INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

SUMMER 2020 | ISSUE 02

ISCBNEWSLETTER

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LETTER FROM ISCB PRESIDENT

Dear ISCB Members & Colleagues,

What a year this has been! 2020 has been a year for the record books. A year of highs and lows for ISCB. Since our last in-person conference in Basel where we celebrated a record-breaking attendance, ISCB has made innumerable progress and hit substantial goals.

ISCB reached our highest membership on record, launched the new ISCBlive program, introduced ISCB Academy webinar series, established new committees to better serve our membership, approved an environmental sustainability policy and so much more. Our society, membership and community reached new heights as we all faced a changed world forcing ISCB to adapt quickly to a new environment.

Since its founding in 1997, the International Society for Computational Biology, Inc. (ISCB), though faced with unforeseen disruption and a changed environment continues to strive for new heights, working towards our goal to be the leading professional society for particpants in the field of computational biology and bioinformatics, serving researchers, practioners, technicians, students and suppliers worldwide. It is because of ISCB's incredible volunteers and membership that it continues to adapt to new demands, envirnonemts and an ever changing field.

This year marks the 28th Intelligent Systems for Molecular Biology (ISMB) conference, a conference which has grown to become the world's largest bioinformatics/computational biology conference. We now introduce this years ISMB 2020 as a 100% virtual conference, bringing our membership and community the largest and most respected computational biology and bioinformatics meeting in the world.

If you are attending ISMB 2020, we hope you take advantage of the ability to browse the schedule at your leisure and even mark the talks that you are most interested in seeing. If you miss a talk, you have access to this platform until October 31, 2020, and all of the talks (and the virtual poster hall) presented will be available on-demand to watch at your convenience.

This issue of the ISCB newsletter is filled with great information including the celebration of the ISCB Fellows, ISCB Award Recipients, the virtual ISMB 2020 Conference Program, and much more.

Again, I would like to personally thank the many volunteers that keep our Society moving forward, the leadership of ISCB for their continued dedication and service, and all ISCB members for their support.

On behalf of the many contributing authors of this newsletter, we hope you enjoy!

Thomas Lengauer

Thomas Lengauer,
ISCB President

2020 ISCB INNOVATOR AWARD

X. SHIRLEY LIU

The International Society for Computational Biology (ISCB) Innovator Award recognizes a scientist who is within two decades of completing her or his graduate degree and has made significant contributions to the field of computational biology. The 2020 awardee is Dr. Xiaole Shirley Liu, Professor of Biostatistics and Computational Biology at the Harvard T.H. Chan School of Public Health and Co-Director of the Center for Functional Cancer Epigenetics at the Dana-Farber Cancer Institute. Liu will be recognized for her award and deliver a keynote presentation at the 2020 ISMB virtual meeting on July 13-16, 2020.

K.SHIRLEY LIU

from Basic Genomics to the Cancer Moonshot

X. Shirley Liu grew up in Tianjin, China and her elder brother sparked her interest in biology at an early age. She transferred from Peking University during her freshman year to pursue her undergraduate degree at Smith College in the United States. Liu was working towards a degree in biochemistry when she took a basic computer literacy course. From that class, Liu became drawn to computer programming and quickly immersed herself in computer science courses in her junior year. In summer 1996, she had a transformative experience, she recalled, “At the recommendations of my advisors Jeanne Powell and Steven Williams, I went to a University of Washington summer workshop in bioengineering and visited several universities in the West Coast. The visit to Stanford helped me realize how I could combine computer science and biology.” Liu graduated summa com laude from Smith College in 1997 with a double major in biochemistry and computer science. She pursued a PhD in the nascent field of biomedical informatics, with a minor in computer science, at Stanford University. At the time, Pat Brown and Ron Davis’ laboratories developed DNA microarrays to study gene expression, transcription regulation, and protein-DNA interactions. Under the guidance of her PhD advisors Douglas Brutlag and Jun Liu, she developed algorithms for finding protein-DNA binding motifs (BioProspector, MDscan, and MotifRegressor) from co-expressed gene clusters and chromatin-immunoprecipitation microarrays (ChIP-chip).

Liu accepted a faculty position right after PhD and became an assistant professor in the Department of Biostatistics and Computational Biology in the Dana-Farber Cancer Institute/Harvard School of Public Health in 2003. She recalled, “I was very lucky to collaborate with many wonderful colleagues at Harvard, especially with Myles Brown early in my faculty career. We share research interests in gene regulation and both believe the power of technology. Myles showed me how to use technologies cost effectively to tackle interesting biological problems, how to be open-minded when data lead us to unexpected results, and how to understand the mechanisms underlying our observations.” They developed numerous algorithms and tools (MAT, MACS, Cistrome, LISA, and MAESTRO) to model transcription factor binding and chromatin dynamics that are important to understand gene regulation in development and diseases. Liu and Brown continue to be close collaborators and have published around 70 papers together. As a member of the ENCODE consortium, Shirley Liu's Lab continued to maintain and update these algorithms and tools, which have helped many other scientists adopt new genomics technologies and generate hypotheses.

Liu became drawn to translational cancer research in 2012 after reading the Pulitzer Prize winning book, The Emperor of All Maladies, by Siddhartha Mukherjee. She had just been tenured and wanted to broaden her research areas and take more risks in her projects. Liu developed new methods (MAGeCK) to design and analyze genome-wide CRISPR/Cas9 knockout screens. Her team used computational approaches integrating large-scale compound and genetic screens, as well as functional genomics profiles from cancer cell lines and tumor cohorts, to refine our understanding of hormone receptor therapies, epigenetic inhibitors, gamma secretase inhibitors, receptor tyrosine kinase inhibitors, and immune checkpoint inhibitors in different cancers. She also developed novel algorithms TIMER and TRUST to comprehensively characterize tumor-infiltrating immune cells and immune receptor repertoires in over 10,000 tumors from The Cancer Genome Atlas. Liu continues to make significant contributions to cancer gene regulation. Liu is the principal investigator of the Cancer Immunologic Data Commons, a part of the NCI Cancer Moonshot project that aims to develop better cancer immunotherapy biomarkers and optimize treatment strategies.

Liu considers her role as a mentor to be a critical part of her job. She said, “I want trainees to explore projects that build on their interests and previous expertise and combine that with my lab’s knowledge on gene regulation. This helps each trainee to develop a unique identity.” She has already mentored 18 trainees who have moved on to tenure track faculty positions and continues to welcome a diverse array of trainees with computational and experimental expertise.

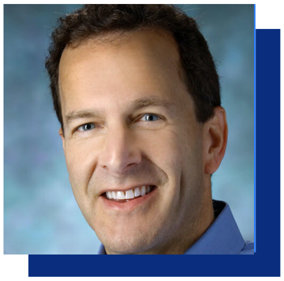
Liu is a highly cited researcher with a prodigious publication record that includes more than 200 papers published by her group, many of them in high-profile journals and highly cited. Liu has served on the editorial boards of leading genomic and computational biology journals throughout her career.

She has also served on a number of conference organizing committees and study sections. She received the Sloan Research Fellowship (2008), has been a Breast Cancer Research Foundation Investigator (2017), and became a Fellow of ISCB (2019). Liu’s open access resources were recognized with the Benjamin Franklin Award for Open Access in the Life Sciences in 2020.

Liu feels deeply honored to be recognized with the ISCB Innovator Award, especially as it comes from her peers in computational biology. She is inspired to continue pursuing projects that advance our understanding of basic biology and can be translated into clinical benefits to cancer patients.

2020 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD
STEVEN SALZBERG

The Outstanding Contributions to ISCB Award was introduced in 2015 to recognize Society members who are more than two decades post-degree and have made lasting and beneficial contributions through their leadership, service, and educational work, or a combination of these areas. Steven L. Salzberg, Bloomberg Distinguished Professor of Biomedical Engineering, Computer Science, and Biostatistics at Johns Hopkins University, and Director of the Center for Computational Biology, is being honored as the 2020 winner of the ISCB Accomplishments by a Senior Scientist Award. He will be recognized and give a keynote address at ISMB 2020 virtual conference being held on July 13-16, 2020.



Steven Salzberg
A Journey between Industry and Academia

Steven Salzberg grew up in Columbia, SC. Throughout his childhood and young adulthood, he was always interested in science and deeply enjoyed reading science fiction. Salzberg was also fascinated by astronomy and considered studying physics. As an undergraduate at Yale University in the 1970's, he explored several majors and thought he had settled on English Literature but added Computer Science as a second major upon taking an introductory computer programming class. He recalled, "This is the kind of math I thought I would really like to study," and he was soon captivated by artificial intelligence (AI) and natural language processing. At the advice of his undergraduate advisor, Salzberg spent a year after graduation gaining more programming experience by working at a local power company in South Carolina, where he worked on an IBM mainframe and used self-training courses to learn COBOL and IBM assembler. Salzberg said, "It was a very boring sort of application, but I was still interested in programming. I liked the idea I could work on something technical, and within a short period of time, I would have results that would do what I intended."

Salzberg returned to Yale and completed his M.S. in computer science. He then joined a startup in Boston during the first blush of AI, although this and many other AI startups failed in the late 1980's due to lack of computing power and other technical limitations.

One of Salzberg's advisors at the startup was AI pioneer Bill Woods, who held an adjunct appointment at Harvard University and later became Salzberg's graduate advisor in the Department of Computer Science. Salzberg had managed to avoid taking any biology classes as an undergraduate, but he heard about the Human Genome Project (HGP) while he was in graduate school in the late 1980's. He said, "The Human Genome Project sounded like the most exciting thing in all of science at the time, and I wanted to be a part of that." While completing his PhD project in machine learning, he started sitting in on biology classes, including a course by the late Stephen Jay Gould, and reading on his own to learn about genomics and genetics. He was determined to figure out a way to using his computing knowledge to get involved in the HGP.

Salzburg continued doing research in machine learning as he started in his first academic position at Johns Hopkins University. He was still curious about genomics and recalled going to a talk in the early 1990's by Temple Smith about sequence differences between exons and introns. It dawned on Salzberg that he could use machine learning to distinguish exons from introns, which could be used as a strategy for gene finding. This became Salzberg's entrance into genomics.

During this time, Salzberg was also introduced to Nobel Laureate Hamilton Smith, a notable microbiologist who discovered type II restriction enzymes. Salzberg recalled, "[Smith] had a secret passion for computer programming. He wanted to talk to computer scientists who were interested in genomics—that was me. And I was interested in learning more about genomics." Salzberg and Smith began working together to understand how computer programs could be made for tasks like gene finding. Smith had also started collaborating with J. Craig Venter, and in 1997, both Smith and Salzberg began working at Venter's non-profit research institute, The Institute for Genomic Research (TIGR). Salzberg became the Director of Bioinformatics at TIGR and developed with his colleague Art Delcher the GLIMMER gene finder, a software system still used today to identify coding regions in bacteria, archaea and viruses. In the early 2000's, the first Mycobacterium tuberculosis genomes were being sequenced by both TIGR and The Sanger Center. This led Salzberg and his colleagues to develop MUMmer, a system that could be used to compare large genomes. He also got involved in the HGP through the development of a gene finder that could analyze the human genome and, with his colleague Mihaela Pertea, also built other eukaryotic gene finders for plant, fungus, and parasite genomes. Salzberg and his colleagues were called upon by the FBI after the 2001 anthrax attacks to analyze the genome of the anthrax bacteria, and that work identified genetic mutations that eventually pinpointed the source of the bacteria to a biodefense lab in Fort Detrick, Maryland. In 2003, Salzberg co-founded the Influenza Genome Sequencing project with David Lipman, which involved the sequencing and analysis of thousands of influenza isolates.

Salzberg then moved to the University of Maryland, College Park in 2005, where he was the Horvitz Professor of Computer Science. He returned to JHU in 2011, where he is currently the Bloomberg Distinguished Professor of Biomedical Engineering, Computer Science, and Biostatistics and the Director of the Center for Computational Biology in the Whiting School of Engineering. As next-generation sequencing (NGS) technology developed, Salzberg's research interests shifted toward developing algorithms for large-scale genome assembly and sequence alignment, including the development of the open-source Tuxedo suite of programs (Bowtie, Tophat and Cufflinks).

Salzberg's current interests include the development of an improved human gene catalog and assembly and annotation of an Ashkenazi human reference genome. Recent technical advances have made this undertaking feasible, and the research community has desperately needed other reference genomes beyond the only publicly available genome, GRCh38. Salzberg is also working with colleagues on developing methods for using shotgun sequencing as a diagnostic tool for infectious diseases. They have tested their techniques on biopsy materials from patients with difficult-to-diagnose brain infections and on samples collected from eye infections, and the technology has the potential to work on a much broad range of infections.

Salzberg has trained numerous students and postdoctoral fellows throughout his time in academia and at TIGR, and he has focused on matching highly motivated individuals with projects that get them excited. Like many computational biologists, Salzberg is continually in search of interesting data associated with problems that matter, whether they involve the nature of the human genome, human health and disease, or any of a much broader range of microbial, plant, and animal genomes.

Salzberg's body of work includes more than 300 publications, including many highly cited manuscripts. His contributions have been recognized through his election as a member of the American Academy of Arts and Sciences, a Fellow of the American Association for the Advancement of Science (AAAS), a Fellow

of the International Society for Computational Biology (ISCB), and a member of the Board of Scientific Counselors of the National Library of Medicine at NIH. All of Salzberg's bioinformatics systems have been released as free, open-source software, and he won the 2013 Benjamin Franklin Award for Open Science for his advocacy of open-source software and of open sharing of genome sequence data. Salzberg is also a contributor to Forbesmagazine and writes a widely read column that debunks pseudoscience and explains scientific and medical findings with honesty and clarity.

Salzberg is greatly honored to be the 2020 recipient of ISCB's Accomplishments by a Senior Scientist award. He has always felt at home at ISMB meetings since their inception and is touched by this award since it is bestowed upon him by his computational biology colleagues.

RSG with DREAM 2020

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

NOVEMBER 16-18, 2020

DETAILS

WHEN
NOVEMBER 16-18, 2020

WHERE
VIRTUAL ISCB EVENT

COST*
ISCB

Professional $100
Post Doc $75
Student $50

Non-Members

Professional $250
Post Doc $175
Student $125

*Reflects Early registration rates. Rates increase on Oct 13

MORE INFO

www.iscb.org/recomb-regsysgen2020

SUBMIT TODAY!

SUBMISSION DEADLINES

Oral presentations & Posters	October 5, 2020
DREAM Challenge Deadlines	Challenge Specific

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
Regulatory and Systems Genomics in Immunology

We welcome submissions on computational and experimental advances regulatory and systems genomics in immunology. Topics include but are not limited to immunological regulatory programs and signaling pathways, genetic and non-genetic sources of self/non-self identification, precision epitope identification and targeting, and immune cell regulation.

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.

THANK YOU TO OUR GENEROUS DONORS

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Mirian Silvera
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2020 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD
JUDITH BLAKE

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. Judith Blake, Professor at the Jackson Laboratory in Bar Harbor, ME, is the 2020 winner of the Outstanding Contributions to ISCB Award and will be recognized at the 2020 ISMB virtual meeting being held on July 13-16, 2020.

Judith Blake
Science and Service Intertwined

Judith Blake has spent most of her career at the Jackson Laboratory in Bar Harbor, ME developing bioinformatics systems for integrating genetic, genomic, and phenotypic information and working to make data from different genomes more accessible for genomics and genetics research. Early in Blake's career at the Jackson Laboratory, she became a principal investigator with the Mouse Genome Informatics (MGI) project, a widely used international open access database resource for the laboratory mouse, providing integrated genetic, genomic, and biological data to facilitate the study of human health and disease. Blake's work on the MGI led to her interest in bio-ontologies. During the 1998 ISMB meeting, she and other colleagues working on genome projects in different model organisms recognized a need for open access bio-ontologies, which are controlled structured vocabularies for molecular biology that support the comparison of data across different genomes. She is one of the founding principal investigators and one of current leaders of the Gene Ontology (GO) Consortium group. Together with her research team, she has spent many years contributing to development of bio-ontology systems and to supporting integration of functional genomics data for mouse, in particular, within MGI and the GO project.

Beyond Blake's contributions to the bioinformatics and data curation communities, she has served ISCB in many ways. She recalls attending the first ISMB meeting at the National Library of Medicine in Bethesda, MD in 1993, which led to the eventual formation of ISCB. Blake said, "Here I found a community of investigators actively engaged in creating new tools and approaches to computational scientific investigations. My colleagues in ISCB shared my excitement as new innovations were developed to understand molecular systems and data." She has come to appreciate how ISCB brings together scientists from academia, industry, and technology in an open and supportive environment that fosters the building of new tools to advance the understanding of biological systems. Blake has served on the ISCB Board of Directors and chaired the ISCB Public Affairs and Policy committee, as well as working on other program and review committees. She has also represented ISCB on the Federation of American Societies for Experimental Biology (FASEB) Board of Directors.

Blake sees many benefits in pursuing scientific service opportunities and said, "I encourage young scientists and trainees to engage in those ISCB activities that match their passions. The opportunity to support their colleagues and to engage in a scientific network will both enhance the interactions of a global network of scientists but will also bring new insights to their own scientific investigations."

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

ISCB is pleased to recognize Dr. Jian Peng, Assistant Professor in the Department of Computer Science at the University of Illinois at Urbana-Champaign as the 2020 winner of the Overton Prize. Peng will be presenting a keynote presentation at the 2020 International Conference on Intelligent Systems for Molecular Biology virtual meeting being held on July 13-16, 2020.

Jian Peng

A Lifelong Love of the Sequence-Structure-Function Relationship

Jian Peng grew up in Yichang, Hubei Province, China to parents who were both university professors. His earliest memories include taking pleasure in his time spent reading from his parents' home library, even when he could not fully comprehend the content of some the books. He recalled, "My parents were college professors, who always gave me the freedom to choose what I liked to do." Peng was 10 years old when his parents gave him his first personal computer. and he was quickly drawn to computer programming. He spent many hours teaching himself to program and read programming books on C/C++, Windows, and data structures. In high school, Peng became interested in chemistry, but he returned to his early interest in computer programming while pursuing his bachelor's and master's degrees in computer science at Wuhan University. As an undergraduate, Peng became deeply interested in mathematical logic and its applications to programming languages and wanted to pursue this topic in graduate school. He said, "I didn't find many places to study this topic. I was fortunate to meet with Professor Jinbo Xu, who was giving a bioinformatics talk at Tsinghua University and kindly showed me several fascinating papers, including his seminal work on the protein side chain packing problem. He suggested that I spend time reading textbooks on machine learning (ML), as he believed that ML would become a very useful tool in computational biology when more data become available."

Peng went on to complete his PhD in 2013 at the Toyota Technological Institute at Chicago under Xu, where his research focused on protein structure prediction and modeling using ML methods. These methods, which are known as RaptorX and are still widely used today, have excelled at alignments of hard targets. Peng then joined Bonnie Berger's lab as a postdoc and expanded his research scope to include systems biology and functional genomics. He recalled, "We have had a great time working on a variety of problems, including structural bioinformatics, compressive genomics, systems biology, and disease genomics. I also really appreciated my time in the lab of (the late) Susan Lindquist, where I learned a lot from experimental and wet lab biologists and found ways to help address important problems in neurodegenerative diseases using my computational skills." He is deeply appreciative of his mentorship under Xu, Berger, and Lindquist not just for the areas of research he worked on with them but also for the lessons he learned in conducting experiments correctly and with rigor.

INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

FIND YOUR LOCAL ISCB!

ISCB AFFILIATE GROUPS

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

The ISCB Affiliates program is designed to forge links between ISCB and regional non-profit membership groups, centers, institutes and networks that involve researchers from various institutions and/or organizations within a defined geographic region involved in the advancement of bioinformatics.





AFRICAN SOCIETY FOR BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (ASBCB)

ASIA PACIFIC BIOINFORMATICS NETWORK (APBIONET)

AUSTRALIAN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SOCIETY (ABACBS)

BIOCANET: CENTRAL AMERICAN NETWORK OF BIOINFORMATICS AND MOLECULAR BIOCOMPUTING

BIOINFORMATICS ITALIAN SOCIETY (BITS)

BIOCLUES INDIA

BOSTON AREA MOLECULAR BIOLOGY COMPUTER TYPES (BAMBCT)

EUROPEAN MOLECULAR BIOLOGY NETWORK (EMBNET)

FACHGRUPPE BIOINFORMATIK (FABI)

GREAT LAKES BIOINFORMATICS CONSORTIUM (GLBC)

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ISRAELI SOCIETY OF BIOINFORMATICS AND COMPUTATIONAL BIOLOGY (ISBCB)

JAPANESE SOCIETY FOR BIOINFORMATICS (JSBI)

KOREAN SOCIETY FOR BIOINFORMATICS (KSBI)

MIDSOUTH COMPUTATIONAL BIOLOGY AND BIOINFORMATICS SOCIETY (MCBIOS)

POLISH BIOINFORMATICS SOCIETY (PBIS)

SOCIEDAD IBEROAMERICANA DE BIOINFORMáTICA, IBEROAMERICAN SOCIETY OF BIOINFORMATICS (SOIBIO)

SOCIETY FOR BIOINFORMATICS IN THE NORDIC COUNTRIES (SOCBIN)

VANCOUVER BIOINFORMATICS USER GROUP (VANBUG)

In 2015, Peng was appointed as an assistant professor in the Department of Computer Science, and affiliated with the College of Medicine, at the University of Illinois at Urbana-Champaign. Peng's perspective in identifying new research topics has evolved with his maturation as an academic. As a student, he was more drawn to problems that he thought were highly interesting, or he was swayed by the "coolness" of a method. Now Peng appreciates that his research interests must also address important scientific problems, and he feels it is critical to convey this concept to his trainees as they apply their knowledge in computation and biology to solve problems that deeply interest them.

Through his research experiences, Peng has learned that scientists are often surprised by unexpected findings. He said, "What I've learned in these years from successes and failures is how capable (and incapable) computational methods can be. Like many artificial intelligence/ML researchers, I was initially focused on developing powerful ML models for problems with large datasets, which hopefully can provide us new biological insights. However, in many important problems, such as those related to protein function and design, disease mutations studies, and functional genomics, the effective sample sizes are much smaller than what we expect for ML." Peng's research has always been driven by understanding the sequence-structure-function relationship. Currently, Peng's research has shifted directions towards using biological insights for developing advanced machine learning models. Like Bayesian methods, he uses known biological insights to serve as the "structural" prior to constrain ML models and generate new hypotheses in line with existing knowledge. Two recent notable projects in this line are the DeepContact algorithm for protein contact map prediction and the Mashup algorithm (with Berger and Cho) for heterogeneous biological network data integration.

He is interested in understanding the functional and structural consequences of protein mutations. Peng appreciates the importance of this area in terms of designing proteins with better and more biologically relevant functions, but also improving the annotation of missense mutations in human genomes for gaining insights in molecular mechanisms of human diseases.

Peng is greatly humbled and honored to receive the 2020 ICSB Overton Prize as it is a recognition from his peers within the ISCB community, and he shares his gratitude with the mentors, students and collaborators that have brought his work to fruition.

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virtual
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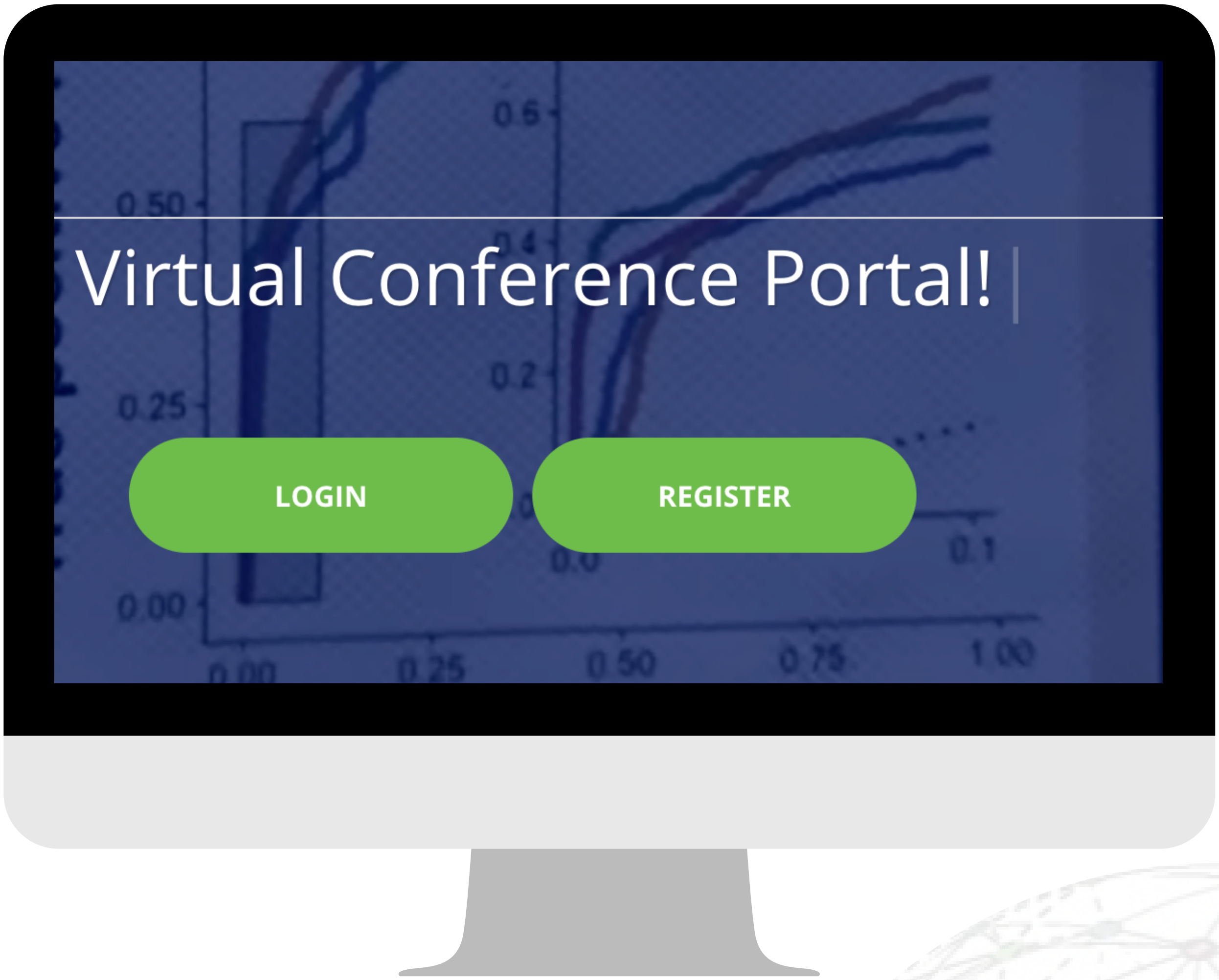
2020



Virtual Conference Portal!

Virtual Conference Programme

Welcome to Virtual ISMB 2020

On behalf of the organizing committee of ISMB 2020 and the Board of Directors of the International Society for Computational Biology (ISCB) we wish you a very warm and appreciative welcome. Though we miss what would have been a warm and heart welcome to Montreal, we look forward to experiencing the city in person in 2024! In the meantime, this virtual gathering promises to be an inventive and thought-provoking meeting for computational biologists in 2020.

This year saw the changing of the world as we knew it. COVID-19 disrupted not only our lives but also how we navigate the scientific world. Instead of cancelling or postponing ISMB 2020, the conference was moved to what we see before us now, a 100% virtual platform. This required an extreme restructuring of the conference, to ensure that ISMB 2020 will deliver to the comfort and safety of your homes, all the great scientific content that you would have enjoyed while attending the conference in Montreal. In addition, to safeguard ISMB's relevance and cutting-edge content, a new track showcasing research on SARS-Cov-2 / COVID-19 was added to an already robust program.

At the heart of the scientific program are the ISCB's Communities of Special Interest (COSIs), enabling intensified community involvement and bolstering its reputation as a conference with a strong scientific and technical program, which showcases the best international developments in the field. This year we have 22 COSIs participating at ISMB 2020 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, Live or on demand sessions from all time zones.

Over the course of the next four days, we will have the opportunity to hear and interact live with speakers delivering over 400 talks presented in 22 Community of Special Interest (COSI) tracks, Special Sessions, Technology Tracks, and Workshop on Bioinformatics Education (WEB). You will also be able to browse the more than 700 posters in the virtual Poster Hall, where authors will stand-by to answer your questions in the chat feature.

All of the sessions will be on a predetermined broadcast schedule. You can browse the schedule at your leisure and even mark the talks that you are most interested in seeing. If you miss something, don't worry! You will be able to access this platform until October 31, 2020, and all of the talks (and the virtual poster hall) presented will be available on-demand to watch at your convenience.

As is the goal every year, ISMB will aim to bring together scientists from computer science, molecular biology, mathematics, statistics and related fields, and provide an intense multidisciplinary forum for disseminating the latest developments in bioinformatics/computational biology in a virtual environment. The virtual platform of the conference will foster fresh dialogues, collaboration, and learning opportunities.

The program includes:

- *Live and on demand sessions to benefit attendees from all time zones*
- *More than 500 expected talks broadcast over the conference days*
- *Exclusive access to the ISMB 2020 on-demand repository of talks and poster presentations for viewing at your leisure after conference*
- *Live question and answer feature to engage with the speaker during sessions*
- *Live chat feature to engage with other participants within your session room*
- *A networking café for video meet ups with colleagues, friends, or future collaborators*
- *Opportunity to explore the virtual exhibit hall to chat & meet with exhibitors*
- *Opportunity to explore the virtual poster hall (yes, all of those great poster presentations in one place!)*

We want to acknowledge all the chairs of the Proceedings, COSIs, COVID-19, Technology Track, Travel Fellowship, Tutorials, and Student Council Symposium committees. Their dedication and leadership during this time has been invaluable, in offering to you an insightful, relevant, and cutting-edge program.

We of course want to extend our appreciation to our conference sponsors and exhibitors for their ongoing support during these trying times. This year's virtual exhibition section will be a key feature for attendees to learn more about publishing opportunities, services, tools, and job openings.

Finally, we wish you all a great virtual conference experience!

Enjoy ISMB 2020

Yours sincerely,

Shoshana Wodak

Conference Co-Chairs

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BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Danielle Albers, *University of Colorado at Boulder, United States*
Cagatay Turkay, *City, University of London, United Kingdom*
Thomas Höllt, *Leiden University Medical Center, The Netherlands*
Michael Krone, *University of Tübingen, Germany*
Michel Westenberg, *Eindhoven University of Technology, The Netherlands*

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

David Kreil, *Boku University Vienna, Austria*
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Paweł P Łabaj, *Austrian Academy of Sciences, and Jagiellonian University, Poland*
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COMPMS: COMPUTATIONAL MASS SPECTROMETRY

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FUNCTION: INCORPORATING CAFA 4: GENE AND PROTEIN FUNCTION ANNOTATION

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HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

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Gang Fang, *Mount Sinai School of Medicine, United States*
Kjong Lehmann, *ETH-Zürich, Switzerland*
Layla Oesper, *Carleton College, United States*

IRNA: INTEGRATIVE RNA BIOLOGY

Yoseph Barash, *University of Pennsylvania, United States*
Klemens Hertel, *University of California, Irvine, United States*
Michelle Scott, *Université de Sherbrooke, Canada*

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Christoph Lippert, *University of Potsdam, Germany*
Sara Mostafavi, *University of British Columbia, Canada*

MICROBIOME

Aaron Darling,*University of Technology Sydney, Australia*
Alice McHardy, *Helmholtz Centre for Infection Research, Germany*
Fernando Meyer, *Helmholtz Centre for Infection Research, Germany*
Alexander Sczyrba, *Bielefeld University, Germany*

MICROBIOME

Aaron Darling,*University of Technology Sydney, Australia*
Alice McHardy, *Helmholtz Centre for Infection Research, Germany*
Fernando Meyer, *Helmholtz Centre for Infection Research, Germany*
Alexander Sczyrba, *Bielefeld University, Germany*

NETBIO: NETWORK BIOLOGY

Martina (Tina) *Kutmon, Maastricht University, Netherlands*
Tijana Milenkovic, *University of Notre Dame, United States*
Natasa Przulj, *Barcelona Supercomputing Center, Spain*

REGSYS: REGULATORY AND SYSTEMS GENOMICS

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Stephen MacKinnon, *Cyclica, Canada*
Venkata Satagopam, *University of Luxembourg*
Mansoor Saqi, *Kings College London, United Kingdom*
Maria Secrier, *University College London, United Kingdom*

VARI: VARIANT INTERPRETATION

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Hannah Carter, *University of California, San Diego, United States*
Antonio Rausell, *Imagine Institute for Genetic Diseases, France*

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Distinguished Keynote Presentations

MONDAY, JULY 13

Elaine Mardis

The Ohio State University College of Medicine

Computational Analysis in Pediatric Cancer Precision Medicine

Introduced by: Francis Ouellette, Conference Co-chair

TUESDAY, JULY 14

ISCB 2020 Innovator Award Keynote

Xiaole Shirley Liu

Biostatistics, Harvard T.H. Chan School of Public Health;
Co-director, Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute
United States

Computational modeling of tumor immunity

Introduced by: Thomas Lengauer, ISCB President

WEDNESDAY, JULY 15

ISCB Overton Prize Keynote

Jian Peng

University of Illinois at Urbana-Champaign

Machine learning for structural and functional genomics

Introduced by: Shoshana Wodak, Conference Co-chair

THURSDAY, JULY 16

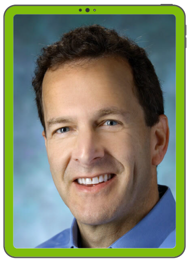
Laxmi Parida

IBM T. J. Watson Research Center

Combinatorics, Statistics and Topology enabling Genomics

Introduced by: David Sankoff, Honorary Conference Chair

THURSDAY, JULY 14



ISCB 2020 Accomplishments by a Senior Scientist Award Keynote

Steven L. Salzberg

Johns Hopkins University

Bioinformatics and genomics: a virtuous cycle driven by technology

Introduced by: Ron Shamir, ISCB Awards Committee Chair

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

www.iscb.org

ISCB Student Council

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

www.iscbsc.org

GOBLET

GOBLET, the Global Organisation for Bioinformatics Learning, Education and Training, is a legally registered foundation whose mission is to cultivate the global bioinformatics trainer community, set standards and provide high-quality resources to support learning, education and training.

www.mygoblet.org

Oxford University Press

Bioinformatics publishes the highest quality scientific papers and review articles with its main focus is on new developments in genome bioinformatics and computational biology.

https://academic.oup.com/BIOINFORMATICS

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https://datascience.nih.gov/

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JAX uniquely amplifies the efforts of the global biomedical research community. We develop and share our research, innovative tools and solutions, ever-expanding data resources, more than 11,000 specialized mouse models and services, and a suite comprehensive educational programs to empower basic scientific research and speed drug discovery across the globe.

https://www.jax.org/

Schedule-at-a-glance
Monday

Monday, July 13

7:45	Posters available for viewing								
9:25	Morning Welcome and Introduction of ISCB 2020 Distinguished Fellows								
9:30	ISMB 2020 Distinguished Keynote, Elaine Mardis								
10:40	CAMDA	Function	iRNA Integrative RNA Biology Community	MLCSB	SYSMOD	Mining	BIOINFO-CORE	Technology Track	Special Session (SST01): Systems Immunology
11:40	Program Break								
12:00	Camda Contiued...	Function Contiued...	iRNA Contiued...	MLCSB Contiued...	SYSMOD Contiued...	Text Mining Contiued...	Bioinfo-core Contiued...	Technology Track	Special Session (SST01): Systems Immunology
12:40	Break, Open Networking Time, BoF								
1:00	ISCB Town Hall								
2:00							WEB 2020	Special Session (SST02)	Special Session (SST01)
3:00	Program Break								
3:20							WEB 2020	Special Session (SST02)	Special Session (SST01)
4:40	Program Break								
5:00							WEB 2020	Special Session (SST02)	Special Session (SST01)

Schedule-at-a-glance
Tuesday

Tuesday, July 14

7:45	Posters available for viewing								
9:25	Welcome & ISCB 2020 Outstanding Contributions Award Presentation to Judith Blake								
9:30	ISCB Innovator Award Keynote, Xiaole Shirley Liu								
10:40	CAMDA	Function	iRNA Integrative RNA Biology Community	MLCSB	EDUCATION Community Of Special Interest	Evolution & Comparative Genomics EvolCompGen	Special Track: NIH/OD Office of Data Science Strategy (ODSS)	SYSMOD	Special Session (SST03):
11:40	Program Break								
12:00	Camda Contiued...	Function Contiued...	iRNA Contiued...	MLCSB Contiued...	Education Contiued...	Evolution & Comparative Genomics Contiued...	Special Track: ODSS Contiued...	Sysmod Continued...	Special Session (SST01): Systems Immunology
12:40	Break, Open Networking Time, BoF								
1:15	Lunch & Learn: F1000 Research								
2:00	Camda Contiued...	Function Contiued...	iRNA Contiued...	MLCSB Contiued...	Education Contiued...	Evolution & Comparative Genomics Contiued...	Special Track: ODSS Contiued...	Special Session (SST04): SCANGEN	Special Session (SST05):
3:00	Program Break								
3:20	Camda Contiued...	Function Contiued...	iRNA Contiued...	MLCSB Contiued...	Education Contiued...	Evolution & Comparative Genomics Contiued...	Special Track: ODSS Contiued...	Special Session (SST04): SCANGEN	Special Session (SST05):
4:40	Program Break								
5:00	Camda Contiued...	Function Contiued...	iRNA Contiued...	MLCSB Contiued...	Education Contiued...	Evolution & Comparative Genomics Contiued...	Special Track: ODSS Contiued...	Special Session (SST04): SCANGEN	Special Session (SST05):

Schedule-at-a-glance
Wednesday

Wednesday, July 15

7:45	Posters available for viewing				
9:25	Morning Welcome and Conference Updates				
9:30	ISCB Overton Prize Award Keynote, Jian Peng				
10:40	3DSIG		HiTSeq	RegSys	biovis
11:40	Program Break				
12:00	3DSIG Contiued...	Bio-ontologies Contiued...	HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...
12:40	Break, Open Networking Time, BoF				
1:00	Lunch and Learn: The Black Women in Computational Biology Network				
2:00	3DSIG Contiued...	Bio-ontologies Contiued...	HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...
3:00	Program Break				
3:20	3DSIG Contiued...	Bio-ontologies Contiued...	HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...
4:40	Program Break				
5:00	3DSIG Contiued...	Bio-ontologies Contiued...	HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...

Schedule-at-a-glance
Wednesday

Wednesday, July 15

7:45	Posters available for viewing				
9:25	Morning Welcome and Conference Updates				
9:30	ISCB Overton Prize Award Keynote, Jian Peng				
10:40	CompMS Computational Mass Spectrometry	MICROBIOME Community Of Special Interest	NetBio	TransMed	Vari-SIG
11:40	Program Break				
12:00	CompMS Contiued...	Microbiome Contiued...	NetBio Continued...	TransMed Continued...	VARI Continued...
12:40	Break, Open Networking Time, BoF				
1:00	Lunch and Learn: The Black Women in Computational Biology Network				
2:00	CompMS Contiued...	Microbiome Contiued...	NetBio Continued...	TransMed Continued...	VARI Continued...
3:00	Program Break				
3:20	CompMS Contiued...	Microbiome Contiued...	NetBio Continued...	TransMed Continued...	VARI Continued...
4:40	Program Break				
5:00	CompMS Contiued...	Microbiome Contiued...	NetBio Continued...	TransMed Continued...	VARI Continued...

Schedule-at-a-glance Thursday

Thursday, July 16

7:45	Posters available for viewing								
9:25	Morning Welcome and Conference Updates								
9:30	ISMB Distinguished Keynote, Laxmi Parida								
10:40	3DSIG		HiTSeq	RegSys	General Comp Bio Talks	CompMS Computational Mass Spectrometry	Special Presentation: COVID-19	NetBio	Special Presentation: *Is biology contributing to the climate crisis? How green is your data centre?*
11:40	Program Break								
12:00	3DSIG Contiued...	Bio-ontologies Contiued...	HiTSeq Contiued...	RegSys Contiued...	General Comp Bio Talks Continued...	CompMS Contiued...	Special Presentation: Continued...	NetBio Continued...	Special Presentation: Continued...
12:40	Break, Open Networking Time, BoF								
12:50	Hackathon Presentations								
2:00	ISCB Accomplishments by a Senior Scientist Award Keynote, Steven L. Salzberg								
3:00	Program break								
3:20	3DSIG Contiued...		HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...	CompMS Contiued...	Special Presentation: Continued...	Special Session (SST06)	Special Session (SST07)
4:20	Program Break								
4:40	3DSIG Contiued...		HiTSeq Contiued...	RegSys Contiued...	biovis Contiued...	CompMS Contiued...	Special Presentation: Continued...	Special Session (SST06) Continued	Special Session (SST07) Continued
6:00	Awards Presentations and Closing Remarks								

Special Sessions

MONDAY, JULY 13 • TUESDAY, JULY 14 • THURSDAY, JULY 16

https://www.iscb.org/ismb2020-program/special-sessions

MONDAY, JULY 13

SST01: SYSTEMS IMMUNOLOGY: COMPUTATIONAL APPROACHES FOR UNDERSTANDING HUMAN IMMUNE SYSTEM AND IMMUNE-RELATED DISEASES

http://sysimm.lji.org/

ORGANIZER(S):

Ferhat Ay, *La Jolla Institute for Allergy and Immunology, United States*
Duygu Ucar, *The Jackson Laboratory for Genomic Medicine, University of Connecticut Health Center, United States*

10:40 AM **John Tsang,** *National Institutes of Health,*
Do differences make a difference: from single cells to humans

11:10 AM **Jane Skok,** *New York University School of Medicine, United States*
The impact of cancer associated CTCF mutations on chromatin architecture and gene regulation

12:00 PM **Bali Pulendran,**
Probing the Immune Response to Vaccination with Systems Biology

2:00 PM **Shuzhao Li** *The Jackson Laboratory for Genomic Medicine*
Chemistry between genes: a proposition for ImmunoMetabolomics

2:30 PM **David Hawkins,**
The role of cis-regulatory elements in cell fate and immune disorders

3:20 PM **Sana Badri** *New York University School of Medicine*
Uncovering B-ALL TF-gene regulatory interactions associated with CRLF2-overexpression

3:30 PM **Bjoern Peters,** *La Jolla Institute for Allergy & Immunology*
Examining waning immunity of B. pertussis vaccination

4:00 PM **Duygu Ucar** The Jackson Laboratory for Genomic Medicine
Sexual dimorphism in human immune system aging

4:20 PM **Bharat Panwar,** *La Jolla Institute for Immunology*
Integrated transcriptomic analysis of SLE reveals IFN-driven cross-talk between immune cells

4:30 PM **James Anibal,** *National Cancer Institute*
Grégoire Altan-Bonnet, *National Cancer Institute*
Semi-connected multilayer perceptron for single-cell profiling

5:00 PM **Ferhat Ay** La Jolla Institute for Immunology,
Interpreting genetic variants through chromatin interaction maps in primary human immune cells

5:20 PM **Kathryn Miller-Jensen**
Exploring the functional consequences of macrophage heterogeneity

5:50 PM **Nathan Lawlor,** The Jackson Laboratory
Dissecting the heterogeneity of protein and transcriptional responses in human blood derived immune cells after T- and monocyte-specific activation

6:00 PM **Benjamin Meckiff,** La Jolla Institute for Immunology
Single-cell transcriptomic analysis of SARS-CoV-2 reactive CD4+ T cells

6:10 PM **Gregory Seumois,** La Jolla Institute for Immunology
Single-cell transcriptomic analysis of allergen-specific T cells in allergy and asthma

Special Sessions

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MONDAY, JULY 13

SST02: BIOINFORMATICS OUTSIDE THE LAB: HOW TO MOBILIZE ONLINE CITIZEN SCIENTISTS TO ACCELERATE RESEARCH

ORGANIZER(S):

Jérôme Waldispühl, *McGill University, Canada*

2:00 PM	**Jérôme Waldispühl,** McGill University	*Introduction*
2:10 PM	**Seth Cooper**	*Foldit and the origin of scientific discovery games in molecular biology*
2:30 PM	**Ginger Tsueng**	*Applying Citizen Science to Biomedical Literature Curation and Beyond*
2:45 PM	**Roman Sarrazin-Gendron** McGill University	*Phylo: How to turn scientific tasks into casual games*
3:20 PM	**Hanna Wayment-Steele**	*Improved RNA secondary structure modeling through crowdsourced RNA design initiatives*
3:35 PM	**Pietro Michelucci**	*Why humans-in-the-loop are needed to tackle the challenges of precision medicine*
3:50 PM	**Daniel McDonald**	*Accelerating Microbiome Science by Empowering Individuals*
4:05 PM	**Firas Khatib**	Gamers and experimentalists collaborate on COVID-19
4:20 PM	**Rhiju Das**	*Crowdsourced design of stabilized COVID-19 mRNA vaccines with Eterna OpenVaccine*
5:00 PM	**Attila Szantner**	*Citizen Science and Videogames - An unlikely marriage*
5:10 PM	**Gabriel Richard**	*Challenges in designing scientific discovery games in AAA games*
5:20 PM	**All speakers**	*Panel Discussion*

TUESDAY, JULY 14

SST03: BIOINFORMATICS OF CORALS

ORGANIZER(S):

Lenore Cowen, *Department of Computer Science, Tufts University, United States*
Judith Klein-Seetharaman, *Department of Chemistry, Colorado School of Mines, United States*
Hollie Putnam, *Department of Biological Sciences, University of Rhode Island, United States*

10:40 AM **Hollie Putnam** *University of Rhode Island*
Tackling the challenge of elucidating reef-building coral holobiont function

11:00 AM **Cheong Xin Chan** *University of Queensland*
Dynamic genome evolution of coral symbionts: a bioinformatics challenge

11:20 AM **Judith Klein-Seetharaman,** *Colorado School of Mines,*
Pipeline for discovery of membrane receptors in non-model organisms: the case of Pocillopora damicornis

12:00 PM **Mónica Medina** *Pennsylvania State University*
Metabolic complementary in phylogenetically divergent coral holobionts

12:20 PM **Debashish Bhattacharya,** *Rutgers University*
Metabolomic analysis of coral holobionts reveals markers of thermal stress

Special Sessions

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https://www.iscb.org/ismb2020-program/special-sessions

TUESDAY, JULY 14

SST04: SCANGEN: SINGLE-CELL CANCER GENOMICS

http://www.scangen.org/

ORGANIZER(S):

Kieran R Campbell, *Lunenfeld-Tanenbaum Research Institute, University of Toronto, Canada*

2:00 PM **Smita Krishnaswamy,** *Yale University,*

Deep Representation Learning for Problems in Biology

2:20 PM **Laura Richards,** *University of Toronto*

Gradient of developmental and injury-response transcriptional states define roots of glioblastoma heterogeneity

2:40 PM **Claudia Kleinman,** *McGill University*

Inferring the origins of pediatric brain tumors by single-cell analysis of the normal developing brain

3:20 PM **Benjamin J. Raphael** *Princeton University*

Copy number aberrations from single-cell sequencing

3:40 PM **Xiangqi Bai** *Chinese Academy of Sciences*

Joint Inference of Clonal Structure using Single-cell DNA-Seq and RNA-Seq data

4:00 PM **Yingxin Lin,** *The University of Sydney*

Integrative analysis of breast cancer survival based on spatial features

5:00 PM **Sohrab Shah,** *Memorial Sloan Kettering Cancer Center*

Single cell whole genome sequencing for studying cancer evolution

5:20 PM **Lingfei Wang,** *Broad Institute of MIT and Harvard*

Normalisr: inferring single-cell differential and co-expression with linear association testing

Special Sessions

MONDAY, JULY 13 • TUESDAY, JULY 14 • THURSDAY, JULY 16

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TUESDAY JULY 14

SST05: HUBMAP: INTEGRATING GENOMICS, IMAGING AND MASS-SPECTROMETRY TO CONSTRUCT SINGLE-CELL HUMAN TISSUE MAPS

ORGANIZER(S):

Ziv Bar-Joseph, *Carnegie Mellon University, United States*
Nils Gehlenborg, *Harvard Medical School, United States*
Ajay Pillai, *National Human Genome Research Institute, United States*

2:00 PM **Michael Snyder,** *Stanford University*

HUBMAP Session Keynote:
HuBMAP Data Collection Plans

2:40 PM **Cole Trapnell,** *University of Washington*

Embryo-scale, single-cell spatial transcriptomics

3:20 PM **Nick Nystrom,** *Pittsburgh Supercomputing Center,*

Infrastructure for Storing Massive Biological Data Sets

3:45 PM **Ziv Bar-Joseph,** *Carnegie Mellon University*

Tools and Pipelines for the Analysis and Integration of HuBMAP data

4:10 PM **Nils Gehlenborg,** *Harvard Medical School*

Visualization and Exploration of Heterogeneous Human Tissue Data Sets

4:35 PM **Katy Borner,** *Indiana University*

Common coordinates for registering human scale data at multiple scales

5:00 PM **Michael Snyder,** *Stanford University,*

Nils Gehlenborg, *Harvard Medical School*

Nick Nystrom, Pittsburgh Supercomputing Center

Ziv Bar-Joseph, *Carnegie Mellon University*

How can I interact with, use, develop methods for and obtain funding to work with HuBMAP data?

THURSDAY, JULY 16

SST06: INTERPRETING THE LIPIDOME – APPROACHES TO EMBRACE THE COMPLEXITY

ORGANIZER(S):

Bobbie-Jo Webb-Robertson, *Pacific Northwest National Laboratory, United States*
Jason McDermott, *Pacific Northwest National Laboratory, United States*
Geremy Clair, *Pacific Northwest National Laboratory, United States*

3:30 PM	**Jennifer Kyle** **Bobbie-Jo Webb-Robertson** *Welcome & Introduction to Lipidomics*
3:40 PM	**Maria Fedorova** *Exploring diversity of natural lipidomes: focus on high accuracy lipid identifications*
4:00 PM	**Lucila Aimo,** *Swiss Institute of Bioinformatics* *SwissLipids, a knowledge resource for lipids and their biology*
4:40 PM	**Geremy Clair** *Lipid Mini-on: a R-based tool for automatic lipid ontology generation and enrichment analysis*
5:00 PM	**J. Bernd Helms** *Towards a holistic view of lipid dynamics using Lipid Ontology (LION)*
5:20 PM	**Matej Oresic** Lipidome in non-alcoholic fatty liver disease: pathway, metabolic models, and biomarkers
5:40 PM	**Egon Willighagen,** *BiGCaT, NUTRIM, Maastricht University* *Integrating lipidomics data with pathway*

Special Sessions

MONDAY, JULY 13 • TUESDAY, JULY 14 • THURSDAY, JULY 16

https://www.iscb.org/ismb2020-program/special-sessions

THURSDAY, JULY 16

SST07: THE BRAIN INITIATIVE CELL CENSUS NETWORK

ORGANIZER(S):
Jesse Gillis, *Cold Spring Harbor Laboratory, United States*

3:20 PM **John Ngai,** *University of California, Berkeley*
Introduction to the Brain Initiative Cell Census Network (BICCN)

3:40 PM **Eran Mukamel,** *University of California San Diego*
Integrating single cell epigenomes into a multimodal brain cell atlas within the BICCN

4:00 PM **Nik Jorstad,** *Allen Institute*
Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse

4:40 PM **Megan Crow,** *Cold Spring Harbor Laboratory,*
Replicability of cell identities in the BICCN

5:00 PM **Zizhen Yao,** *Allen Institute*
A taxonomy of transcriptomic cell types across isocortex and hippocampal formation in adult mouse

5:20 PM **Alex Dobin,** *Cold Spring Harbor Laboratory*
Cross-species alternative isoform usage in BICCN brain cell types

5:40 PM **Brian Herb,** *University of Maryland,*
Utilizing NeMO archive's multimodal brain-wide data in your research, and how to feature your own data on the archive

COVID-19 Special Track

THURSDAY, JULY 16

https://www.iscb.org/cms_addon/conferences/ismb2020/tracks/covid-19

10:40 AM **Thomas Lengauer,** *ISCB President*

Introduction and COVID Repository

10:50 AM **Richard Neher** *Biozentrum University of Basel*

Real-time tracking of SARS-CoV-2 spread and evolution

11:30 AM **Snehalika Lall,** *Indian Statistical institute*

Identifying novel SARS-CoV2–human protein interactions using graph embedding

12:00 PM **Matthew Raybould,** *University of Oxford*

CoV-AbDab: the Coronavirus Antibody Database

12:15 PM **Philippe Le Mercier,** *Allen Institute*

Annotation of SARS-CoV-2 in ViralZone: From proteins to virus life cycle.

12:30 PM **Michal Linial,** *The Hebrew University*

The SARS-CoV-2 exerts a distinctive strategy for interacting with the ACE2 human receptor

3:00 PM **Jake McGreig,** *University of Kent*

Differentially conserved amino acid positions reflect differences in SARS-CoV-2 and SARS-CoV behaviour

3:15 PM **Mohammed El-Kebir,** *University Of Illinois at Urbana-Champaign*

Characterization of SARS-CoV-2 viral diversity within and across hosts

3:30 PM **Qingyu Chen,** *NIH*

Curation at Scale: Computational approaches to support curation in LitCovid

3:45 PM **Bjoern Gruening,** *Uni-Freiburg*

Tools, Workflows and Infrastructure for Open and Reproducible Analysis of SARS-CoV-2 Data

4:20 PM **Nina H. Fefferman** *University of Tennessee*

Invited Talk

5:00 PM **Jeffrey Law,** *Virginia Tech*

Identifying Human Interactors of SARS-CoV-2 Proteins and Drug Targets for COVID-19 using Network-Based Label Propagation

5:15 PM **Varun Mittal,** *NLPCore*

Viruses, Visualization, and Validation: Interactive mining of COVID-19 literature

5:30 PM **Brian Le,** *UCSF*

Transcriptomics-based drug repositioning pipeline identifies therapeutic candidates for COVID-19

5:45 PM **Sean O'Donoghue,** *CSIRO & Garvan*

Systematic modeling of COVID-19 protein structures

POSTERS

MONDAY, JULY 13 • TUESDAY, JULY 14 • THURSDAY, JULY 16

https://www.iscb.org/cms_addon/conferences/ismb2020/posters.php

Poster Session A:

July 13 & July 14 7:45 AM - 9:15 AM EDT

Bioinfo-core
CAMDA COSI
COVID-19
Education COSI
EvoCompGen COSI
Function / CAFA 4
MLCSB COSI
SCANGEN (Special Session)
SysMod COSI
Systems Immunology (Special Session)
Text Mining

July 14 between 10:40 am - 2:00 pm EDT

iRNA COSI

Poster Session B:

July 15 and July 16 7:45 am - 9:15 am EDT

3DSIG COSI
Bio-Ontologies COSI
BioVis COSI
CompMS COSI
COVID-19
HitSeq COSI
MICROBIOME COSI
NetBio COSI
RegSys COSI
TransMed COSI
VarI COSI
General Comp Bio

3DSIG COSI

COSI TRACK PRESENTATIONS

Wednesday, July 15th

10:40 AM **Eli Draizen,** University of Virginia,

Deep Learning of Protein Structural Classes: Any Evidence for an 'Urfold'?

11:00 AM **Genki Terashi,** Purdue University

EM Map Segmentation and De Novo Protein Structure Modeling for Multiple Chain Complexes with MAINMAST

11:10 AM **Daisuke Kihara,** Purdue University

Protein Contact Map De-noising Using Generative Adversarial Networks

11:20 AM **Badri Adhikari,** University of Missouri-St. Louis

Deep Learning Protein Contacts and Real-valued Distances Using PDNET

11:30 AM **Tomer Sidi,** Ben-Gurion University of the Negev

Redundancy-Weighting the PDB for Detailed Secondary Structure Prediction

12:00 PM **3DSIG Keynote**

Genki Terashi, Purdue University

Thinking Deeply About Protein Structure Prediction

2:00 PM **Yang Shen,** Texas A&M University

De Novo Protein Design for Novel Folds with Guided & Conditional Wasserstein GAN

2:10 PM **Ravinder Abrol,** California State University, Northridge

The vestibule role of membrane-water interface as the intermediate stage in a new three-stage model for helical membrane protein folding

2:20 PM **Antoniya Aleksandrova,** NINDS - NIH

Detecting Symmetry in Membrane Proteins

2:40 PM **Joanna Slusky,** University of Kansas

Evolutionary pathways of repeat protein topology in bacterial outer membrane proteins

3:20 PM **Amara Jabeen,** Macquarie University

BIO-GATS: A tool for automated GPCR template selection through a biophysical approach for homology modeling.

3:30 PM **Bhumika Arora,** Monash University

Modeling of G protein-coupled receptor structures : Improving the prediction of loop conformations and the usability of models for structure-based drug design

3:40 PM **F Fraternali,** King's College London

Nanocapsule Designs for Antimicrobial Resistance

3:50 PM **Katrin Schöning-Stierand,** Universität Hamburg Center for Bioinformatics (ZBH)

GeoMine: A Web-Based Tool for Chemical Three-Dimensional Searching of the PDB

4:00 PM **Fergus Imrie,** University of Oxford,

Generating Property-Matched Decoy Molecules Using Deep Learning

4:20 PM **Gwangho Lee,** Pusan National University

In silico selection of RNA aptamers for a target protein based on discriminative classifiers and the Monte-Carlo tree search

5:00 PM **Jeffrey A. Ruffolo,** Johns Hopkins University

Proceedings Presentation: Geometric Potentials from Deep Learning Improve Prediction of CDR H3 Loop Structures

5:20 PM **Debswapna Bhattacharya,** Auburn University

Proceedings Presentation: QDeep: distance-based protein model quality estimation by residue-level ensemble error classifications using stacked deep residual neural networks

5:40 PM **Spencer Krieger,** University of Arizona

Proceedings Presentation: Boosting the accuracy of protein secondary structure prediction through nearest neighbor search and method hybridization

3DSIG COSI

COSI TRACK PRESENTATIONS

Thursday, July 16th

10:40 AM	**Fei He,**	*University of Missouri-Columbia,*	*Quality Assessment of Protein Docking Models Based on Graph Neural Network*
11:00 AM	**Qifang Xu,**	*Fox Chase Cancer Center,*	*ProtCID: A data resource for structural information on protein interactions*
11:20 AM	**Sd Lam,**	*Universiti Kebangsaan Malaysia*	*SARS-CoV-2 spike protein predicted to bind strongly to host receptor protein orthologues from mammals, but not fish, birds or reptiles*
12:00 PM	**Yiwei Li,**	*University of Western Ontario*	*DELPHI: accurate deep ensemble model for protein interaction sites prediction*
12:20 PM	**Matthew Raybould,**	*University of Oxford*	*Evidence of Antibody Repertoire Functional Convergence through Public Baseline and Shared Response Structures*
3:20 PM	**Jarjapu Mahita,**	*Dartmouth College*	*Computational epitope binning of protein binders*
3:30 PM	**Aya Narunsky,**	*Tel Aviv University*	*How proteins evolved to recognize an ancient nucleotide?*
3:40 PM	**Avital Sharir-Ivry,**	*McGill University*	*Nature of long-range evolutionary constraint in enzymes: Insights from comparison to non-catalytic ligand binding sites*
4:00 PM	**Michal Linial,**	*The Hebrew University of Jerusalem*	*Studying de novo mutations via structural alterations in protein-protein interaction: STXBP1 associated neuronal pathology*
4:40 PM	**Bian Li,**	*Yale University*	*Predicting changes in protein thermostability upon point mutation with deep 3D convolutional neural networks*
5:00 PM	**Khalique Newaz,**	*University of Notre Dame*	*Network analysis of synonymous codon usage*
5:10 PM	**N. Suhas Jagannathan,**	*National University of Singapore*	*In silico ensemble modeling suggests binding-induced expansion as a possible functional mechanism for two endocytic proteins.*
5:20 PM	**Maria I. Freiberger,**	*UBA-CONICET-IQUIBICEN*	*Frustration leads to fuzzy interactions in disordered proteins*
5:40 PM	**Alexandre G. De Brevern,**	*Université de Paris*	*Protein local conformations analyses in ordered and intrinsically disordered proteins in the light of a structural alphabet*

Bio-Ontologies COSI

COSI TRACK PRESENTATIONS

Wednesday, July 15th

10:40 AM Bio-Ontologies Keynote

Michael Gruninger

The crisis of content

11:20 AM **John-Marc Chandonia,** *Berkeley National Lab*

CORAL: A platform for FAIR, rigorous, self-validated data modeling and integrative, reproducible data analysis

12:00 PM **Yang Wang,** *Guizhou University Medical College*

Ontology-based collection and analysis of natural and lab animal hosts of human coronaviruses

12:20 PM **Yongqun He** *University of Michigan*

CIDO Diagnosis: COVID-19 diagnosis modeling, representation and analysis using the Coronavirus Infectious Disease Ontology

2:00 PM **Núria Queralt-Rosinach,** *Leiden University Medical Center*

Modeling quantitative traits for COVID-19 case reports

2:20 PM **Senay Kafkas,** *King Abdullah University Of Science and Technology*

Using ontologies to extract disease-phenotype associations from literature

2:40 PM **Tiffany Leung,** *Maastricht University*

Representing Physician Suicide Claims as Nanopublications

3:20 PM **Remzi Çelebi,** *Maastricht University*

Metadata standards for the FAIR sharing of vector embeddings in Biomedicine

3:40 PM **Runar Reve,** *King Abdullah University Of Science and Technology*

Applying GWAS on UK Biobank by using enhanced phenotype information based on Ontology-Wide Association Study

4:00 PM **Stefanie Seltmann,** *Charité - Universitätsmedizin Berlin*

hPSCreg-CLO: ontological representation of human pluripotent stem cell lines from the hPSCreg

4:20 PM **Tiffany J. Callahan,** *University of Colorado*

A Framework for Automated Construction of Heterogeneous Large-Scale Biomedical Knowledge Graphs

5:00 PM Bio-Ontologies Keynote

Karin Verspoor

COVID-SEE: Enabling scientific evidence exploration through semantics in a time of crisis

Bio-Ontologies COSI

COSI TRACK PRESENTATIONS

Thursday, July 16

10:40 AM **Chengxin Zhang,** *University of Michigan*
Detecting Gene Ontology misannotations using taxon-specific rate ratio comparisons

11:00 AM **Bjoern Peters,** *La Jolla Institute for Allergy & Immunology*
COB as a Community Resource

11:10 AM **Randi Vita,** *La Jolla Institute for Allergy & Immunology*
A Structured Model for Immune Exposures

12:00 PM **Toshiyuki T. Yokoyama,** *University of Tokyo*
Semantic Variation Graphs: Ontologies for Pangenome Graphs

12:30 PM **Jennifer R. Smith,** *Medical College of Wisconsin*
RGD: Data and tools to aid the discovery of precision models of human disease

ISCB TOWN HALL

MONDAY JULY 13

12:45 PM - 1:45 PM

Join us at the ISCB Town Hall meeting on Monday, July 13, from 12:45 PM - 1:45 PM to learn more about the latest programs, initiatives, and conferences. This is also your chance to help shape the future of ISCB by providing feedback and suggestions.

BIOINFO-CORE COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 13

10:40 AM **Eric Merzetti**
BioNet Alberta: A network based approach to Bioinformatic capacity building in Alberta

10:50 AM **R. Krishna Murthy Karuturi,** *The Jackson Laboratory*
Mentoring and Managing Staff in Bioinformatics Cores
Using Generative Adversarial Networks

11:00 AM **Madelaine Gogol**
Chickens in Space: our experiences with spatial transcriptomics on the 10x Visium and slide-seq platforms

11:10 AM **Simone Marini,** *University of Florida*
Multi-sample, multi-condition analysis in scRNAseq data sets

11:20 AM **Breakout session 1**

12:00 PM **Breakout session 2**

12:20 PM **Breakout summaries**

BIOVIS COSI

COSI TRACK PRESENTATIONS

Wednesday, July 15th

10:40 AM **Cagatay Turkay,** *University of Warwick*
BioVis Opening

10:50 AM **BioVis Keynote:**
Hendrik Strobelt
Visualization and Human-AI collaboration for biomedical tasks

12:00 PM **Christian Dallago,** *Technical University of Munich*
bio_embeddings: python pipeline for fast visualization of protein features extracted by language models

12:10 PM **Jon Hill,** *Boehringer Ingelheim Pharmaceuticals Inc,*
Grid-Constrained Dimensionality-Reduction for Single-Cell RNA-Seq Summarization

12:20 PM **Maria Stephenson,** *Canada's Michael Smith Genome Sciences Centre*
RNA-Scoop: interactive visualization of isoforms in single-cell transcriptomes

12:30 PM **Antonios Somarakis,** *LUMC*
ImaCytE: Visual Exploration of Cellular Micro-environments for Imaging Mass Cytometry Data

2:10 PM **BioVis Keynote**
Marinka Zitnik
Machine Learning for Drug Repurposing

3:20 PM **Marwan Abdellah,** *Blue Brain Project / EPFL*
Proceedings Presentation *Interactive visualization and analysis of morphological skeletons of brain vasculature networks with VessMorphoVis*

3:40 PM **Peter Mindek,** *TU Wien*
Multi-Scale Procedural Animations of Microtubule Dynamics Based on Measured Data

3:50 PM **Bjorn Sommer,** *Royal College of Art*
Towards an Immersive Analytics Application for Anatomical Fish Brain Data

4:00 PM **Jiaqi Wu,** *University of Illinois at Urbana Champaign*
Proceedings Presentation: *ClonArch: Visualizing the Spatial Clonal Architecture of Tumors*

4:20 PM **Florian Ganglberger,** *VRVis Research Center*
A Web-based Framework for the Exploration of Heterogeneous Spatial Big Brain Data

4:30 PM **Heba Sailem,** *University of Oxford*
PhenoPlot-v2 a flexible tool for visualising microscopy data

5:00 PM **Kari Lavikka,** *University of Helsinki*
Grammar-Based Interactive Genome Visualization

5:10 PM **Hsiang-Yun Wu,** *TU Wien*
Metabopolis: scalable network layout for biological pathway diagrams in urban map style

5:20 PM **Josiah Seaman,** *Max Planck Institute*
Pantograph - Scalable Interactive Graph Genome Visualization

5:30 PM **Anthony Federico,** *Boston University*
A framework for the analysis, visualization, and comparison of multiple multi-omics networks

5:40 PM **Selim Kalayci,** *Icahn School of Medicine at Mount Sinai*
ProNetView-ccRCC: A web-based portal to interactively explore clear cell renal cell carcinoma proteogenomics networks

5:50 PM **Fritz Lekschas,** *Harvard University*
Interactive Visual Pattern Search in Epigenomic Data

6:00 PM **Cagatay Turkay,** *University of Warwick*
BioVis Closing

CAMDA COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 13

10:50 AM CAMDA Keynote:
Rita Colwell
Climate, Oceans, and Human Health: Cholera as a paradigm for prediction infectious diseases

12:00 PM **Dimitri Perrin,** *Queensland University of Technology*
Metagenomic Geolocation using Read Signatures

2:00 PM **Dorothy Ellis,** *University of Florida*
Unraveling city-specific microbial signature and identifying sample origin for the data from CAMDA 2020 Metagenomic Geolocation Challenge

2:20 PM **Dimitar Vassilev,** *Sofia University*
Spatial models for assessment of bacterial classification relevant to AMR

2:40 PM **Samuel Anyaso-Samuel,** *University of Florida*
Metagenomic Geolocation Prediction Using an Adaptive Ensemble Classifier

3:20 PM **Maximilian Miller,** *Rutgers University*
Separation of Mystery-Samples using mi-faser and forest embedding

3:40 PM **Cory Gardner,** *Saint Louis University*
Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation

4:00 PM **Carlos Loucera**
Towards a metagenomics interpretable model for understanding the transition from adenoma to colorectal cancer

5:00 PM **Mohammad Arifur Rahman,** *GMU*
Proceedings Presentation: *IDMIL: An alignment-free interpretable deep multiple instance learning (MIL) for predicting disease from whole-metagenomic data*

5:20 PM **Paweł Łabaj**
DNA Based Methods in Intelligence - Moving Towards Metagenomics

CAMDA COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY 14

10:45 AM CAMDA Keynote:
Aedin Culhane
Challenges and tools for integrative analysis of single cell 'omics data

12:00 PM **Seungjun Ahn,** *University of Florida*
Effect of Tumor Purity on The Analysis of Gene Expression Data

12:20 PM **Maria Peña-Chilet,** *CIBERER*
Mechanistic models of CMap drug perturbation functional profiles

2:00 PM **CAMDA CAFE**

3:20 PM **Witold Rudnicki,** *University of Bialystok*
Prediction of Drug Induced Liver Injury with different data sets and different end points

4:00 PM **Peter Tran,** *Saint Louis University*
Improving Deep Learning Performance on Prediction of Drug-Induced Liver Injury

4:20 PM **Junguk Hur,** *University of North Dakota*
Gene expression signature-based machine learning classifier of drug-induced liver injury

5:00 PM **Hossein Sharifi Noghabi,** *Simon Fraser University*
Proceedings Presentation: *AITL: Adversarial Inductive Transfer Learning with input and output space adaptation for pharmacogenomics*

5:20 PM **Sunkyu Kim,** *Korea University*
Proceedings Presentation: *Improved survival analysis by learning shared genomic information from pan-cancer data*

5:40 PM **Closing remarks and awards**

COMPMS COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY. 15

CompMS
Computational Mass Spectrometry

10:45 AM **Yasset Perez-Riverol,** *EMBL-EBI*
Community standard for reporting the experimental design in proteomics experiments: From samples to data files

11:00 AM **Meena Choi,** *Northeastern University*
MassIVE.quant: a community resource of curated quantitative mass spectrometry-based proteomics datasets

11:20 AM **Nuno Bandeira,** *University of California San Diego*
CoronaMassKB: an open-access platform for sharing of mass spectrometry data and reanalyses from SARS-CoV-2 and related species

11:30 AM **Anthony Valente,** *University of Washington Genome Sciences*
Prediction of Drug Induced Liver Injury with different data sets and different end points

12:00 PM **Dan Guo,** *Northeastern University*
Proceedings Presentation: *Deep multiple instance learning classifies subtissue locations in mass spectrometry images from tissue-level annotations*

12:20 PM **Melanie Christine Föll,** *University of Freiburg*
Mass spectrometry imaging in the age of reproducible medical science

12:30 PM **Matthew Sinnott,** *Birkbeck College and UCL*
Combining Information from Crosslinks and Monolinks in the Modelling of Protein Structures

2:00 PM **CompMS Keynote**
Sunkyu Kim, *Korea University*
Proceedings Presentation: *Improved survival analysis by learning shared genomic information from pan-cancer data*

2:40 PM **Laurent Gatto,** *UCLouvain*
MSnbase, efficient and elegant R-based processing and visualisation of raw mass spectrometry data

2:50 PM **Matthias Fahrner,** *University of Freiburg*
Democratizing DIA analysis on public cloud infrastructures via Galaxy

3:20 PM **Eralp Dogu,** *Mugla Sitki Kocman University*
Isolation forests improve the capability to detect quality problems in mass spectrometry-based proteomics

3:40 PM **Matthew The,** *KTH Stockholm*
Focus on the spectra that matter by clustering of quantification data in shotgun proteomics

4:00 PM **Tsung-Heng Tsai,** *Kent State University*
Selection of features with consistent profiles improves relative protein quantification in mass spectrometry experiments

4:20 PM **Seunghyuk Choi,** *Hanyang University*
Proceedings Presentation: *MutCombinator: Identification of mutated peptides allowing combinatorial mutations using nucleotide-based graph search*

5:00 PM **Yun-En Chung,** *University of Ottawa*
MealTime-MS: A machine learning-guided real-time mass spectrometry analysis for protein identification and efficient dynamic exclusion

5:20 PM **Lei Wang,** *Indiana University*
Reducing false peptide-spectrum matches in peptide identification using spectrum clustering

5:40 PM **Kaiyuan Liu,** *Indiana University*
Full-Spectrum Prediction of Peptides Tandem Mass Spectra using Deep Neural Network

5:50 PM **Andy Lin,** *University of Washington*
Strategies for controlling false discovery rate when only a subset of peptides in a sample are of interest

COMPMS COSI

COSI TRACK PRESENTATIONS

THURSDAY, JULY 16

CompMS
Computational Mass Spectrometry

10:40 AM **Shuzhao Li,** *Jackson Laboratory for Genomic Medicine*
An invitation to Computational Metabolomics

10:50 AM **Jeff Xia,** *McGill University*
The Journey of MetaboAnalyst

11:00 AM **Kai Dührkop,** *Friedrich-Schiller-University Jena*
Classes for the masses: Systematic classification of unknowns using fragmentation spectra

11:20 AM **Soha Hassoun,** *Tufts University*
Pathway-Activity Likelihood Analysis and Metabolite Annotation for Untargeted Metabolomics using Probabilistic Modeling

12:00 PM **CompMS Keynote**
David Wishart
In Silico Metabolomics - Tools to Illuminate the Dark Matter of the Metabolome

3:20 PM **Douglas Walker,** *Mount Sinai*
A call to create a true exposome database for untargeted chemical profiling

3:40 PM **Sebastian Böcker,** *Friedrich-Schiller-University Jena*
ZODIAC: database-independent molecular formula annotation using Gibbs sampling reveals novel small molecules

3:50 PM **Justin Jj van der Hooft,** *Wageningen University*
Spec2Vec: Improved mass spectral similarity scoring through learning of structural relationships

4:00 PM **Robert Ahrends,** *University of Vienna*
LipidCreator workbench to probe the lipidomic landscape

4:10 PM **Steffen Neumann,** *Leibniz Institute of Plant Biochemistry*
The metaRbolomics Toolbox in Bioconductor and beyond

4:40 PM **Cecilia Noecker**
Using metabolic models to integrate microbiomes and metabolomes

4:00 PM **CompMS Keynote**
Tsung-Heng Tsai, *Kent State University*
Selection of features with consistent profiles improves relative protein quantification in mass spectrometry experiments

EDUCATION COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY. 14

10:40 AM **Education Keynote**
Bérénice Batut, *University of Freiburg*
Empowering usable, and comprehensive bioinformatics training

11:20 AM **Anna Swan** *EMBL-EBI*
Online learning from EMBL-EBI with the new and improved Train online

12:00 PM **Zahra Mungloo-Dilmohamud,** *University of Mauritius*
Classes for the masses: Systematic classification of unknowns using fragmentation spectra

12:20 PM **Tony Wildish,** *European Bioinformatics Institute*
Staff Education to Accelerate the Cloud Adoption

2:00 PM **Verena Ras,** *University of Cape Town*
IMPLEMENTATION OF ADVANCED BIOINFORMATICS EDUCATION ACROSS AFRICA

2:20 PM **Patricia Carvajal-Lopez,** *EMBL-EBI*
DIAGNOSING THE HEALTH OF BIOINFORMATICS EDUCATION IN LATIN AMERICA

2:40 PM **Diana Marek,** *SIB Swiss Institute of Bioinformatics*
Applying best practices to enhance bioinformatics training in Switzerland

3:20 PM **Russell Schwartz,** *Carnegie Mellon University*
Data Science Training for Experimental Biology Graduate Students

3:40 PM **Peter Causey-Freeman,** *University of Manchester*
Embedding skills for a new profession by teaching programming in an immersive and authentic environment

4:00 PM **Joshua Kangas,** *Carnegie Mellon University*
An Introduction to Modern Computational Biology through Microbiome Research for High School Students

4:20 PM **Mihai Pop,** *University of Maryland, College Park*
Introducing genome assembly to the general public through interactive word games

5:00 PM **Rochelle E. Tractenberg,** *Georgetown University and the Collaborative for Research on Outcomes and -Metrics*
Guidelines for curriculum and course development in higher education and training

5:20 PM **Education Keynote**
Cecilia Noecker
Using metabolic models to integrate microbiomes and metabolomes

EVOLCOMPGEN COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY. 14

Evolution &
Comparative Genomics
EvolCompGen

10:40 AM **Erin Molloy,** *University of Illinois at Urbana-Champaign*
Proceedings Presentation: FastMulRFS: Fast and accurate species tree estimation under generic gene duplication and loss models

11:00 AM **Carolin Kosiol,** *University of St Andrews*
Species tree estimation with selection

11:10 AM **Wataru Iwasaki,** *The University of Tokyo*
Graph Splitting: A Graph-Based Approach for Superfamily-Scale Phylogenetic Tree Reconstruction

11:20 AM **Zhe Yu,** *University of Ottawa*
Gaps and runs in syntenic alignments

11:30 AM **VerenaSamuel Briand, Ras,** *University of Montreal*
A Solution to the Labeled Robinson-Foulds Distance Problem

12:00 PM **Amin Emad,** *McGill University*
Tissue-guided LASSO for prediction of clinical drug response using preclinical samples

12:20 PM **Hazal Koptagel,** *KTH Royal Institute of Technology*
A Probabilistic Framework for Cell Lineage Tree Reconstruction

12:30 PM **Esaie Kuitche Kamela,** *Université de Sherbrooke*
Splicing-structure-based selection of protein isoforms improves the accuracy of gene tree reconstruction

12:40 PM **Yufeng Wu,** *University of Connecticut*
Proceedings Presentation: Inference of Population Admixture Network from Local Gene Genealogies: a Coalescent-based Maximum Likelihood Approach

2:00 PM **Dongjoon Lim,** *McGill University*
Proceedings Presentation: EvoLSTM: Context-dependent models of sequence evolution using a sequence-to-sequence LSTM

2:20 PM **Giltae Song,** *Pusan national University*
Gene annotation refinement software using synteny based mapping

2:30 PM **Lauren McKinnon,** *Brigham Young University*
A Comprehensive Analysis of the Phylogenetic Signal in Ramp Sequences in 211 Vertebrates

2:40 PM **Gurmeet Kaur,** *NCBI NIH*
Highly-regulated and diverse NTP-based biological conflict systems with implications for emergence of multicellularity

2:50 PM **David Sankoff,** *University of Ottawa*
Integrated synteny- and similarity-based inference on the polyploidization-fractionation cycle

3:20 PM **Ron Zeira,** *Princeton University*
Proceedings Presentation: Copy Number Evolution with Weighted Aberrations in Cancer

3:40 PM **Linda K. Sundermann,** *University of Toronto*
Reconstructing Tumor Evolutionary Histories and Clone Trees in Polynomial-time with SubMARine

3:50 PM **Christine Charvet,** *Delaware State University*
Structural and transcriptional variation linked to protracted human frontal cortex development

4:00 PM **John Lee,** *Cold Spring Harbor Laboratory*
CoCoCoNet: Conserved and Comparative Co-expression Across a Diverse Set of Species

4:10 PM **Soumitra Pal,** *National Institute of Health*
Modeling gene expression evolution with EvoGeneX uncovers differences in evolution of species, organs and sexes

4:20 PM **Metin Balaban,** *University of California San Diego*
Proceedings Presentation: Phylogenetic double placement of mixed samples

5:00 PM **Palash Sashittal,** *University Of Illinois at Urbana-Champaign*
Proceedings Presentation: Sampling and Summarizing Transmission Trees with Multi-strain Infections

5:20 PM **Janani Ravi,** *Michigan State University*
An integrative computational evolutionary approach to understand the protein repertoire in bacterial pathogens

EVOLCOMPGEN COSI

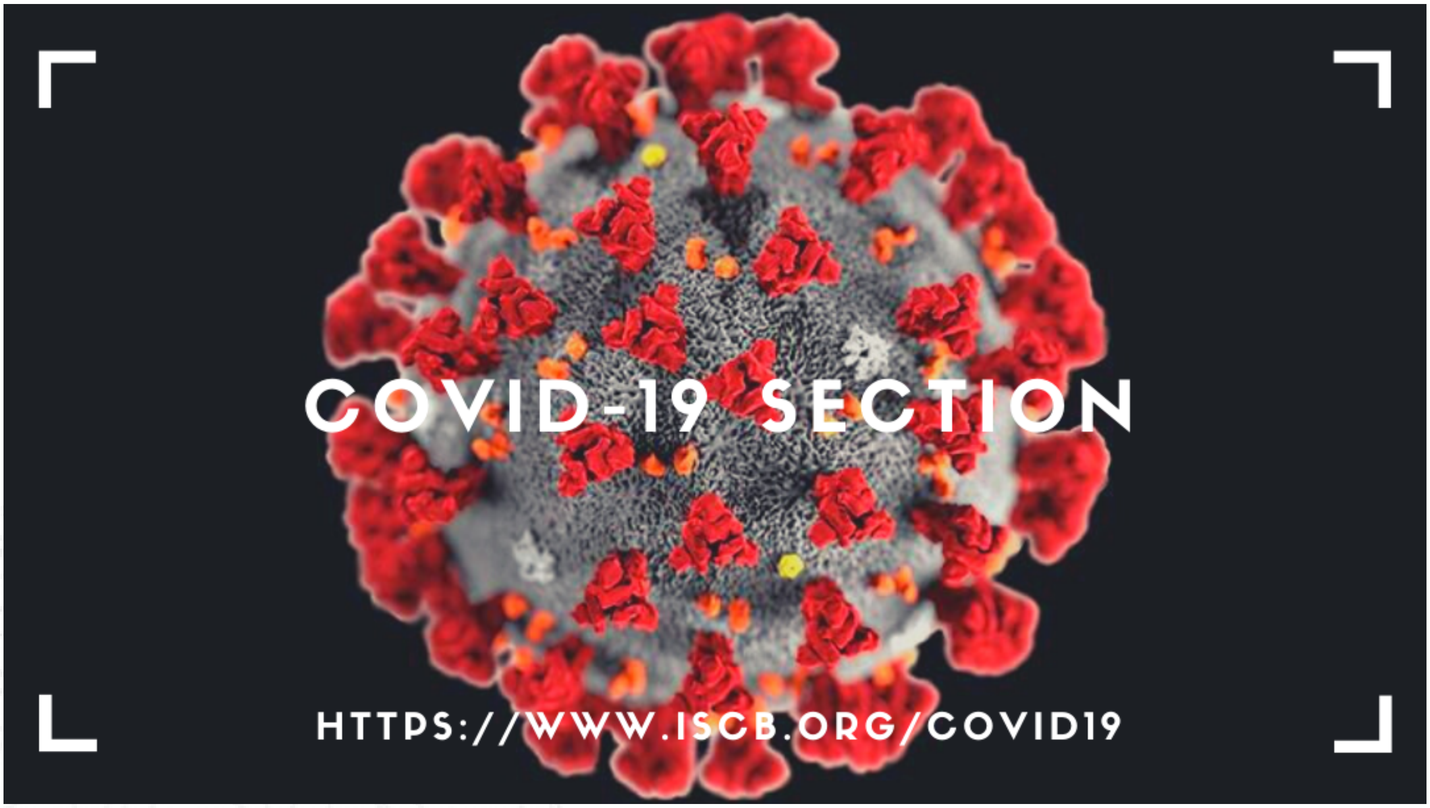
COSI TRACK PRESENTATIONS

TUESDAY, JULY. 14

5:30 PM **Malay Basu,** University of Alabama
Reading the book of life: the language of proteins

5:40 PM **Edward Braun,** Univeristy of Florida
What is the structure of the 'evolutionary model space' for proteins?

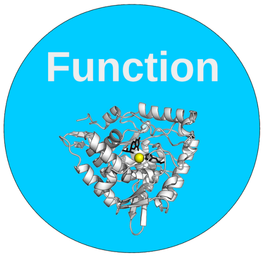
5:50 PM **Avital Sharir-Ivry,** McGill University
On quantifying evolutionary importance of protein sites: A tale of two measures



FUNCTION COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 13



10:40 AM **Function COSI Keynote**
Richard J. Roberts
DNA methylases – computation, experiments and new biology

12:00 PM **Rabie Saidi,** *EMBL-EBI*
Update on Protein Functional Annotation in UniProt in 2020

12:20 PM **Nicola Bordin,** *University College London*
Pruning the Protein Jungle: recent developments in the CATH-Gardener function analysis and prediction pipeline.

2:00 PM **Alex Warwick Vesztrocy,** *University of Lausanne*
Proceedings Presentation: Benchmarking Gene Ontology Function Predictions Using Negative Annotations

2:20 PM **Matthew Hahn,** *Indiana University*
Proceedings Presentation: The Ortholog Conjecture Revisited: the Value of Orthologs and Paralogs in Function Prediction

2:40 PM **Dina Svetlitsky** *Ben Gurion University of the Negev*
Proceedings Presentation: Discovery of multi-operon colinear syntenic blocks in microbial genomes

3:20 PM **Function COSI Keynote**
Carolyn Lawrence-Dill *Iowa State University,*
Saving Time at the Bench and in the Field: Predicting Gene Function and Phenotype in Crops

4:00 PM **Maxat Kulmanov,** *King Abdullah University of Science and Technolog*
DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier

4:20 PM **Lizhi Liu,** *Fudan University*
HPOLabeler: Improving Prediction of Human Protein-Phenotype Associations by Learning to Rank

5:00 PM **Constance Jeffery,** *University of Illinois at Chicago*
Enzymes, Moonlighting Enzymes, Pseudoenzymes: Similar in Sequence, Different in Function

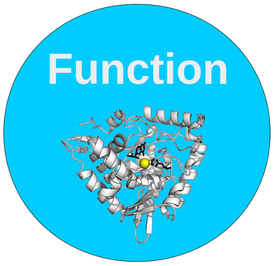
5:20 PM **Yanbin Yin,** *University of Nebraska-Lincoln*
eCAMI: simultaneous classification and motif identification for enzyme annotation

5:40 PM **Meet Barot,** *New York University*
Learning sequence, structure and network features for protein function prediction

FUNCTION COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY 14



10:40 AM **Function COSI Keynote**
Gary Bader, *University of Toronto*

11:20 AM **Wayne Hayes,** *UCI*
Cross-species functional prediction by global network alignment

12:00 PM **Damiano Piovesan,** *University of Padova*
Silvio Tosatto, *University of Padova*
Yisu Peng *Northeastern University*
Predrag Radivojac, *Northeastern University*
CAFA4 overview

2:00 PM *CAFA4 Talk1*

2:20 PM *CAFA4 Talk 2*

2:40 PM *CAFA4 Talk 3*

3:20 PM **Amelia Villegas-Morcillo,** *University of Granada*
Unsupervised protein embeddings outperform hand-crafted sequence and structure features at predicting molecular function

3:40 PM **Maria Littmann,** *(TUM*
Embeddings allow GO annotation transfer beyond homology

4:00 PM **Yuki Kagaya,** *Tohoku University*
ContactPFP: Protein Function Prediction Using Predicted Contact Information

4:20 PM **Ehsaneddin Asgari,** *University of California, Berkeley*
Fine-tuning of Language Model-Based Representation for Protein Functional Annotation

5:00 PM **Damiano Piovesan,** *University of Padova*
INGA protein function prediction for the dark proteome

5:20 PM **Kyle Hippe,** *Pacific Lutheran University*
CaoLab: Protein function and disorder prediction from sequence based on RNN

5:40 PM **John Hover,** *Cold Spring Harbor Laboratory*
Protein function inference via curated aggregate co-expression networks.

GENERAL COMP BIO

COSI TRACK PRESENTATIONS

THURSDAY, JULY 16

10:40 AM **Nour Almadhoun,** *Bilkent University*
Proceedings Presentation: Inference Attacks Against Differentially-Private Query Results from Genomic Datasets Including Dependent Tuples

11:00 AM **Florian Schmidt** *A-Star Institute Singapore*
RCA2 - An improved framework for reference-based clustering of single cell transcriptomes

11:20 AM **Joseph Bonello,** *University of Malta*
Automating FAIR assessment scores

12:00 PM **Mark Lennox,** *Queen's University Belfast*
DeepPS: a transformer model for predicting general and kinase-specific phosphorylation sites

12:20 PM **Ian Reddin,** *University of Kent*
Drug-adapted cancer cell lines reveal drug-induced heterogeneity and enable the identification of biomarker candidates for the acquired resistance setting

3:20 PM **Yannik Schälte** *Helmholtz Zentrum München*
Proceedings Presentation: Efficient Exact Inference for Dynamical Systems with Noisy Measurements using Sequential Approximate Bayesian Computation

3:40 PM **Kalaivani Raju,** *Mogrify Limited*
Mogrify: A computational framework to convert between cell types

4:00 PM **Carlos Outeiral Rubiera,** *University of Oxford*
Investigating the potential of quantum computing for protein folding

4:10 PM **Trang T. Le,** *University of Pennsylvania*
Analysis of ISCB honorees and keynotes reveals disparities

4:40 PM **Amirali Aghazadeh,** *University of California, Berkeley*
Proceedings Presentation: CRISPRLand: Interpretable Large-Scale Inference of DNA Repair Landscape Based on a Spectral Approach

5:00 PM **Pablo Camara,** *University of Pennsylvania*
Single-cell transcriptomic analysis of highly-multiplexed cytometry data via antigen mapping

5:20 PM **Mehrdad Bakhtiari,** *University of California San Diego*
Variable Number Tandem Repeats mediate the expression of proximal genes

5:40 PM **Prashant Emani,** *Yale University*
Inferring identifying characteristics through pooling of information across genotypic trajectories

HITSeq COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **HITSeq COSI Keynote**
Karen Migan *UC Santa Cruz*
Genetic and epigenetic maps of human centromeric regions

12:00 PM **Tatiana Dvorkina,** *Saint Petersburg State University*
Proceedings Presentation: The String Decomposition Problem and its Applications to Centromere Analysis and Assembly

12:20 PM **Chirag Jain,** *National Institutes of Health*
Proceedings Presentation: Weighted minimizer sampling improves long read mapping

12:40 PM **Alla Mikheenko,** *Saint Petersburg State University*
Proceedings Presentation: TandemTools: mapping long reads and assessing/improving assembly quality in extra-long tandem repeats

2:00 PM **Sebastian Niehus,** *Berlin Institute of Health (BIH)*
PopDel detects large deletions jointly in tens of thousands of genomes

2:20 PM **Nathan Lapierre,** *University of California*
Metalign: Efficient alignment-based metagenomic profiling via containment min hash

2:40 PM **Harun Mustafa,** *ETH Zürich*
META^2: Memory-efficient taxonomic classification and abundance estimation for metagenomics with deep learning

3:20 PM **Kristoffer Sahlin,** *Stockholm University*
Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis

3:40 PM **Ying Chen,** *Genome Institute of Singapore*
Reference-guided transcript discovery and quantification for long read RNA-Seq data

4:00 PM **Jonas A. Sibbesen,** *University of California Santa Cruz*
Improving RNA-seq mapping and haplotype-specific transcript inference using variation graphs

4:20 PM **Hirak Sarkar,** *University of Maryland*
Proceedings Presentation: Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data

5:00 PM **HITSeq COSI Keynote**
Hagen Tilgner, *Weill Cornell Medicine*
Hitseq Keynote: Cell-type specific isoform expression of coding and non-coding genes

HITSeq COSI

TRACK PRESENTATIONS

THURSDAY, JULY 16

10:40 AM **HITSeq COSI Keynote**
Michel Schatz, *Johns Hopkins University*
Genomics 2020: Real-time Nanopore signal mapping, learned index structures, and comparisons across hundreds of thousands of genomes

12:00 PM **Ermin Hodzic,** *Simon Fraser University*
Proceedings Presentation: Identification of Conserved Evolutionary Trajectories in Tumors

12:20 PM **Matthew Myers,** *Princeton University*
Proceedings Presentation: Identifying tumor clones in sparse single-cell mutation data

12:40 PM **Farid Rashidi Mehrabadi,** *National Institutes of Health*
Proceedings Presentation: PhISCS-BnB: A Fast Branch and Bound Algorithm for the Perfect Tumor Phylogeny Reconstruction Problem

3:20 PM **Ken Chen,** *University of Texas MD Anderson Cancer Center*
Single-cell copy number lineage tracing enabling gene discovery

3:40 PM **Qiuyu Lian,** *Tsinghua University*
Proceedings Presentation: Artificial-Cell-Type Aware Cell Type Classification in CITE-seq

4:00 PM **Benjamin DeMeo,** *Massachusetts Institute of Technology*
Proceedings Presentation: Hopper: A Mathematically Optimal Algorithm for Sketching Biological Data

4:40 PM **Xinrui Lyu,** *ETH Zürich*
Proceedings Presentation: Mutational Signature Learning with Supervised Negative Binomial Non-Negative Matrix Factorization

5:00 PM **Hongyu Zheng,** *Carnegie Mellon University*
Proceedings Presentation: Improved Design and Analysis of Practical Minimizers

5:20 PM **Camille Marchet,** *EBI*
Proceedings Presentation: REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets

5:40 PM **Xian Chang,** *University of California Santa Cruz*
Proceedings Presentation: Distance Indexing and Seed Clustering in Sequence Graphs

MICROBIOME COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **MICROBIOME COSI Keynote**
Niranjan Nagarajan, *Genome Institute of Singapore*
Assembling and modelling complex microbiomes mediating host-pathogen interactions

11:20 AM **Satria Ardhe Kautsar,** *Wageningen University*
Charting the secondary metabolic diversity of 209,211 microbial genomes and metagenome-assembled genomes

11:30 AM **Harihara Subrahmaniam Muralidharan,** *University of Maryland, College Park*
PIRATE- Phage Identification fRom Assembly-graph varianT Elements

12:00 PM **Anuradha Wickramarachchi,** *Australian National University*
Proceedings Presentation: MetaBCC-LR: Metagenomics Binning by Coverageand Composition for Long Reads

12:20 PM **Jacquelyn S Meisel,** *University of Maryland, College Park*
Assembly graph-based variant discovery reveals novel dynamics in the human microbiome

12:30 PM **Theodora Lo,** *Canada's Michael Smith Genome Sciences Centre*
Meta-NanoSim: metagenome simulator for nanopore reads

2:00 PM **MICROBIOME COSI Keynote**
Amy Willis
The analysis of microbiome data from biased high-throughput sequencing

2:40 PM **Sylvain Riondet,** *Genome Institute of Singapore*
PLoT-ME: Pre-classification of Long-reads for Memory Efficient Taxonomic assignment

2:50 PM **Caitlin Simopoulos,** *University of Ottawa*
pepFunk: an R shiny app and workflow for peptide-centric functional analysis of metaproteomic microbiome data

3:20 PM **Vitor C. Piro,** *Hasso Platner Institute*
Proceedings Presentation: ganon: precise metagenomics classification against large and up-to-date sets of reference sequences

3:40 PM **Patrick Smyth,** *University of Ottawa*
Studying the dynamics of the gut microbiota using metabolically stable isotopic labeling and metaproteomics

3:50 PM **Dmitry Rodionov,** *Sanford-Burnham-Prebys Medical Discovery Institute*
Phenotypic characterization of complex microbial communities

4:00 PM **Alice McHardy,** *Helmoltz Centre for Infection Research*
Introduction to CAMI

4:10 PM **Alex Sczyrba,** *Bielefeld University*
Assembly results for second round of CAMI challenges

4:20 PM **Fernando Meyer,** *Helmoltz Centre for Infection Research*
(Taxonomic) binning results for the second round of CAMI challenges

4:30 PM **David Koslicki,** *Pennsylvania State University*
Profiling results for the second round of CAMI challenges

4:40 PM **Benoit Kunath,** *Luxembourg Centre for Systems Biomedicine*
Expanding CAMI towards metaproteomics

5:00 PM **Caroline Weis,** *ETH Zurich*
Proceedings Presentation: Topological and kernel-based microbial phenotype prediction from MALDI-TOF mass spectra

5:20 PM **Jakob Nissen,** *Technical University of Denmark*
Deep learning for binning and high resolution taxonomic profiling of microbial genomes

5:30 PM **Derek Reiman,** *University of Illinois at Chicago*
MiMeNet: Exploring the Microbiome-Metabolome Relationships using Neural Networks

5:40 PM **Luis Pedro Coelho,** *Fudan University*
Machine-learning based prospection of antimicrobial peptides (AMPs) from metagenomes using Macrel

5:50 PM- **Shaojun Pan,** *Fudan University*
Identifying short open reading frames (smORFs) with deep learning

MLCSB COSI

TRACK PRESENTATIONS

MONDAY, JULY 13

10:40 AM **Debora Marks**
Emergent pathogens, vaccines and therapeutics : how can computation accelerate discovery?

12:00 PM **Yang Zhang,** *Carnegie Mellon University*
Proceedings Presentation: Cancer mutational signatures representation by large-scale context embedding

12:20 PM **Aayush Grover,**
International Institute of Information Technology
Proceedings Presentation: MHCAttnNet: Predicting MHC-Peptide Bindings for MHC Alleles Classes I & II Using An Attention-Based Deep Neural Model

2:00 PM **Anshul Kundaje,** *Stanford University*
Deep learning at base-resolution reveals motif syntax of the cis-regulatory code

3:20 PM **Alex Tseng,** *Stanford University*
Fourier-transform-based attribution priors improve the stability and interpretability of deep learning models for regulatory genomics

3:40 PM **Ron Schwessinger,** *University of Oxford*
Dissecting the grammar of chromatin architecture using megabase scale DNA sequence with deep neural networks and transfer learning

4:00 PM **Asa Thibodeau,** *The Jackson Laboratory for Genomic Medicine*
CoRE-ATAC: A Deep Learning model for the Classification of Regulatory Elements from single cell and bulk ATAC-seq data

4:20 PM **Jacob Schreiber,** *University of Washington*
Zero-shot imputations across species are enabled through joint modeling of human and mouse epigenomics

4:40 PM **Chendi Wang** *The University of British Columbia*
A Combined Species Model using Branched Multitask Routing Networks

5:00 PM- **Zichen Wang,** *University of California, Los Angeles*
Proceedings Presentation: Towards Heterogeneous Information Fusion: Bipartite Graph Convolutional Networks for In Silico Drug Repurposing

5:20 PM **Srivamshi Pittala,** *Dartmouth College*
Learning Context-aware Structural Representations to Predict Antigen and Antibody Binding Interfaces

5:30 PM **Jannis Born,** *ETH Zurich*
PaccMann^RL: Designing anticancer drugs from transcriptomic data via reinforcement learning

5:40 PM **Amin Emad,** *McGill University*
Tissue-guided LASSO for prediction of clinical drug response using preclinical samples

5:50 PM **Nadav Brandes,** *The Hebrew University of Jerusalem*
Quantifying gene selection in cancer through protein functional alteration bias

MLCSB COSI

TRACK PRESENTATIONS

TUESDAY, JULY 14

10:40 AM **Maria Chikina,** *University of Pittsburgh*
Finding concise descriptors of genomic data

12:00 PM **Steven M. Hill,** *University of Cambridge*
PCausal network learning using a semi-supervised approach

12:20 PM **Assya Trofimov,** *IRIC - Université de Montréal*
Proceedings Presentation: Factorized embeddings learns rich and biologically meaningful embedding spaces using factorized tensor decomposition

2:00 PM **Ayse Dincer,** *Univeristy of Washington*
Adversarial Deconfounding Autoencoder for Learning Robust Gene Expression Embeddings

2:20 PM **Shaoheng Liang,**
The University of Texas MD Anderson Cancer Center
Latent periodic process inference from single-cell RNA-seq data

2:40 PM **Stefan Stark,** *ETH Zürich*
SCIM: Universal Single-Cell Matching with Unpaired Feature Sets

3:20 PM **Helena Todorov,** *Ghent University*
Proceedings Presentation: TinGa: fast and flexible trajectory inference with Growing Neural Gas

3:40 PM **Kai Cao,** *Chinese Academy of Sciences*
Proceedings Presentation: Unsupervised Topological Alignment for Single-Cell Multi-Omics Integration

4:00 PM **Jacob Kimmel,** *Calico Life Sciences, LLC*
scNym: Semi-supervised neural networks for single cell identity classification

4:20 PM **Rebecca Santorella,** *Brown University*
Gromov-Wasserstein based optimal transport to align single-cell multi-omics data

4:30 PM **David Wang,** *University of Pennsylvania*
A Non-Parametric Bayesian Framework for Detecting Coregulated Splicing Signals in Heterogeneous RNA Datasets with Applications to Acute Myeloid Leukemia

5:00 PM **Nikolaus Fortelny,** *CeMM Center*
Knowledge-primed neural networks enable biologically interpretable deep learning on single-cell sequencing data

5:10 PM **Yichen Zhang,** *University of British Columbia*
DeepPLIER: a deep learning approach to pathway-level representation of gene expression data

5:20 PM **David Merrell,** *University of Wisconsin*
Inferring Signaling Pathways with Probabilistic Programming

5:30 PM **Peter Koo,** *Cold Spring Harbor Laboratory*
Can We Trust Convolutional Neural Networks for Genomics?

NETBIO COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **NetBio Keynote**
Albert-Laszlo Barabasi
Network Medicine: From Cellular Networks to the Human Diseasome

11:20 AM **Noel Malod-Dognin,** *Barcelona Supercomputing Center (BSC)*
Proceedings Presentation: Chromatin network markers of leukemia

12:00 PM **Anja Gumpinger,** *Havard Medical School*
Proceedings Presentation: Prediction of cancer driver genes through network-based moment propagation of mutation scores

12:20 PM **Mostafa Karimi,** *Texas A&M University*
Proceedings Presentation: Network-principled deep generative models for designing drug combinations as graph sets

2:00 PM **NetBio Keynote:**
Anastasia Baryshnikova
Genome-wide phenotypic screens: the total is greater than the sum of the parts

2:40 PM **2:40 PM** *Technical University of Munich*
BiCoN: Network-constrained biclustering of patients and omics data

2:50 PM **Cagatay Dursun,** *Marquette University*
PhenoGeneRanker: A Tool for Gene Prioritization Using Complete Multiplex Heterogeneous Networks

3:20 PM **Marieke Kuijjer,** *University of Oslo*
Understanding tissue-specific gene regulation by miRNAs

3:40 PM **Robin Haw,** *Ontario Institute for Cancer Research*
The Reactome Pathway Knowledgebase: Variants, Dark Proteins and Functional Interactions

3:50 PM **Benjamin Harris,** *Cold Spring Harbor Laboratory*
Multiscale Co-expression in the Brain

4:00 PM **Kayla Johnson,** *Michigan State University*
A comparison of normalization and transformation techniques for constructing gene co-expression networks from RNA-seq data

4:10 PM **Qi Li,** *University of Notre Dame*
Supervised prediction of aging-related genes from a dynamic context-specific protein interaction subnetwork

4:20 PM **Kapil Devkota,** *Tufts University*
Proceedings Presentation: GLIDE: Combining Local Methods and Diffusion State Embeddings to Predict Missing Interactions in Biological Networks

5:00 PM **Mengshi Zhou,** *Case Western Reserve University*
Proceedings Presentation: Combining phenome-driven drug target prediction with patients' electronic health records-based clinical corroboration towards drug discovery

5:20 PM **Midori Iida,** *Kyushu Institute of Technology,*
Proceedings Presentation: Network-based characterization of disease-disease relationships in terms of drugs and therapeutic targets

5:40 PM **Chun-Yu Lin,** *National Chiao Tung University*
Membrane protein-regulated networks across human cancers

NETBIO COSI

TRACK PRESENTATIONS

THURSDAY, JULY 16

10:40 AM **NetBio Keynote**
Roded Sharan
A systematic approach to orient the human protein-protein interaction network

11:20 AM **Torsten Gross,** *Humboldt University*
Proceedings Presentation: Identifiability and experimental design in perturbation studies

12:00 PM **Yu Xia,** *McGill University*
Estimating Dispensable Content in the Human Interactome

12:20 PM **Emily Ackerman,** *University of Pittsburgh*
Identifying Regulators of Infection in Virus-Host Networks

12:30 PM **Jordan Berg,** *University of Utah*
Modeling and Identifying Regulatory Patterns within Chaotic Metabolic Networks

REGSYS COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **Shaun Mahony,** *The Pennsylvania State University*
RegSys Introduction

10:45 AM **REGSYS Keynote**
Wyeth Wasserman, *University of British Columbia*
Detection of functional cis-regulatory variations causal for rare genetic disorders

11:20 AM **Divyanshi Srivastava,** *The Pennsylvania State University*
Hox binding specificity is directed by DNA sequence preferences and differential abilities to engage inaccessible chromatin

12:00 PM **Abhimanyu Banerjee,** *Stanford University*
Deep learning models of 422 C2H2 Zinc Finger transcription factor binding profiles reveal alternate combinatorial DNA binding sequence preferences

12:20 PM **Yi Liu,** *University of Chicago*
Proceedings Presentation: Fully Interpretable Deep Learning Model of Transcriptional Control

2:00 PM **REGSYS Keynote**
Sara Mostafavi, *University of British Columbia*
Deep Learning of Immune Differentiation

2:40 PM **Irene Kaplow,** *Carnegie Mellon University*
A guide to predicting activity of enhancer orthologs in hundreds of species

3:20 PM **Christoph J. Thieme,** *MDC Berlin*
Comparison of chromatin contacts maps from GAM and Hi-C reveals method specific interactions linked with active and inactive chromatin

3:40 PM **Abbas Roayaei Ardakany,** *la jolla institute for allergy and immunology*
Proceedings Presentation: Fully Interpretable Deep Learning Model of Transcriptional Control

4:00 PM **Brittany Baur,** *University of Wisconsin-Madison*
Deciphering the role of 3D genome organization in breast cancer susceptibility

4:20 PM **Jeffrey Wang,** *La Jolla Institute for Immunology*
dcHiC: Differential Compartment Analysis of Hi-C datasets.

5:00 PM **REGSYS Keynote**
Dana Pe'Er, *Memorial Sloan Kettering Cancer Center*
A single cell lens into regulatory inference

5:40 PM **Aditya Pratapa,** *Virginia Tech*
How to build regulatory networks from single-cell gene expression data

REGSYS COSI

TRACK PRESENTATIONS

THURSDAY, JULY 16

10:40 AM **REGSYS Keynote**
Francesca Luca *The Pennsylvania State University*
Genetic regulation of gene expression, environmental contexts and disease risk

11:20 AM **Lucia Ramirez-Navarro,** *Universidad Nacional Autónoma de México*
Characterization of regulatory variants in promoters with enhancer activity and their relation with human diseases

12:00 PM **Jennifer Zou,** *UCLA*
Learning global patterns of epigenetic variation across individuals

12:20 PM **Zeyang Shen,** *University of California San Diego*
Proceedings Presentation: MAGGIE: leveraging genetic variation to identify DNA sequence motifs mediating transcription factor binding and function

3:20 PM **REGSYS Keynote**
Christina Leslie
A unified atlas of CD8 T cell dysfunctional states in cancer and infection

4:00 PM **Christian Lee,** *Ontario Institute of Cancer Research*
Investigating regional somatic mutation rate variation across functional elements in whole cancer genomes

4:40 PM **REGSYS Keynote**
Quaid Morris, *Memorial Sloan Kettering Cancer Centre*
RNA-binding proteins and their targets

5:20 PM **Shaoke Lou,** *Yale University*
Proceedings Presentation: TopicNet: a framework for measuring transcriptional regulatory network change

5:40 PM **Shilu Zhang,** *University of Wisconsin-Madison*
Defining cell type-varying networks of chromatin marks and transcription factors underlying cell-fate transition dynamics

iRNA COSI

TRACK PRESENTATIONS

MONDAY, JULY 13

10:40 AM **iRNA Keynote**
Ana Conesa, *University of Florida*
The Functional Iso-Transcriptomics toolset to leverage long reads sequencing for unraveling isoform transcriptional networks from single cells.

11:20 AM **Fairlie Reese,** *University of California, Irvine*
Swan: a Python library for the analysis and visualization of long-read transcriptomes

11:30 AM **Andrey D. Prjibelski,** *St. Petersburg State University*
IsoQuant: isoform analysis and quantification with long error-prone transcriptomic reads

12:00 PM **Xi Wang,** *German Cancer Research Center*
Full-length transcriptome reconstruction reveals a large diversity of RNA and protein isoforms in rat hippocampus

12:10 PM **Baraa Orabi,** *The University of British Columbia,*
Freddie: Annotation-free Isoform Discovery Using Long-Read Sequencing

12:20 PM **Shamsuddin Bhuiyan,** *The University of British Columbia*
Prioritizing genes likely to have functionally distinct splice isoforms using long read RNA-seq data

12:30 PM **Yoseph Barash,** *University of Pennsylvania*
iRNA Panel Discussion: Long-read RNA-seq

2:00 PM **Étienne Fafard-Couture,** *Université de Sherbrooke*
Inferring snoRNA characteristics from their abundance profile in healthy human tissues

2:20 PM **Athanasios Zovoilis,** *University of Lethbridge*
Dissecting the role of SINE non-coding RNAs in amyloid pathology: An integrative RNA genomics approach.

2:40 PM **Ziynet Nesibe Kesimoglu,** *Marquette University*
Inferring competing endogenous RNA (ceRNA) interactions in cancer

3:20 PM **Shuze Wang,** *University of Michigan*
Single Cell Chromatin Accessibility Delineates Cellular Identities of the Neonatal Organ of Corti

3:40 PM **Avi Srivastava,** *Stony Brook university*
Proceedings Presentation: A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification

4:00 PM **iRNA Keynote**
Athma A. Pai
The race to the 3' end: tracking mRNA cleavage diversity in real time

5:00 PM **Anupama Jha,** *University of Pennsylvania*
RBP-Pokedex: Prediction of RBP knockdown effect via DNN experiment modeling

5:20 PM **Hiroki Takizawa,** *University of Wisconsin-Madison*
Proceedings Presentation: Finding the Direct Optimal RNA Barrier Energy and Improving Pathways with an Arbitrary Energy Model

5:40 PM **Teresa Müller,** *University Freiburg*
Proceedings Presentation: The locality dilemma of Sankoff-like RNA alignments

6:00 PM *iRNA: Social Hour*

iRNA COSI

TRACK PRESENTATIONS

TUESDAY, JULY 14

10:40 AM **Ploy Pratanwanich,** *Genome Institute of Singapore*
Detection of differential RNA modifications from direct RNA sequencing of human cell lines

11:00 AM **Noel-Marie Plonski,** *Kent State University*
RNA editing landscapes: a new model for biomarkers discovery in neurological disease

11:20 AM **Ali Imami,** *University of Toledo*
BORE - Detecting RNA Editing Events comfortably

11:30 AM **Yoseph Barash,** *University of Pennsylvania*
iRNA: Poster Session

2:00 PM **iRNA Keynote**
Jérôme Waldispühl, *McGill University*
Non-canonical base pair interactions improve the scalability and accuracy of the prediction and analysis of RNA 3D structures

2:40 PM **Yu Li,** *KAUST*
RNA Secondary Structure Prediction By Learning Unrolled Algorithms

2:50 PM **Tom MacDougall,** *Université de Montréal*
Elucidating the Automatically Detected Features Used By Deep Neural Networks for RFAM family classification

3:20 PM **Liang Huang,** *Oregon State University*
Proceedings Presentation: LinearPartition: Linear-Time Approximation of RNA Folding Partition Function and Base Pairing Probabilities

3:40 PM **Zichao Yan,** *McGill University,*
Proceedings Presentation: Graph neural representational learning of RNA secondary structures for predicting RNA-protein interactions

4:00 PM **Elena Matveishina,** *Lomonosov Moscow State University*
Practical Guidance for Genome-Wide RNA:DNA Triple Helix Prediction

4:10 PM **Osvaldo Rivera,** *University of Pennsylvania*
Splicing variations contribute to the functional dysregulation of genes in acute myeloid leukemia.

4:20 PM **Yang Pan,** *UCLA,*
PEGASAS: A pathway-guided approach for analyzing pre-mRNA alternative splicing during cancer progression

5:00 PM **iRNA Keynote**
Eric Lécuyer
Systematic approaches to study the subcellular localization properties of RNAs and RNA Binding Proteins

5:40 PM **Yoseph Barash,** *University of Pennsylvania*
iRNA: concluding Remarks

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MARK YOUR CALENDARS

SYSMOD COSI

TRACK PRESENTATIONS

MONDAY, JULY 13

10:35 AM **Laurence Calzone**
Introduction to SysMod 2020

10:40 AM **Diana Széliová,** University of Natural Resources and Life Sciences
Maintenance energy is essential for accurate predictions of intracellular fluxes in CHO

11:00 AM **Sanjeev Dahal,** Queen's University
Using genome-scale model of metabolism and macromolecular expression (ME-model) to study biofilm development in Pseudomonas aeruginosa PAO1

11:20 AM **Jean-Christophe Lachance,** Université de Sherbrooke
Genome-scale metabolic modelling reveals key features of a minimal gene set

12:00 PM **Paul Francois,** McGill University
Robotic mapping and generative modelling of cytokine response

2:00 PM **Douglas A. Lauffenburger ,**
Cross-Species Translation of Biological Information via Computational Systems Modeling Frameworks

2:40 PM **Yin Hoon Chew,** Icahn School of Medicine at Mount Sinai
Towards a Human Whole-Cell Model: A Prototype Model of Human Embryonic Stem Cells

3:20 PM **Daniel Lobo,** UMBC
Whole-body regeneration and size-dependent fission controlled by a self-regulated Turing system in planaria

3:40 PM **Matteo Barberis,** University of Surrey
Clb3-centered regulations are pivotal for autonomous cell cycle oscillator designs in yeast

4:00 PM **Serhan Yılmaz,** Case Western Reserve University
Robust Inference of Kinase Activity Using Functional Networks

4:20 PM **Stephen Kotiang** Wichita State University
Probabilistic Factor Graph Modeling and Analysis of Biological Networks

5:00 PM **Mukta G. Palshikar,** University of Rochester
Executable models of pathways built using single-cell RNAseq data reveal immune cell heterogeneity in people living with HIV and atherosclerosis

5:20 PM **Jason Ko,** UMBC
Modeling Sorting, Intercalation, and Involution Tissue Behaviors due to Regulated Cell Adhesion

5:40 PM **Juilee Thakar,** University of Rochester,
Closing remarks of the first SysMod day

SYSMOD COSI

TRACK PRESENTATIONS

TUESDAY, JULY 14

10:40 AM **Maria Anna Rapsomaniki,** *IBM Research Zurich*
A stochastic hybrid model for DNA replication incorporating protein mobility dynamics

11:00 AM **Carolyn Cho ,**
Quantitative and Systems Pharmacology (QSP) and Model-Informed Drug Development (MIDD) of a "Smart" Insulin

12:00 PM **Jürgen Zanghellini,** *University of Vienna,*
Cellular robustness is not a byproduct of environmental flexibility

12:20 PM **Andreas Dräger,** *IBMI*
Closing remarks of the SysMod meeting 2020

TRANSMED COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **TRANSMED Keynote**
Jason H. Moore, *University of Pennsylvania*
20 Challenges of AI in Medicine

11:20 AM **Rui Zhu,** *Indiana University,*
Proceedings Presentation: Privacy-preserving Construction of Generalized Linear Mixed Model for Biomedical Computation

12:00 PM **Soufiane Mourragui,** *Delft University of Technology and the Netherlands Cancer Institute, Netherlands*
A versatile non-linear transfer learning framework for correcting pre-clinical-based predictors of drug response

12:30 PM *Q&A*

2:00 PM **Yifeng Tao,** *Carnegie Mellon University*
Proceedings Presentation: Robust and accurate deconvolution of tumor populations uncovers evolutionary mechanisms of breast cancer metastasis

2:20 PM **Rune Linding,** *Humboldt-Universität zu Berlin,*
Deep Hidden Physics Modeling of Cell Signaling Networks

2:30 PM **Yu-Chiao Chiu,** *The University of Texas at San Antonio*
A deep transfer learning model for extending in vitro CRISPR-Cas9 viability screens to tumors

2:40 PM **Colin Semple,** *The University of Edinburgh*
The evolution of homologous repair deficiency in high grade serous ovarian carcinoma

2:50 PM *Q&A*

3:20 PM **Lei Du,** *Northwestern Polytechnical University*
Proceedings Presentation: Identifying diagnosis-specific genotype-phenotype associations via joint multi-task sparse canonical correlation analysis and classification

3:40 PM **Jannis Born,** *ETH Zurich*
POCOVID-Net: Automatic Detection of COVID-19 From a New Lung Ultrasound Imaging Dataset (POCUS)

4:00 PM **Handan Melike Donertas,** *EMBL-EBI*
Drug repurposing to improve health and lifespan in humans

4:20 PM **Arvind Singh Mer,** *University of Toronto*
Patient Derived Xenografts Based Pharmacogenomics for Precision Medicine

4:30 PM *Q&A*

5:00 PM **Johannes Griss,** *EMBL-EBI)*
ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis

5:10 PM **TRANSMED Keynote**
Atul Butte, *Priscilla Chan and Mark Zuckerberg Distinguished Professor of Pediatrics. Bioengineering & Therapeutic Sciences, and Epidemiology & Biostatistics at UCSF*
TBD

5:50 PM **Maria Secrier,** *University College London*
Closing remarks

VARI COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 15

10:40 AM **Kelley Harris ,**
New techniques for tracing mutation spectrum evolution: from linear inverse modeling to yeast reporter assays

11:20 AM **Marzieh Eslami Rasekh,** *Boston University*
Population-specific VNTR Alleles in the Human Genome

12:00 PM **Arjun Bhattacharya,** *University of North Carolina at Chapel Hill*
Multi-omic strategies for transcriptome-wide prediction and association studies

12:20 PM **Joseph Atemia,** *icipe*
Mining next-generation genome sequencing data for genetic diversity assessment of eastern Africa finger millet blast fungus

12:30 PM **Yi-Fei Huang,** *Pennsylvania State University*
Unified inference of missense variant effects and gene constraints in the human genome

2:00 PM **Lincoln Stein,** *Ontario Institute for Cancer Research*
Somatic variant calling and interpretation in the Pan-Cancer Analysis of Whole Genomes project

2:40 PM **Remo Monti,** *Hasso Plattner Institute*
Seak marries regulatory genomics deep learning with rare-variant association tests

2:50 PM **Alex Kaplun ,** *Northwestern Polytechnical University*
Proceedings Presentation: Identifying diagnosis-Go Big Or Go Home: PCR-free WGS Long And Short Read Orthogonal Test Eliminates The Need For Multiple Platform Genetic Tests

3:20 PM **Berk Alpay,** *University of Connecticut*
Proceedings Presentation: Combinatorial and statistical prediction of gene expression from haplotype sequence

3:40 PM **Patrick May,** *Luxembourg Centre for Systems Biomedicine*
Gene family information facilitates classification of disease-causing variants and identification of pathogenic variant enriched regions

3:50 PM **Zishuo Zeng,** *Rutgers University*
A novel framework to evaluate deleteriousness of synonymous variants

4:00 PM **Joseph Chi-Fung Ng** *King's College London*
Missense variants in health and disease affect distinct functional pathways and proteomics features

4:10 PM **Silvia Benevenuta,** *University of Torino*
Calibrating variant-scoring methods for clinical decision making

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4:20 PM **VARI Keynote**
Muhammed Hasan Çelik, *Technical University of Munich*
Missense variant effect landscapes across environments and genetic backgrounds.

5:40 PM **Michal Linial,** *The Hebrew University of Jerusalem*
Proceedings Presentation: BIRD: Identifying Cell Doublets via Biallelic Expression from Single cells

TECHNOLOGY TALK

PRESENTATIONS

MONDAY, JULY 13TH

10:40 AM **Michael Reich,** *University of California*
The GenePattern Notebook Environment

11:00 AM **Suhaib Mohammed,** *EMBL-EBI)*
Expression Atlas: A platform for integrating and displaying expression data from tissues to single cells

11:20 AM **Pablo Moreno,** *EMBL-EBI)*
HiSCiAp: User-friendly, scalable tools and workflows for single-cell analysis

NIH/OD OFFICE OF DATA SCIENCE STRATEGY (ODSS) TALK

PRESENTATIONS

TUESDAY, JULY 14TH

10:40 AM **Susan Gregurick,** *NIH*

Introduction to the ODSS Data Science Sessions

11:00 AM **Atul Butte,** *UCSF*

10 lessons we learned in 10 days about clinical data interoperability in the COVID crisis

11:20 AM **Joseph Loscalzo,** *Brigham and Women's Hospital*

Network Medicine Framework for Drug Repurposing

12:00 PM **Hoifung Poon,** *Microsoft Research*

Machine Reading for Precision Medicine

12:20 PM **Elaine Nsoesie,** *Boston University*

Internet and Remote Sensing Data for Public Health Surveillance

2:00 PM **Timnit Gebru,** *Google Research*

Lessons from Archives: Strategies for Collecting Sociocultural Data in Machine Learning

2:20 PM **Bradley Malin** *Vanderbilt University*

Data Sharing Challenges for Biomedical AI

2:40 PM **Matthew DeCamp,** *University of Colorado*

Ethics, Bias, and the Adoption of AI in Biomedicine

3:20 PM **Alex T. Bui,** *UCLA*

Internet and Remote Sensing Data Training at the Intersection: Bringing Together Computation and Biomedicine

3:40 PM **Kara Hall,** *SciTS*

TBA

4:00 PM **Ivet Bahar,** *University of Pittsburgh*

TBA

4:20 PM **Philip Payne,** *Washington University Institute for Informatics*

Integrating Biomedical Informatics and Data Science to Prepare the Precision Medicine Workforce

4:45 PM **Session Speakers**

Panel Discussion

WEB 2020

PRESENTATIONS

MONDAY, JULY 13

Track Chairs
Michelle Brazas, Cath BrooksbanK, Nicola Mulder, Patricia Palagi

2:00 PM **Michelle Brazas,** *Ontario Institute for Cancer Research*
Introduction to WEB 2020

2:04 PM **Michelle Brazas,** *Ontario Institute for Cancer Research*
RECENT ONLINE TRAINING EXPERIENCES - THE UNIVERSITY EXPERIENCE

2:05 PM **Tugce Bilgin,** *Columbia University*
Teaching the Virus: Lessons from the Online Age

2:25 PM **Javier De Las Rivas,** *GOBLET*
Overview 1

2:30 PM **Bruno Gaeta,** *University of New South Wales*
Overview 2

2:35 PM **Nicola Mulder,** *University of Cape Town,*
Overview 3

2:40 PM **Tugce Bilgin,** *Columbia University*
Group discussion on University specific aspects of online training: Resources in place, numbers taught, assessment methods

3:19 PM **Cath Brooksbank,** *EMBL-EBI*
RECENT ONLINE TRAINING EXPERIENCES - SHORT-COURSE EXPERIENCE

3:20 PM **Patricia M. Palagi,** *SIB Swiss Institute of Bioinformatics*
Overview 4

3:25 PM **Sarah L. Morgan,** *EMBL-EBI*
Overview 5

3:30 PM **Rachade Hmamouchi,** *Bioinformatics.ca,*
Overview 6

3:35 PM **Rachade Hmamouchi,** *Bioinformatics.ca*
Group discussion on short-course specific aspects of online training: Technologies used, hands-on facilitation, numbers taught

3:53 PM **Nicola Mulder,** *University of Cape Town*
BEST PRACTICES IN ONLINE TRAINING

3:55 PM **Kate Hutchinson,** *Fred Hutchinson Cancer Research Center*
Best practices from the experience: the Carpentries

4:10 PM **Rachael Ainsworth,** *Software Sustainability Institute*
Best practices from the experience: Software Sustainability

4:25 PM **Venkata Pardhasaradhi Satagopam,**
University of Luxembourg
Education Summit report

5:00 PM **Patricia Palagi,** *SIB Swiss Institute of Bioinformatics*
FILLING THE GAPS IN ONLINE LEARNING

5:55 PM **Michelle Brazas,** *Ontario Institute for Cancer Research*
Closing of WEB 2020

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VIRTUAL ISCB STUDENT COUNCIL SYMPOSIUM 2020

Wim Cuypers *(SCS 2020 Chair)*
Dr. Melike Dönertaş *(SCS 2020 Co-chair)*
Jasleen Grewal *(SCS 2020 Co-chair)*

The ISCB Student Council Symposium (SCS) is the flagship event of the ISCB Student Council, and the year 2020 marks the 16th edition of this event. The COVID-19 pandemic almost prevented us from doing what we love most: sharing our passion for Computational Biology research. Luckily, with help from the ISCB, our sponsor Harvard Medical School, and a panel of independent reviewers, we were able to construct an exciting virtual symposium program for the first virtual SCS:

- *Two keynote speakers, Prof. Elana J Fertig and Prof. Hamed S. Najafabadi*
- *Nine student/early career researcher talks*
- *Almost 40 posters and corresponding flash talks*
- *A career panel, moderated by Dr. Bruce Seet, with panelists Dr. Anne Mullin, Dr. Rita Strack and Dr. Anthony Fejes*
- *An invited talk by Jenea Adams, representing The Black Women In Computational Biology Network*
- *Best poster and best talk prizes*

COVID-19 IMPACT SURVEY FOR EARLY CAREER RESEARCHERS

Dr. Farzana Rahman *(SC representative to the ISCB Board of Directors)*
Dr. R. Gonzalo Parra *(SC Vice Chair) on behalf of the ISCB Student Council's Executive Team*

COVID-19 has affected us all. Our way of work and lives have changed dramatically due to the SARS-COV-2 pandemic. The ISCB Student Council has created COVID-19 survey focusing COVID-19's impact on Early Career Researchers (ECR). The outcome of this survey will help us to better understand the situation and impact caused by the global pandemic on the members of the ECRs in the field of Computational biology and Bioinformatics. Therefore, we invite the global ECRs to share their views by filling in the survey. Survey Link: http://iscbsc.org/COVID-19_Impact_Survey

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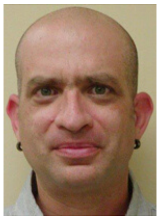

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upcoming

EVENTS OF INTEREST

iSCB

INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

The 9th National Conference on Bioinformatics and Systems Biology of China

Oct 08, 2020 through Oct 11, 2020

http://ccbsb2020.dtces.com/en.html

2nd International Symposium on Mathematical and Computational Oncology

Oct 08, 2020 through Oct 10, 2020

http://www.ismco.net

16th International Symposium on Bioinformatics Research and Applications

Dec 01, 2020 through Dec 04, 2020

https://isbra.confreg.org/

BIOSTEC 2021 – 14th International Joint Conference on Biomedical Engineering Systems and Technology

Feb 11, 2021 through Feb 13, 2021

http://www.biostec.org

3rd Interdisciplinary Signaling Workshop

Jul 19, 2021 through Jul 23, 2021

http://signallingworkshop.org

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