of Basel, Switzerland*
SWISS-MODEL: Homology modelling of protein structures and complexes

5:00 PM **Erich Baker,** *Baylor University, United States*
GeneWeaver.org: A RESTful service for multi-species data integration in functional genomics

5:20 PM **Ian Sillitoe,** *UCL, United Kingdom*
CATH: Tools and datasets to analyse protein structure, sequence and function

Birds of a Feather

TUESDAY, JULY 23 • WEDNESDAY, JULY 24 • THURSDAY, JULY 25

12:45 PM – 1:45 PM

https://www.iscb.org/ismbeccb2019-program/ismbeccb2019-bof

TUESDAY, JULY 23

The ISCB code of conduct

Organizers: Lucia Peixoto, ***Washington State University, United States***, and
Casey Greene, ***University of Pennsylvania, United States***

ROOM: BOSTON 1/2 (GROUND FLOOR)

WEDNESDAY, JULY 24

Actionable ways to increase diversity in our community: Next steps for ISCB EDI TaskForce

Organizer: Malvika Sharan, ***EMBL Heidelberg, Germany***

ROOM: BOSTON 1/2 (GROUND FLOOR)

Dos and Don'ts checklist for computational training

Organizer: Sara El-Gebali, ***EMBL-EBI***

ROOM: SHANGHAI 1/2 (GROUND FLOOR)

Integrative queryable genomics with InterMine

Organizer: Yo Yehudi, ***University of Cambridge, United Kingdom***

ROOM: SHANGHAI 3/4 (GROUND FLOOR)

Welcome to BOSC (the Bioinformatics Open Source Conference)

Organizer: Monica Munoz-Torres, ***BOSC***

ROOM: DELHI (GROUND FLOOR)

Portable data analysis workflows with the CWL standards – CWL v1.1 update and community meetup

Organizers: Michael R. Crusoe, ***ELIXIR-NL & ELIXIR Interoperability Platform***

ROOM: KAIRO 1/2 (GROUND FLOOR)

Bioinformaticians in Aging & Senescence Research

Organizer: Georg Fuellen, ***Rostock University Medical Center, Germany***

ROOM: OSAKA/SAMARKAND (3RD FLOOR)

THURSDAY, JULY 25

Open Bioinformatics Foundation Board Meeting

Organizer: Heather Wiencko, ***OBF***

ROOM: DELHI (GROUND FLOOR)

Cytoscape Roadmap and Feedback

Organizer: Scooter Morris, ***University of California, San Francisco, United States***

ROOM: SHANGHAI 3/4 (GROUND FLOOR)

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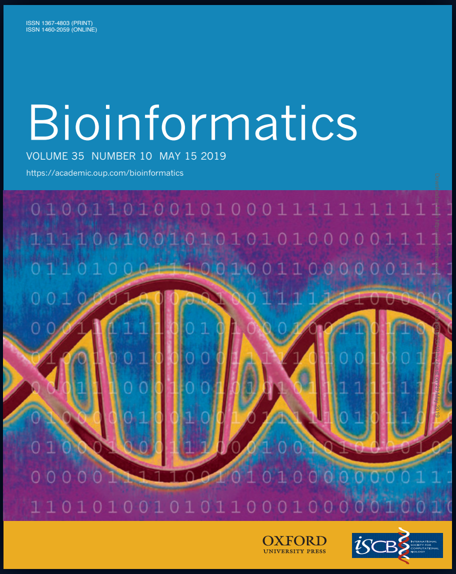

ISCB CONGRATULATES THE 2019 ISCB FELLOWS

The ISCB Fellows program was created to honor members who have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. During the 2009 inaugural year of the program, the ISCB Board of Directors unanimously conferred Fellows status on the seven winners-to-date of the ISCB Accomplishment by a Senior Scientist Award. 2019 marks the 10th anniversary of the program. Each year since 2010, ISCB has sought Fellows nominations from our members, with eligibility restrictions based on selection criteria focused most heavily on the significance of scientific contributions, and service to our field and to ISCB.

This year we were pleased to receive many excellent nominations, and the Fellows Selection Committee members carefully considered each one. Ultimately, four nominees were elected as this year's newest Fellows:

Vineet Bafna, Professor, Computer Science and Engineering, University of California, San Diego (UCSD), United States; an innovator who developed many bioinformatics algorithms for solving important biological problems and a leading researcher in the area of Cancer Genomics, Population Genetics, and Proteogenomics.

Vineet Bafna is the current director of the Bioinformatics and Systems Biology PhD Program (BISB) at UCSD. He joined the UCSD faculty on July 1, 2003, after seven years in the biosciences industry. After receiving his B.Tech from the Indian Institute of Technology in 1989, he was awarded a Ph.D. in Computer Science from Pennsylvania State University in 1994 and was a postdoctoral researcher at its Center for Discrete Mathematics and Theoretical Computer Science for two years. From 1996-99, Bafna was a senior investigator at SmithKline Beecham, conducting research on DNA signaling, target discovery and EST assembly. From 1999 to 2002, he worked at Celera Genomics, ultimately as Director of Informatics Research, at a time when Celera was decoding the human genome. Bafna has been on the Steering and Program Committees of the past several annual International Conferences on Research in Computational Biology (RECOMB), and is on the editorial board of the Journal of Bioinformatics and Computational Biology (JBCB). He has published over two dozen articles in major journals and conference proceedings. Bafna is a leading expert in bioinformatics. He has published on many aspects of this emerging field, including genome rearrangements, multiple alignments, RNA structure, gene finding, DNA signals, mass spectrometric data analysis, and human population genetics.

Eleazar Eskin, Professor, Computer Science, Human Genetics, University of California, Los Angeles, United States; a leading computer scientist working on computational problems in human genetics and educator and developer of advanced educational programs for computer scientists, biologists, and statisticians, in computational biology.

Eleazar Eskin received his PhD in Computer Science from Columbia University in 2002, and conducted postdoctoral studies at Hebrew University in Jerusalem. After serving as Assistant Professor in Residence at UCSD (2003-2006), he moved to UCLA, where he received a prestigious Sloan Foundation Research Fellowship (2009). After moving up through the ranks at UCLA and receiving multiple university teaching prizes along the way, he is now serves as the inaugural chair for the UCLA Department of Computational Medicine, jointly housed in the UCLA David Geffen School of Medicine and Samueli School of Engineering. He is also a Professor in the Departments of Computer Science and Human Genetics. Eleazar's current research interests are in the relationship between human variation and human disease. His group's research attempts to understand the genetic basis of disease by analyzing human variation data and attempting to discover functional variants which contribute to disease. Indeed, he has consistently been in the notable position of having the most accepted papers to RECOMB. Eleazar is the recipient of the Alfred P. Sloan Foundation fellowship. .He has served as Associate editor of Americal Journal of Human Genetics (2012-2015) and Genetics (2015-present). He has done lots of service for ISCB-related conferences and over the last several years has run the popular Computational Genomics Summer Institute (CGSI) at UCLA, which brings together top researchers in the field with the common goal of educating the next generation.

Xiaole Shirley Liu, Professor, Biostatistics, Harvard T.H. Chan School Of Public Health, Harvard School of Public Health, Co-director, Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, United States; an innovative and prolific computational cancer biologist.

X. Shirley Liu is a Professor in the Department of Biostatistics and Computational Biology at the Dana-Farber Cancer Institute and Harvard School of Public Health. Born in China, she did two years of undergraduate studies at Peking University before transferring to Smith College where she received her BA in Biochemistry and Computer Science in 1997. She received her PhD in Biomedical Informatics and a PhD minor in Computer Science from Stanford University in 2002. Liu is a leading computational biologist with expertise in cancer epigenetics. Her research focuses on integrating data from ChIP-seq, RIP-seq, DNase-seq, MNase-seq, RNA-seq, and other high throughput genomics data to model the specificity and function of transcription factors, chromatin regulators and lncRNAs in tumor development, progression, drug response and resistance. Her laboratory has developed a number of widely used algorithms for transcription factor motif finding, ChIP-chip/seq and DNase-seq data analysis. In epigenetics, she and colleagues generated the first high-throughput nucleosome map of the human genome and were the first to use the dynamics of nucleosome and DNase hypersensitivity to predict driving transcription factors and their genome-wide binding in a biological process. In cancer biology, she and colleagues identified the function of estrogen receptor, androgen receptor, and FoxA1 in breast and prostate cancers, found the direct targets of NOTCH1 in T-LL, and reported the switch of EZH2 from a transcriptional repressor as part of the PRC2 to a transcriptional co-activator in hormone independent prostate cancers. She received a Sloan Research Fellowship in 2008; was named a Yangtze River Scholar and 1000 Talent Scholar in China in 2012 and 2013, resp; and received the Richard E. Weitzman Outstanding Early Career Investigator Award in 2016.

ISCB-Africa ASBCB Conference on Bioinformatics

Kumasi, Ghana
November 11-15, 2019

CONFERENCE TOPICS

- Data governance
- Challenging traditional research ecosystems in Africa
- Data for OneHealth
- Open Science and Open Data
- AI in genomics and precision medicine
- Informatics for Biobanks
- Pathogens genomics
- Metagenomics
- Population Genetics, Variation and Evolution
- Plant genomics (omics)
- Biomedical Ethics
- Drug design and discovery
- General Bioinformatics and Computational Biology
- Bioinformatics Education

WHEN
November 11-15, 2019

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Kumasi, Ghana

COST*
ISCB & ASBCB Members
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Non-Members
Professional $350 | Student & Post Doc $200

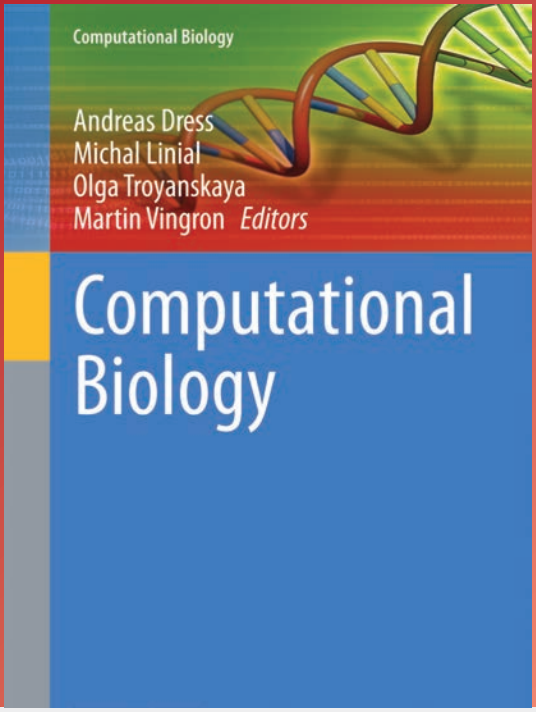
https://www.iscb.org/iscbafrica2019

SUBMISSION DEADLINES

- Abstract Submission	August 30, 2019
- Poster Submission	September 30, 2019

Marie-France Sagot, Director of Research (DR1) INRIA, Head of Erable-BAOBAB Teams, INRIA Grenoble Rhône-Alpes & Laboratoire de Biométrie et Biologie Évolutive (LBBE), Université Claude Bernard, Universite Claude Bernard, France; a key figure linking the South-American and European bioinformatics communities. She is best known for her sharp algorithmic work. Specifically, her work on exact algorithms for structured or approximate motif search using suffix trees was foundational in the analysis of transcriptional regulatory sequences.

Marie-France Sagot was born in Brazil where she obtained a BSc in Computer Science in 1991 at the University of São Paulo, Brazil. She then went to France, her second country, where she obtained a PhD and Habilitation in Theoretical Computer Science in 1996 and 2000, respectively, at the University of Marne-la-Vallée. She was appointed Junior Researcher at the Pasteur Institute in Paris from 1997 to 2001, before joining the French National Institute of Research in Computer Science and Control (Inria) and the Laboratory of Biometry and Evolutionary Biology at the University of Lyon (UCL) and CNRS, France, where she currently serves as Director of Research Class Exceptional (DR0) Inria and head of the Inria European team ERABLE and UCL-CNRS team BAOBAB. Her main research interests are computational biology, algorithmics, and combinatorics. In computational biology, she is more specifically interested in genomics, NGS, small RNAs, (co-) evolution and (co-)phylogeny, biological networks including metabolism and regulation, and symbiosis. She co-founded the French National Conference on Bioinformatics (JOBIM) and is a member since its founding of the Steering Committee of the European Conference on Computational Biology (ECCB).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15 YEARS DEVELOPING THE NEXT GENERATION OF COMPUTATIONAL BIOLOGISTS

By: Nilson Coimbra (Co-chair — SCS 2019), Amel Bekkar (Chair — SCS 2019), Alexander Monzon (Manager — SCS 2019) and Farzana Rahman (ISCB Board of Directors Representative)

In July 2019, the ISCB Student Council (ISCB-SC) will celebrate its 15th anniversary during the ISMB/ECCB 2019. Over its fifteen years of operation, the ISCB Student Council has grown to over 400 registered members and more than 1000 volunteers across the globe. Our volunteers work hard to uphold the ISCB-SC mission that includes promoting the development of the next generation computational biologists, organising scientific events, offering networking opportunities, soft-skills training, educational resources, and career advice, to foster the exchange of ideas and knowledge[1].

The Student Council Symposium (SCS) has emerged to be the most fulfilling flagship event toward the success series of SC aligned to our mission[2]. Through the commitment of the local Regional Student Groups (RSGs) in Africa, Europe, Latin-America and Asia Pacific, we set the flag of our SC symposiums in Europe , Latin America and Africa constituting satellite events to their corresponding continental ISCB conferences (ECCB, ISCB-LA and ISCB Africa). To find out more information about your local RSG and upcoming regional events, visit our booth 3 during ISMB/ECCB 2019 in Basel.

Make sure you visit us during the ISMB/ECCB 2019 and let us know how we can further our mission creating opportunities for students and researchers or ask us how to get involved. Don’t forget to connect with the Student Council via our website (iscbsc.org) and social media channels (Twitter: @iscbsc & Facebook: /iscbsc); these are our main sources for staying in touch with the global computational biology student community. More information about the SC can also be found on Wikipedia[1] (where we welcome your help in keeping our entry up to date).

We encourage you to get in touch with your peers to find out about events and initiatives for computational biology students — no matter where in the world you are. If you would like to volunteer in our activities, please register at volunteer.iscbsc.org or visit Booth 3 during ISMB/ECCB 2019!

Figure 01: Word cloud from the titles of accepted abstracts as talks at the 15th SCS at ISMB/ECCB 2019

STUDENT COUNCIL SYMPOSIUM 2019

The ISCB Student Council Symposium is our flagship event. This annual gathering brings together students, post docs and early-career researchers in the fields of Computational Biology and Bioinformatics. This one-day event is organized mostly by students and early career scientists from all over the world. It provides, for many of them, a first opportunity to present their work to an international audience and to network with those that will become their peers and potential collaborators at later career stages.

This year we reach the 15th edition of the symposium and we are pleased to offer more than 25 presentation (full/flash) and over 60 posters representing a wide variety of topics. We are delighted to have on board two outstanding keynotes: Dr. Christophe Dessimoz (Group Leader, Swiss Institute for Bioinformatics), Dr. Barbara Treutlein (Max Planck Research Group Leader/Tenure-Track Assistant Professor at TU Munich — Germany), and an industrial talk from Dr. Fabian Birzle (Senior Principal Scientist Bioinformatics — Roche Pharmaceutical Research and Early Development). Thanks to the generous support of our sponsors: Harvard Medical School, Roche, Cambridge University Press, Swiss Institute of Bioinformatics, Springer Nature, PLOS and Oxford Academic, we have been able to provide travel fellowships to 5 students.

You can help us spread the world about the SCS 2019 by letting your colleagues know, referring to our website and using the hashtag #SCS19 on social media. Keep in touch with the latest SCS 2019 activities at symposium.iscbsc.org. We look forward to welcoming you on July 21st, in the beautiful city of Basel!

REFERENCES

[1] Parisi D, Olguín-Orellana GJ, Draizen EJ et al. Nurturing tomorrow’s leaders: The ISCB Student Council Symposia in 2018 [version 1; peer review: not peer reviewed]. F1000Research 2019, 8(ISCB Comm J):34

[2] Hassan M, Namasivayam AA, DeBlasio D, et al.: Reflections on a journey: a retrospective of the ISCB Student Council symposium series. BMC Bioinformatics. 2018; 19(Suppl 12): 347.

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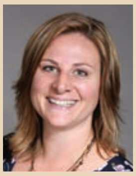

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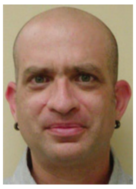

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OF INTEREST

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https://www.ptbi.org.pl/website/conferences/ptbi2019/

International Symposium on Mathematical and Computational Oncology (ISMCO)

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GIW/ABACBS 2019

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AUSTRALIA — NSW — SYDNEY

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https://www.abacbs.org/conference2019/about

2019 ISCB Student Regional Group — Southeast USA Computational Biology Symposium

**UNITED STATES — FL —
ST. PETERSBURG**

DEC 13, 2019 THROUGH DEC 14, 2019

http://rsg-se-usa.iscbsc.org/

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