ISCBNEWSLETTER

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Featuring the ISMB 2022 Conference Programme

NEWSLETTER

CONFERENCE PROGRAMME

COSI SCHEDULES

WELCOME BACK TO OUR MEMBERSHIP!

ISCB'S CEO, DIANE KOVATS

Dear ISCB Members & Colleagues ,

As ISCB enters its 25th year being your professional society of choice, I would like to mark this momentous occasion by welcoming you to another edition of the ISMB, ISCB's flagship conference. Whether you are reading this from Madison, enroute to Madison, or joining us virtually, welcome and thank you for taking the time to be here.

Back in January 2021, ISCB made history when it welcomed its first female president into office, Christine Orengo from University College London in United Kingdom. Since that time, under Christine's stewardship, ISCB has been faced with continued disruption and a permanently changed environment. We continue to have to set new goals and reevaluate how we approach experiences for our membership. It is because of ISCB's incredible volunteers and membership that it continues to adapt to new demands, environments, and an ever-changing field. We might be a small society, but we are a mighty one. We faced a total world shut down, adapted, and have come out stronger. Thank you for helping us whether the storm.

Over the last 25 years, ISCB has continued to grow as an organization. We are closing in on pre pandemic membership numbers with 3,000+ members from 80 plus countries. In having to reevaluate our conference experiences and learning to adapt, we have introduced a new hybrid conference experience for our members and the greater bioinformatics community.

ISMB 2022 offers both an in-person experience as well as a fully immersive virtual experience so both experiences don't miss a beat. In addition to a fully interactive and immersive hybrid experience, conference attendees get exclusive access to the content well beyond the conference days!

As we know its almost impossible to attend all the sessions one wants to attend with more than 500 talks in ten concurrent sessions, now you don't have to worry about it. Miss a talk? Catch it after the conference!

In addition to the development of our new hybrid conference model, as a Society, we continue to strive to enhance scientific networking and research dissemination opportunities for our membership. ISCB is beyond pleased to have introduced ISCB Nucleus to it's members and colleagues. In a day and age where one point access is key, ISCB now offers access into its core through ISCB. Nucleus. Inside ISCB Nucleus, you will find all the archived ISCBacademy webinars and trainings from 2020 – present, as well as the live upcoming webinar sessions and training. You will also find a section where our Communities of Special Interest (COSIs) and Affiliated Regional Groups are featured. Finally, within the Collaboration Hub you can engage in online dialogue within community specific forums or in the global news feed. You can network and connect with fellow researchers through our people search, and (coming soon) have impromptu live meet ups.

This ever evolving and expanding platform is an exclusive ISCB member benefit. New content and features will be added as we work to meet the needs of our audience.

WELCOME BACK TO OUR MEMBERSHIP!
ISCB'S CEO, DIANE KOVATS

ISCB Nucleus also welcomes those outside of our membership to come and engage. ISCB Nucleus is the one stop shop for ISCB members and as ISCB continues to grow, so will ISCB Nucleus. Please check it out and of course, I welcome your feedback.

As always, thank you for your continuous support of our Society. We continue to grow, supporting one another as we work towards our goal to be the leading professional society for participants in the field of computational biology and bioinformatics, serving researchers, practitioners, technicians, students, and suppliers worldwide. Thank you for sticking with us and we hope you enjoy everything ISMB 2022 has to offer, sore feet and all!

Whether you are attending ISMB 2022 in-person or virtually, we hope you will attend the ISCB Town Hall, Monday, July 11 (6:15 pm - 7:30 pm CDT). During this session, you will get to learn about all programs as well as new plans and initiatives at ISCB! We will also celebrate some of our Society achievements. I hope to see you there!

Consider continuing the journey with us by volunteering, renewing your membership, and helping to grow our community by inviting a friend. We advance as an organization because of our dedicated members.

I look forward to meeting many of you here in Madison.

Sincerely,

Diane E. Kovats, CAE, CMP, DES
Chief Executive Officer

HOW YOU CAN SUPPORT ISCB

Dontate Now!

ANNA TRAMANTANO FUND

The goal of the Anna Tramontano Fellowship Fund is help reduce the financial burden to the students who are offered these internships by providing travel support. We hope that by providing financial support, reducing costs to the PIs, we will be able to increase the number of internships offered in a given year.

STUDENT FELLOWSHIP CAMPAIGN

YOU can make a difference in the future of computational biology and bioinformatics by supporting tomorrow's researchers. By donating to ISCB student fellowships, you are investing in the future of our science..

GENERAL RESOURCES FUND

ISCB delivers valuable information about training, education, employment, and relevant news, and provide an influential voice on government and scientific policies that are important to our members and benefit the public. Your membership and generous support helps to make these activities possible.

SPONSOR MEMBERSHIP DUES OF MEMBERS FROM DEVELOPING COUNTRIES

Your contribution will help those in developing countries who cannot afford membership to join and benefit from ISCB.

https://www.iscb.org/support-iscb

2022 ISCB INNOVATOR AWARD
NÚRIA LÓPEZ-BIGAS

Each year, ISCB recognizes a scientist who is within two decades of completing her or his graduate degree and has made significant contributions to field of computational biology. The 2022 ISCB Innovator Award winner is Dr. Núria López-Bigas, Group Leader and ICREA Research Professor of the Biomedical Genomics Group at the Institute for Research in Biomedicine, Barcelona, Spain. She will receive her award and give a keynote address at the 30thConference on Intelligent Systems for Molecular Biology (ISMB) in Madison, WI being held from July 10-14, 2022.

Núria López-Bigas:
Taking Aim at Cancer

Núria López-Bigas was born in Monistrol de Montserrat, a small town near Barcelona and had very broad interests as a young child, but her inclination toward biology emerged asa high school student, after which she pursued a B.Sc. in Biology at the University of Barcelona. López-Bigas went on to complete her Ph.D. in Biology at the Oncologic Research Institute, University of Barcelona under the mentorship of Xavier Estivill. Her dissertation research focused on the molecular causes of hereditary deafness, and she gained experience tackling questions in Mendelian genetics and validating findings in mouse models of deafness. In 2002, López-Bigas shifted her interest toward computational biology and pursued a postdoc at the European Bioinformatics Institute (EBI) in Cambridge, England under the mentorship of Christos Ouzounis. She recalled the effort that accompanied this shift and said, “It was a different time and there were very few formal training opportunities in bioinformatics, so I had to teach myself how to code.” López-Bigas’s work focused on computational comparative genomics at a time when only a handful of complete genomes existed, and she studied mutations involved in disease, much in the vein of her Ph.D. research on hereditary deafness. She also developed experience in using and analyzing microarrays. López-Bigas was supported by the Human Frontiers Science Program (HFSP) as a postdoc, which supported her research at EBI for two years, then provided her with an opportunity to pursue a project in her home country for the final year. She returned to Spain for this period and joined the laboratory of Roderic Guigó at the Centre for Genomic Regulation in Barcelona, Spain.

López-Bigas began her career as an independent scientist in 2006 and was selected to be a Group Leader and Ramon y Cajal Researcher at the Universitat Pompeu Fabra in Barcelona, Spain. This position was organized as a five-year contract and included only minimal financial support to start her lab, but she also obtained a HFSP Career Development Award which provided some extra funding to get started. López-Bigas recalled, “I started slowly, and focused only on computational biology, no wet lab, and this really helped me make progress.” Her lab studied cancer genetics and they focused on copy number alterations and expression differences because of the availability of arrays and techniques that could measure these genetic features. And then the first cancer genomes were starting to be sequenced.

López-Bigas recalled, “It was clear there were lots of mutations in tumors, and we thought it was important to understand how these mutations appear and which ones cause cancer across cancer types.” This research led to her interest in identifying mutations that drive tumorigenesis, and her group has published several pivotal studies detailing how different mutational processes affect specific cells and tissues, and how defects in DNA damage repair pathways alter mutation rates. López-Bigas and her team have also been at the forefront of developing software and data infrastructure for cancer research,

including their IntOGen pipeline that has been used to build a compendium of mutational cancer driver genes (www.intogen.org), which provide critical insights into mechanisms that contribute to tumorigenesis. They have also developed the Cancer Genome Interpreter tool that is used to evaluate the biological and clinical impacts of mutations detected in tumor samples and guide treatment (www.cancergenomeinterpreter.org). After the 5 year contract, in 2011, López-Bigas was selected as an ICREA Research Professor, which is a permanent position paid by the Catalan government.

In 2016, López-Bigas and her research group moved to the Institute for Research in Biomedicine (IRB Barcelona). She has expanded her computational biology lab and has built up a wet lab to give her group the ability to generate their own data and not be only dependent on publicly available datasets. With these expanded capabilities, López-Bigas is now using deep sequencing to compare tumor tissue and resected non-tumor tissue from the same patients to gain insight into cancer driver mutations and how small clonal cell clusters might undergo positive selection and turn into tumors.

The COVID-19 pandemic temporarily shut down López-Bigas's wet lab, but her group was able to continue their computational biology studies since each lab member had a laptop and the ability to connect to the computer cluster. In addition, López-Bigas stepped forward with her team to use their genomics knowledge to help analyze SARS-CoV-2 viral sequences in 2020. She collaborated with scientists in Austria, including Christoph Bock and Andreas Bergthaler, to carry out a genomic epidemiology study of superspreader events and understand factors contributing to mutational dynamics and viral transmission. Members of her team also helped build up the SARS-CoV-2 PCR testing infrastructure in Spain. López-Bigas and her team have now returned full focus on cancer genomics research but were gratified by the opportunities to use their scientific knowledge and skills to help during the pandemic.

López-Bigas has been thankful for her mentorship as a young scientist, which provided her with both intellectual freedom and opportunities to learn new skills. As the mentor of numerous postdocs and students, she has worked hard to create a lab environment where trainees are engaged and collaborative. She said, "As a mentor, I try to get people excited about their projects, motivate them, and encourage collaboration within the lab. An important part of my job is to make the right environment so people can jump into the lab, learn from each other and do interesting science."

As a leader in the field of computational cancer biology, López-Bigas has served her peers in various capacities, including organizing several meetings related cancer genomics and sequencing for ISMB. She has served as a reviewer of grant proposals and research articles and has been a member of scientific advisory boards of large institutions such as the Finland Institute of Molecular Medicine, the Gustave Roussy Cancer Institute and Open Targets. Her work and service have been recognized by numerous awards and honors, including election as a member of European Molecular Biology Organization (EMBO) and a Fellow of ISCB. She is deeply touched by her recognition with the 2022 ISCB Innovator Award and said, "I was surprised to be selected and humbled and happy. It means the bioinformatics community appreciates and recognizes the work of my group."

2022 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD
RON SHAMIR

Each year ISCB recognizes outstanding contributions by a leader in the fields of computational biology and bioinformatics with the Accomplishments by a Senior Scientist Award. This award is the highest honor conferred by ISCB to a scientist who has made significant contributions to research, education, and service to the field and ISCB. Ron Shamir, Professor of Computer Science at Tel Aviv University in Israel, is being recognized as the 2022 recipient of the ISCB Accomplishments by a Senior Scientist Award. He will receive his award and give a keynote address at the 30th Conference on Intelligent Systems for Molecular Biology (ISMB) in Madison, WI being held from July 10-14, 2022.

Ron Shamir
Founding Father of Israeli Bioinformatics

Ron Shamir grew up in Jerusalem, Israel with broad interests in the humanities, science, and mathematics. Shamir was very close to his grandmother who was a pharmacist and had studied chemistry, although he does not recall discussing science with her, and he actually aspired to be an author in his youth. As a high school student at Gymnasia Rehavia in Jerusalem, Shamir became more interested in mathematics, and he recalled, "I had an inspiring math teacher, who really encouraged me. Math problems were like riddles or puzzle-solving challenges. It was fun, and I found that math comes naturally to me."

Shamir started his BSc in mathematics and physics at Tel Aviv University and then completed his degree at Hebrew University of Jerusalem. He pursued graduate studies in operations research (OR), so he could work on a project that connected math with real-world problems, and enrolled in a PhD program at the University of California-Berkeley (UC Berkeley). Shamir's PhD research focused on the average case analysis of the Simplex algorithm for linear programming, which fell somewhere between OR and computer science. His PhD advisors at UC Berkeley were Richard (Dick) Karp and Ilan Adler, who he considers pivotal mentors in his career. Shamir said, "Working with them completely transformed my perspective on academic research, and even though I got into grad school with no such intention, I left wishing to try for a career in academia. I have been collaborating with them ever since. Dick has always been an amazing role model to me, and I have learned immensely from him. By sheer coincidence, a few years after my graduation, we both independently got into the emerging field of computational biology and worked on physical mapping algorithms. It was a great pleasure working together in this new field. Dick Karp is one of the giants of theoretical computer science, and his championing and involvement in the young field of computational biology gave it great credibility and helped establish the new area as a bona fide scientific discipline."

Shamir went on to his first position as a lecturer at Tel Aviv University in the Department of Computer Science where he worked on graph algorithms and optimization. He spent his first sabbatical at Rutgers University, where he worked on temporal reasoning, which is a problem in which event intervals placed along a timeline are subject to various constraints. Gene Lawler had listened to Shamir give a talk about his work, and he recalled, "[Lawler] told me, 'This is a great model for physical mapping of DNA,' by replacing time intervals with clones and the timeline with the chromosome. This encounter changed my life. I started reading about DNA and the genome and was hooked. My wife Michal is a biochemist, so I could ask her all the trivial questions about biology, DNA, etc. It was 1990 and the early beginnings of the Human Genome Project, and there was a lot of excitement about the prospects of combining computation and genomics.

I dove into this new area, which did not even have a name then, and was not disappointed." Shamir has gone on to pioneer various algorithmic techniques in genomics, including analysis of microarray data, regulatory motifs, genome rearrangements, and network biology.

Among Shamir's contributions, he developed elegant algorithms for the analysis of regulatory motifs and protein-protein interactions. Previous approaches have dissected network and similarity data separately, but Shamir and his group developed approaches to analyze these types of data jointly. This led to the discovery of functional modules through the identification of connected networks in the interaction data that exhibited high internal similarity. Shamir continues to be fascinated with topics related to modularity, and he said, "I find myself coming back to the fundamental problem of cluster discovery again and again over the years, and more recently in module discovery based on a combination of similarity and network-based data. This area of study is 100 years old, or 2400 years old, if you start from Aristotle, and is still a lively research area. In a very different direction, I am doing more research on digital medicine in recent years, working on electronic medical records in collaboration with clinicians. This is a tough field. Unlike genomics, where all data is open and well organized, medical data is much more difficult to work with in terms of both data access and data organization. Moreover, physicians are extremely busy work partners and are primarily concerned about treating patients. For them, science only comes second, which makes collaborations more challenging. Nonetheless, this type of research offers a chance to influence disease trajectories and even save lives, so I continue to work in this field." Most recently, Shamir worked with three of his students and with physicians to analyze COVID-19 inpatient data. They developed a machine learning model for predicting the deterioration of patients 7-30 hours before this process starts and have obtained some promising results. They continue to validate this model by analyzing larger and more diverse datasets, which now include nearly 10,000 patients.

Shamir is well known for making his bioinformatics tools, like the Expander expression analysis suite, readily available to the research community as user-friendly software tools. Some of these tools have been written for a specific project with no intention to be broadly useful, but have become unexpectedly popular, such as the simple UNIX program HYDEN he developed with his student Chaim Linhart to design degenerate primers, which is still downloaded hundreds of times per year. He is a pioneer of bioinformatics education and has been posting bioinformatics lecture notes online since 1997, making his course notes some of the of the most widely used and influential bioinformatics educational materials to date. Shamir has been a deeply committed mentor and advisor throughout his career and encourages his students to choose their own projects, through which he advises and guides their research. He also makes his students draft their own research papers and considers the interaction and joint revision process, which includes corrections and rewrites, to be a key part of their education. Throughout the pandemic, Shamir has been constantly adjusting how his lab interacts, be it through virtual meetings or in-person encounters, and he has tried hard to hold face-to-face meetings with his team as much as possible, in order to help keep their training and development moving forward. Shamir added: "I have been extremely lucky in having incredibly talented, creative and driven students. The interaction with them, and later observing their development into great independent scientists and industry leaders, is extremely gratifying. This is the part of my career I am proudest of."

Shamir's research and leadership have been critical to establishing a globally respected Israeli bioinformatics program. He has published over 300 papers, including five with more than 1,000 citations. Shamir established the joint Life Sciences/Computer Science bioinformatics BSc program and founded the Edmond J. Safra Center for Bioinformatics at Tel Aviv University.

He was named the Sackler Chair in Bioinformatics in 2003, and his work and service have been recognized by numerous awards, including the Landau National Prize in the Sciences (2010), RECOMB Test of Time Awards (2011 and 2016), Kadar Family Prize for outstanding research, Tel Aviv University (2017), and election as an ACM Fellow by the Association for Computing Machinery (2012) and an ISCB Fellow by the International Society for Computational Biology (2012).

As the 2022 recipient of the ISCB Accomplishments by a Senior Scientist Award, Shamir is deeply honored by this recognition bestowed upon him by his peers, and only wishes his parents were alive to share in this award. He recounted, "As a young faculty member in computer science, I entered an exciting research adventure in an embryonic field that did not even have a name yet. In retrospect, this was a very risky choice before tenure. Seeing how the field developed and matured and being able to help shape it have been great pleasures. This award sums up the path I have taken as a scientist in the past thirty years. I am truly indebted to the society and to the community for it."

THANK YOU TO OUR GENEROUS DONORS

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2022 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD
REINHARD SCHNEIDER

Each year, the Outstanding Contributions to ISCB Award recognizes an ISCB member for noteworthy service contributions toward the betterment of ISCB through exemplary leadership, education, and service. The 2022 Outstanding Contributions to ISCB Award recipient is Reinhard Schneider.

Reinhard Schneider
A Voice for Bioinformatics Education

Reinhard Schneider is Full Professor in Bioinformatics, Head of Bioinformatics Core Facility, and Head of the ELIXIR Luxembourg Node at the University of Luxembourg. His research interests include developing and improving algorithms related to structure/function predictions of proteins. Schneider has devoted more than 20 years of service to ISCB in various capacities. He became an ISCB member in 1997 but became more involved as a co-organizer of ISMB with Thomas Lengauer in 1999. Schneider joined the ISCB Board of Directors in 2005 at a time when the Society was experiencing financial turmoil. His experiences working with startups helped him work with other board members to improve the management and financial stability of the organization. Schneider worked with Bettina Roth to redesign the ISCB web portal and improved features related to membership and registration, thus making the member portal user-friendly and reliable. Schneider introduced an option for members to purchase multi-year memberships, and he helped introduce other member benefits, and together these strategies boosted both membership and revenue.

Schneider served as ISCB Vice President from 2005 to 2009 and ISCB Treasurer from 2009 to 2016. His time as treasurer included developing an investment strategy for a portion of ISCB funds, which has given the Society greater financial stability.

Beyond these roles, Schneider has served on various committees related to ISCB's annual meetings, including ISMB/ECCB2007 (Vienna), ISMB2008 (Toronto), ISMB/ECCB2009 (Stockholm), ISMB2010 (Boston), ISMB/ECCB2011 (Vienna), ISMB2012 (Long Beach), ISMB/ECCB2013 (Berlin), ISMB2014 (Boston), and ISMB/ECCB2015 (Dublin). He has co-organized several international ISCB affiliated meetings in Africa, Asia, and Latin America, including ISCB Africa (2010: Bamako, Mali; 2011: Cape Town, South Africa) in cooperation with the African Society for Computational Biology and Bioinformatics (ASBCB), ISCB Latin America (2010: Montevideo, Uruguay; 2014: Belo Horizonte, Brazil), and most recently ISCB Asia (2011: Kuala Lumpur, Malaysia; 2012: Shen Zhen, China; 2013: Seoul, South Korea). His involvement with meeting organization includes helping launch and support the live coverage of ISMB via microblogging, making it one of the first life science conferences providing coverage in this manner. This initiative was started at ISMB2008 in Toronto and continues today.

Schneider is deeply gratified by his work in helping establish the ISCB Student Council (ISCBSC). He said, “It was great to see the enthusiasm of younger people getting involved in ISCB and to help them establish the ISCBSC with its own activities. I have invited very good students from developing nations to my lab through the ISCBSC internship initiative and hope these types of programs can help students launch their careers.”

Schneider is thankful for his diverse experiences with ISCB and encourages trainees to seek similar opportunities. He said, “It is important to learn skills that are outside of a typical graduate program, like management and organization skills, and how to work with others on different types of teams.” Schneider will be remembered as one of the ISCB’s leaders who helped financially secure the Society and broaden the ISCB membership. He will continue to support the ISCB community as a lifetime ISCB member.

F1000RESEARCH IS DELIGHTED TO ANNOUNCE BIOINFORMATICS GATEWAY

F1000Research is delighted to announce the launch of the Bioinformatics Gateway, a dedicated venue for open research in collaboration with the ISCB. The Gateway is a home for all research related to the subject of Bioinformatics, welcoming a range of article types to maximize impact and reach. The rapid publication model offered by F1000Research means your research is quickly and openly available. All publications will undergo fully transparent open post-publication peer review following in-house editorial checks.

If you are interested in contributing an article to the gateway, would like to propose a themed collection in a subject related to the gateway or otherwise have any questions, please get in contact with us via research@f1000.com.

We’ve recently launched the following thematic special collections in our Bioinformatics Gateway centered on the following themes:

Machine Learning in Genomics
This article collection aims to promote the latest research applying machine learning approaches to advance genomic research. We welcome submissions of research involving the development and/or application of machine learning methods to genomic data sets including, but not limited to, genome sequencing, gene expression, single-cell genomics, functional genomics, or nuclear organization.
Submission deadline: 15th September 2022

Plant Computational and Quantitative Genomics
This collection invites contributions that present computational studies, software solutions, databases, and online services that focus on the use of sequence-variant information in plants. The envisioned scope of studies ranges from variant calling, profiling of SNPs in genomic regions with the goal to identify sequence motifs, to the identification of candidate genes via GWAS, and the application and development of statistical/machine learning models for genomic selection and their use in breeding projects.
Submission deadline: 20th September 2022

Bioinformatics in Cancer Research
We welcome submissions (e.g., research articles, brief reports, method articles, and reviews) on computational cancer research, including but not limited to, digital pathology and computer vision, sequence analysis, structural biology related to therapeutic development, survival prediction, plus deep learning and computational approaches that study the following areas: the interface between the microbiome and the immune system, the tumour-immune interface, intra and extra tumoral cell-cell crosstalk, prediction of ideal therapy combinations and mechanistic basic biology. Research that is time-sensitive and requires rapid publication is particularly encouraged for submission.
Submission deadline: 30th November 2022

If you are interested in submitting to these collections, please get in touch with us via vinitha.raghavan@f1000.com

2022 ISCB OVERTON PRIZE
PO-RU LOH

The ISCB Overton recognizes the research, education, and service accomplishments of early or mid-career scientists who are emerging leaders in computational biology and bioinformatics. The Overton Prize was established in 2001 to honor the untimely loss of G. Christian Overton, a leading bioinformatics researcher and a founding member of the ISCB Board of Directors.

The 2022 Overton Prize winner is Dr. Po-Ru Loh, Assistant Professor in the Division of Genetics and Center for Data Sciences, Brigham and Women's Hospital and Harvard Medical School, and Associate Member of the Broad Institute of MIT and Harvard. He will receive his award and give a keynote address at the 30thConference on Intelligent Systems for Molecular Biology (ISMB) in Madison, WI being held from July 10-14, 2022.

Po-Ru Loh
From Math Olympiad to Millions of Genomes

Po-Ru Loh grew up in Madison, WI and was encouraged to study arithmetic and algebra from a young age. He recalls liking mathematics in school because of his familiarity with the subject matter, and he also developed an interest in solving mathematical puzzles and competing with his older brother to solve riddles in Brian Bolt's Mathematical Funfair book. As a middle and high school student, Loh's interest in math was further stoked by math competitions, including MathCounts and the Math Olympiad, and he went on to be a 2002 and 2003 Gold medalist, and top scorer on US team in the International Mathematical Olympiad. However, Loh's early encounters with science were somewhat discouraging, as he recalled: "My first experiences with science involved growing lima beans and mealworms. My beans didn't sprout, and my mealworms died. It wasn't until high school that I realized that science had a quantitative side, and I became more interested."

Loh received a B.S. in mathematics from the California Institute of Technology in 2007, during which time he was a second-place finisher in both the Google Code Jam and the TopCoder Open. He strongly considered being a pure mathematician as an undergraduate but eventually realized he wanted to work on problems with more direct real-world relevance.

Loh ended up pursuing a Ph.D. in applied mathematics at MIT and considers his entry into computational biology to be somewhat accidental. He said, "I had no idea what field of study to pursue, so upon matriculating, I simply browsed through faculty research interests and spent my first year sampling an eclectic mix of courses in different fields that sounded interesting. Computational biology was one of them, and it caught my eye as a growing field with interesting algorithmic challenges." Loh joined Bonnie Berger's lab and went on to develop a dissertation project focused on compressive genomics. He worked on algorithms that computed directly on compressed genomic data, which allowed for analyses to keep pace with data generation.

In 2013, Loh began his postdoc under the mentorship of Alkes Price at Harvard T.H. Chan School of Public Health and dove further into computational genetics. With Price, he pioneered ultra-efficient algorithms facilitating biobank-scale genomics through the development of two widely used computational genetics tools, BOLT-LMM and Eagle2. These tools have been used to analyze millions of genomes and have brought to light numerous loci that shape human health and disease.Loh became an Assistant Professor in the Division of Genetics and Center for Data Sciences, Brigham and Women's Hospital and

Harvard Medical School, and Associate Member of the Broad Institute of MIT and Harvard in 2018. During his time as a postdoc and a tenure-track faculty member, Loh has had some unexpected findings that have impacted his research. He said, “The most surprising findings in my research thus far have been unexpectedly strong associations between inherited genetic variants and various human traits, ranging from height to clonal hematopoiesis. Prior to these projects, I had always thought of myself as a tool-builder. I developed statistical methods to help answer questions in genetics, but I left the application of these methods to the “real” geneticists. I was quite shocked the first time that my analyses uncovered new biological knowledge that neither I nor any of my collaborators expected. But these new findings made sense, could be validated, and were ultimately very satisfying. These experiences have shifted my path substantially, increasing my appetite for taking on projects driven by biological questions rather than only method development, and leading me to pursue several projects investigating genomic structural variation.”

Loh’s current interests include studying very rare coding variants and genomic structural variants using computational methods that leverage haplotype sharing withing biobank cohorts, as well as developing methods to detect mosaic chromosomal alterations and understand how they relate to cancer and other genetic disorders. He is irrepressibly enthusiastic and curious and said, “At the moment, I am particularly intrigued by the potential to leverage population-scale whole-genome sequencing to learn more about genomic variants that have typically been difficult to ascertain – specifically, structural variants and somatic variants. However, I would not be surprised if I find myself working on entirely new research directions five years from now. My trajectory thus far has been greatly influenced by serendipitous encounters, and given the rate at which new “omic” data sets and data types become available, it seems essential to keep an eye out for important new resources and the challenges and opportunities they bring.”

Loh is deeply appreciative of his mentors Berger and Price, and he recognizes their investment in him as a scientist, which included helping him identify projects that leveraged his existing skills, pushing him to expand his skills and knowledge, and helping him chart a path to independence. Soumya Raychaudhuri and Richard Maas have also been instrumental in guiding Loh through the establishment of his independent research group. His mentorship has deeply shaped how he works with graduate students and postdocs in his lab.

As an early career scientist, Loh has been extremely productive, with over 70 publications, >17,000 citations and numerous awards and fellowships. Loh has consistently developed open-source software tools that are used by the computational biology community, and he has served on program committees for ISMB and RECOMB. Loh is particularly grateful for his recognition with the Overton Prize and said, “It is an incredible honor to receive this award. When I first attended the ISMB conference as a graduate student ten years ago, I never imagined I could one day be selected for the Overton Prize. I am tremendously grateful to all the mentors, collaborators, and trainees who contributed to the work recognized by this award and to my development as a scientist.”

ISMB
2022
MADISON
JULY 10-14, 2022

Hybrid
CONFERENCE PROGRAMME

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

Welcome to ISMB 2022

On behalf of the organizing committee of ISMB 2022 and the Board of Directors of the International Society for Computational Biology (ISCB) we wish you a very warm and appreciative welcome. If you are here in Madison, welcome back to in-person and if you are joining us from somewhere else, welcome to this hybrid conference experience! We waited patiently, carefully crafting this return to ensure a safe conference, and now we are opening conference doors once again. We encourage you to take full advantage of these exciting and intense few days of collaboration, fresh dialogue, and innumerable learning opportunities.

Each day of the conference scientific programme includes outstanding keynote lectures and technical talks (corresponding to both published and unpublished work), thematically organized in the Communities of Special Interest (COSI) tracks. In addition, there are workshops, special sessions, a virtual students organized symposium, and poster sessions. And of course, we cannot forget about our Exhibit Hall - Grand Terrace where you can meet with our 15 conference exhibitors while grabbing a coffee during breaks. This year's exhibition features commercial and non-profit providers of bioinformatics tools, technologies, and publications. We hope you take advantage of everything the conference has to offer, especially the endless opportunities to meet, network, and connect with your fellow computational biologists.

For those joining us online, you also have the opportunity to interact with all of the ISMB 2022 participants within the collaboration hub. In the forums section, you can chat with your fellow colleagues and friends in designated forum space or even start a conversation of your own. While viewing a live session, you can chat and ask questions. Poke around the exhibit hall where you too can learn about the commercial and non-profit providers of bioinformatics tools, technologies, and publications.

ISMB 2022 Programme Overview:
- 5 Distinguished Keynote presentations, including our three 2022 ISCB Award Winners
- 22 community-led COSI Tracks and workshops
- 4 Special Sessions (Computational Immunology, Digital Agriculture, Genome Privacy and Security, and COVID-19)
- Special Track: NIH-NSF Smart Health
- 12 Technology Track presentations
- 11 Pre-conference Tutorials (6 virtual & 5 in person)
- Recruiter Information Sessions
- More than 900 posters available throughout the conference and presented by their authors in multiple sessions.

It's a lot of science and information packed into four days. Don't worry if you miss something, everything will be available via the conference platform as on-demand viewing through Nov. 30, 2022.

As Conference Chairs, we appreciate the support of the very many volunteers who have helped guide the development of the conference and of course all the reviewers who have played an essential role towards forging the scientific program of the conference.

We want to acknowledge all the chairs of the Proceedings, COSIs, Special Sessions, 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.

As many of you know, without Diane Kovats, ISCB Chief Executive Officer, Steven Leard, the ISMB Conference Director, and the entire ISCB team there would be no ISMB meeting! This year we thank them for enabling the return to an in person meeting while also respecting the conditions and offering a hybrid experience. We are immensely grateful to Diane, Steven and their teams for the dedication and effort that they put into organizing all the logistics of this very parallel and complex meeting.

Let’s have a great ISMB 2022!

Yours sincerely,

Mona Singh Iddo Friedberg Keith Dunker

Conference Co-Chairs

ISMB
2022
MADISON

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Associate Professor
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Princeton University
Department of Computer Science

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Professor Emeritus of Biochemistry
& Molecular Biology
Indiana University
School of Medicine

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Iddo Friedberg, Iowa State University, United States

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Steven Leard, ISMB Conference Director, Canada

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Robert Beiko, Dalhousie University, Canada

BIOMEDICAL INFORMATICS

Maria Secrier, University College London, United Kingdom
Barbara Engelhardt, Princeton University, United States

EVOLUTIONARY, COMPARATIVE, AND POPULATION GENOMICS

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Lars Arvestad, Stockholm University, Sweden

GENOME PRIVACY AND SECURITY

Hyunghoon Cho, Broad Institute of MIT and Harvard, United States

GENOMIC SEQUENCE ANALYSIS

Carl Kingsford, Carnegie Mellon University, United States
Rob Patro, University of Maryland, United States

MACROMOLECULAR SEQUENCE, STRUCTURE, AND FUNCTION

Yann Ponty, CNRS/LIX, Polytechnique, France
Jérôme Waldispühl, McGill University, Canada

REGULATORY AND FUNCTIONAL GENOMICS

Jian Ma, Carnegie Mellon University, United States
Saurabh Sinha, University of Illinois, United States

SYSTEMS BIOLOGY AND NETWORKS

Marinka Zitnik, Harvard University, United States
Tijana Milenkovic, University of Notre Dame, United States

EQUITY-FOCUSED RESEARCH

Casey Greene, University of Colorado's Anschutz Medical Campus, United States

GENERAL COMPUTATIONAL BIOLOGY

Mohammed El-Kebir, *University of Illinois, United States*
Su-in Lee, University of Washington, United States

Scientific Organizing Committee

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3D-SIG: STRUCTURAL BIOINFORMATICS AND COMPUTATIONAL BIOPHYSICS

Douglas Pires, The University of Melbourne, Australia
Rafael Najmanovich, University of Montreal, Canada

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Madelaine Gogol, Stowers Institute, United States
Rodrigo Ortega Polo, Agriculture and Agri-Food Canada
Alberto Riva, University of Florida, United States

BIO-ONTOLOGIES

Tiffany Callahan, University of Colorado Denver, United States
Robert Hoehndorf, King Abdullah University of Science & Technology, Saudi Arabia

BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE

Nomi L. Harris (Chair), Lawrence Berkeley National Laboratory, United States
Karsten Hokamp, Trinity College Dublin, Ireland
Hervé Ménager, Institut Pasteur, France
Monica Munoz-Torres, University of Colorado Anschutz Medical Campus, United States
Deepak Unni, European Molecular Biology Laboratory, Heidelberg, Germany
Nicole Vasilevsky, University of Colorado Anschutz Medical Campus, United States
Jason Williams, Cold Spring Harbor Laboratory, United States
Peter Cock (ex officio, Open Bioinformatics Foundation (OBF), United Kingdom

BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Jan Byška, Masaryk University, Czech Republic
Helena Jambor, TU Dresden, Germany
Michael Krone, University of Tübingen, Germany
Heba Sailem, University of Oxford, United Kingdom
Qianwen Wang, Harvard University, United States

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

Joaquin Dopazo, Fundación Progreso y Salud, Spain
David Kreil, Boku University Vienna, Austria
Paweł P Łabaj, Austrian Academy of Sciences, and Jagiellonian University, Poland
Wenzhong Xiao, Harvard Medical School, United States

COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Wout Bittremieux, University of California San Diego, United States
Isabell Bludeau, Max Planck Institute of Biochemistry, Germany
Lindsay Pino, University of Pennsylvania, United States
Timo Sachsenberg, University of Tübingen, Germany

EDUCATION: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS EDUCATION AND TRAINING

Annette McGrath, Australian Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
Patricia M. Palagi, SIB Swiss Institute of Bioinformatics, Switzerland
Russell Schwartz, Carnegie Mellon University, United States
Wai Keat Yam, International Medical University, Malaysia

EQUITY-FOCUSED RESEARCH

Casey Greene, University of Colorado's Anschutz Medical Campus, United States

EVOLCOMPGEN: EVOLUTION & COMPARATIVE GENOMICS

Edward L. Braun, University of Florida, United States
Nadia El-Mabrouk, University of Montreal, Canada
Wataru Iwasaki, University of Tokyo, Japan
Giltae Song, Pusan National University, Korea
Janani Ravi, Michigan State University, United States

FUNCTION: INCORPORATING CAFA 4: GENE AND PROTEIN FUNCTION ANNOTATION

Dukka KC, Michigan Technological University, United States
Iddo Friedberg, Iowa State University, United States
Kimberly Reynolds, University of Texas Southwestern Medical Center, United States
Mark Wass, University of Kent, United Kingdom

HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

Can Alkan, *Bilkent University, Turkey*
Christina Boucher, *University of Florida, United States*
Ana Conesa, *University of Florida, United States*
Francisco M. De La Vega, *Stanford University, United States*
Dirk Evers, *Dr. Dirk Evers Consulting, Germany*
Birte Kehr, *Universitätsklinikum Regensburg, Germany*
Kjong Lehmann, *ETH-Zürich, Switzerland*

IRNA: INTEGRATIVE RNA BIOLOGY

Yoseph Barash, *University of Pennsylvania, United States*
Klemens Hertel, *UC Irvine, United States*
Athma Pai, *University of Massachusetts Medical School, United States*
Michelle Scott, ***University of Sherbrooke, Canada***

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Catalina Vallejos, *The University of Edinburgh, United Kingdom*
Marinka Zitnik, *Harvard University, United States*

MICROBIOME

Alice McHardy, *Helmholtz Centre for Infection Research, Germany*
Alexander Sczyrba, *Bielefeld University, Germany*
Zhong Wang, *Joint Genome Institute, United States*

NETBIO: NETWORK BIOLOGY

Martina (Tina) Kutmon, *Maastricht University, Netherlands*
Tijana Milenkovic, *University of Notre Dame, United States*

REGSYS: REGULATORY AND SYSTEMS GENOMICS

Shaun Mahony, *Penn State University, United States*
Anthony Mathelier, *University of Oslo, Norway*
Alejandra Medina-Rivera, *National Autonomous University of Mexico*
Lonnie Welch, *Ohio University, United States*

SUSTAINABILITY RESEARCH IN COMPUTATIONAL BIOLOGY

Ana Conesa, Spanish National Research Council (CSIC), Spain

Scientific Organizing Committee

COSI TRACK LEADS & ABSTRACT CHAIRS

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Andreas Dräger, *University of Tübingen, Germany*
Reihaneh Mostolizadeh, *University of Tübingen, Germany*
Anna Niaraki, *Université d'Évery, France*
Bhanwar Puniya, *University of Nebraska-Lincoln, United States*

TEXT MINING

Cecilia Arighi, *University of Delaware, United States*
Lars Juhl Jensen, *University of Copenhagen, Denmark*
Robert Leaman, *NCBI/NLM/NIH, United States*
Zhiyong Lu, *NCBI/NLM/NIH, United States*

TRANSMED: TRANSLATIONAL MEDICINE INFORMATICS & APPLICATIONS

Sanne Abeln, *Vrije Universiteit Amsterdam, Netherlands*
Irina Balaur, ***University of Luxembourg***
Wei Gu, *University of Luxembourg*
Heba Sailem, *University of Oxford, United Kingdom*
Venkata Satagopam, *University of Luxembourg*
Maria Secrier, *University College London, United Kingdom*

SPECIAL SESSIONS

SPECIAL SESSION: COMPUTATIONAL IMMUNOLOGY

Yuri Pritykin, *Princeton University, United States*

SPECIAL SESSION: COVID-19

Thomas Lengauer, *Max Planck Institute for Informatics, Germany*
Shoshana Wodak, *VIB-VUB Center for Structural Biology, Belgium*

SPECIAL SESSION: DIGITAL AGRICULTURE

Jennifer L. Clarke, *University of Nebraska-Lincoln, United States*
Noah Fahlgren, *The Donald Danforth Plant Science Center, United States*
Camilo Valdes, *University of Nebraska-Lincoln, United States*

SPECIAL SESSION: GENOME PRIVACY AND SECURITY

Bonnie Berger, *Massachusetts Institute of Technology, United States*
Hyunghoon Cho, *Broad Institute of MIT and Harvard, United States*

TRAVEL FELLOWSHIPS COMMITTEE

Luis Pedro Coelho, *Fudan University, China*
Priscila Grynberg, *Embrapa, Brazil*
Kana Shimizu, *Waseda University, Japan*

VARI: VARIANT INTERPRETATION

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

GENERAL COMPUTATIONAL BIOLOGY

Xin Gao, *King Abdullah University of Science and Technology (KAUST), Saudi Arabia*
Sara Mostafavi, *University of Washington, United States*

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

Distinguished Keynote Presentations

SUNDAY, JULY 10, 2022 AT 6:30 PM - 7:30 PM CDT

Tanya Berger-Wolf

The Ohio State University

Imageomics: Images as the Source of Information about Life

Introduced by: Iddo Friedberg, Conference Co-chair; Iowa State University, United States

MONDAY, JULY 11, 2022 AT 8:45 AM - 9:45 AM CDT

ISCB Overton Prize Keynote

Po-Ru Loh

Broad Institute of MIT and Harvard

Haplotype-informed discovery of hidden genetic variants influencing human traits

Introduced by: Mona Singh, Conference Co-chair; Princeton University, United States

TUESDAY, JULY 12, 2022 AT 8:45 AM - 9:45 AM CDT

Aïda Ouangraoua

Université de Sherbrooke

Gene evolution at transcript level: challenges and existing solutions

Introduced by: Keith Dunker, Honorary Conference Chair; Professor Emeritus, Indiana University School of Medicine, United States

WEDNESDAY, JULY 13, 2022 AT 8:45 AM - 9:45 AM CDT

ISCB Accomplishments by a Senior Scientist Award Keynote

Ron Shamir

Blavatnik School of Computer Science

Integration, modularity and network analysis for understanding disease

Introduced by: Christine Orengo, ISCB President; University College London, United Kingdom

THURSDAY, JULY 14, 2022 AT 8:30 AM - 9:30 AM CDT

ISCB Innovator Award Keynote

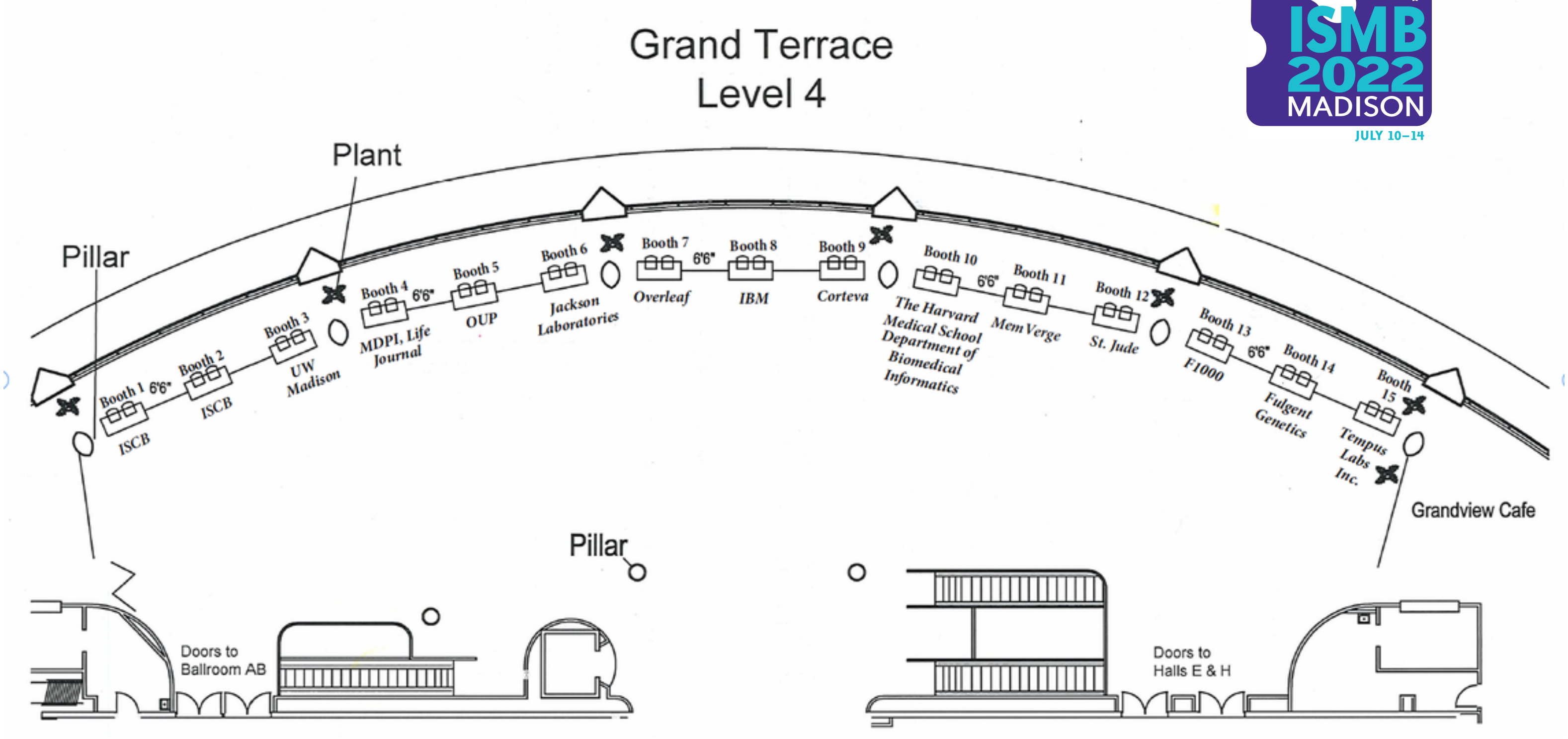
Núria López-Bigas

Institute for Research in Biomedicine

Comprehensive identification of cancer driver mutations

Introduced by: Janet Kelso, ISCB Treasurer; Max Planck Institute for Evolutionary Anthropology, Germany

ISMB 2022 Exhibitors and Recruiters



Onsite & Virtual Exhibitors

1 International Society for Computational Biology

2 ISCB Education Committee/GOBLET/ ISCB Student Council

3 University of Wisconsin, Madison

4 MDPI, Life Journal

5 Oxford University Press

6 Jackson Laboratories

7 Overleaf

8 IBM

9 Corteva

10 Harvard Medical School Department of Biomedical Informatics

11 MemVerge

12 St. Jude Children's Research Hospital

13 F1000

14 Fulgent Genetics

15 Tempus Labs Inc

Virtual Only Exhibitors

V16 Goblet

V17 Frontiers

V18 Syngenta Crop Protection, LLC

Schedule-at-a-glance
Sunday, July 10

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JULY 10–14

All times in Central Time Zone

9:00AM - 4:30PM	ISCB Board of Directors Meeting
	
4:00PM - 6:00PM	Exhibition Open Room: Grand Terrace
6:15PM - 6:30PM	ISMB 2022 Conference Welcome Room: Madison ABCD
6:30PM - 7:30PM	 Distinguished Keynote Speaker Tanya Berger-Wolf, The Ohio State University Introduced by: Iddo Friedberg, Conference Co-chair
7:30PM - 9:00PM	Networking Reception - Monona Terrace Rooftop Garden - Level Five

Schedule-at-a-glance
Monday, July 11

All times in Central Time Zone

7:30AM - 8:30AM	Virtual Poster Session (via Conference Platform)
	
8:30AM-8:45AM	Morning Welcome & Introduction of ISCB Distinguished Fellows 2022
8:45AM - 9:45AM	 ISCB Overton Prize Keynote: Po-Ru Loh, Brigham and Women's Hospital and Harvard Medical School Introduced by: Mona Singh, Conference Co-chair
9:45AM - 10:30AM	Caffeinate and Connect with exhibitors (Coffee Break) Room: Grand Terrace
10:30AM - 12:30PM	Sessions

SysMod COSI: Computational Modeling of Biological Systems (Room: Madison A)

Function COSI: Protein Function Annotation (Room: Madison B)

General Computational Biology Talks (Room: Madison CD)

iRNA COSI: Integrative RNA Biology (Room: Lecture Hall)

CAMDA COSI: Critical Assessment of Massive Data Analysis (Room: EH)

Bioinfo Core Workshop (Room: FI)

Special Session: Computational Immunology (Room: GJ)

CompMS COSI: Computational Mass Spectrometry (Room: KOPL)

Text Mining COSI (Room: MQRN)

Junior Principal Investigators COSI: Funding a Computational Biology Lab (Technology Theatre Community Terrace)

12:30PM - 2:30PM	Lunch and Ideation Hall (Poster Session A) Room: Exhibit Hall A (Level 1)
10:30AM - 12:30PM	Sessions Continue

SysMod COSI Continues

Function COSI Continues

General Computational Biology Continues

iRNA COSI Continues

CAMDA COSI: Continues

WEB 2022 (Room: FI)

Special Session: Computational Immunology Continues

CompMS COSI Continues

Text Mining COSI Continues

Technology Track (Technology Theatre Community Terrace)

3:30PM - 4:00PM	Coffee Break (Caffeinate and Connect with exhibitors) Room: Grand Terrace
4:00PM - 6:00PM	Sessions Continue

SysMod COSI Continues

Function COSI Continues

General Computational Biology Continues

iRNA COSI Continues

CAMDA COSI: Continues

WEB 2022 (Room: FI)

Special Session: Computational Immunology Continues

CompMS COSI Continues

Text Mining COSI Continues

Technology Track (Technology Theatre Community Terrace)

6:15PM - 7:30PM	 ISCB Town Hall (Lecture Hall, Level Four)
6:15PM - 7:15PM	Virtual Poster Session (via Conference Platform)

Schedule-at-a-glance
Tuesday, July 12

All times in Central Time Zone

7:30AM - 8:30AM Virtual Poster Session (via Conference Platform)

8:30AM-8:45AM Morning Welcome & ISCB Outstanding Contributions Award Presentation to Reinhard Schneider Room: Madison ABCD

8:45AM - 9:45AM

ISCB Distinguished Keynote:
Aïda Ouangraoua, Université de Sherbrooke
Introduced by:
Keith Dunker, Honorary Conference Chair

9:45AM - 10:30AM Caffeinate and Connect with exhibitors (Coffee Break) Room: Grand Terrace

10:30AM - 12:30PM Sessions

- **TransMed COSI: Translational Medical Informatics** (Room: Madison A)
- **HitSeq COSI: High-throughput Sequencing** (Room: Madison B)
- **NetBio COSI: Network Biology** (Room: Madison CD)
- **iRNA COSI: Integrative RNA Biology** (Room: Lecture Hall)
- **CAMDA COSI: Critical Assessment of Massive Data Analysis** (Room: EH)
- **VarI COSI: Variant Interpretation** (Room: FI)
- **Education COSI: Computational Biology Education** (Room: GJ)
- **Special Track: NIH-NSF Smart Health Program** (Room: KOPL)
- **Special Session: Digital Agriculture** (Room: MQRN)
- **Technology Track** (Technology Theatre Community Terrace)

12:30PM - 2:30PM Lunch and Ideation Hall (Poster Session A) Room: Exhibit Hall A (Level 1)

10:30AM - 12:30PM Sessions Continue

- TransMed COSI Continues
- HitSeq COSI Continues
- NetBio COSI Continues
- iRNA COSI Continues
- CAMDA COSI: Continues
- VarI COSI Continues
- Education COSI Continues
- Special Track: NIH-NSF Smart Health Program Continues
- Special Session: Digital Agriculture Continues
- Technology Track Continues

3:30PM - 4:00PM Coffee Break (Caffeinate and Connect with exhibitors) Room: Grand Terrace

4:00PM - 6:00PM Sessions Continue

- TransMed COSI Continues
- HitSeq COSI Continues
- NetBio COSI Continues
- iRNA COSI Continues
- CAMDA COSI: Continues
- VarI COSI Continues
- Education COSI Continues
- **Special Session: Genome Privacy and Security** (Room: KOPL)
- Special Session: Digital Agriculture Continues
- Technology Track Continues

6:15PM - 7:30PM
Birds of a Feather (BoF): Strategies for Team Science in the Age of Hybrid and Remote Work Room: KOPL
Birds of a Feather (BoF): Bioinformatics in the cloud for newcomers Room: MQRN

6:15PM - 7:15PM Virtual Poster Session (via Conference Platform)

Schedule-at-a-glance
Wednesday, July 13

All times in Central Time Zone

7:30AM - 8:30AM	Virtual Poster Session (via Conference Platform)
8:30AM-8:45AM	Morning Welcome, Room: Madison ABCD
8:45AM - 9:45AM	 ISCB Accomplishments by a Senior Scientist Award Keynote: Ron Shamir, Tel Aviv University Introduced by: Christine Orengo, ISCB President
9:45AM - 10:30AM	Caffeinate and Connect with exhibitors (Coffee Break) Room: Grand Terrace
10:30AM - 12:30PM	Sessions

RegSys COSI: Regulatory and Systems Genomics (Room: Madison A)	**BOSC COSI** (Room: Lecture Hall)	**Evolution and Comparative Genomics COSI** (Room: GJ)
HitSeq COSI: High-throughput Sequencing (Room: Madison B)	**3DSIG COSI: Structural Bioinformatics and Computational Biophysics** (Room: EH)	**BioVis COSI: Biological Data Visualization** (Room: KOPL)
MLCSB COSI: Machine Learning in Computational and Systems Biology (Room: Madison CD)	**MICROBIOME COSI** (Room: FI)	**Bio-Ontologies COSI** (Room: MQRN)

12:30PM - 2:30PM	Lunch and Ideation Hall (Poster Session A) Room: Exhibit Hall A (Level 1)
10:30AM - 12:30PM	Sessions Continue

RegSys COSI Continues	**BOSC COSI** Continues	**Evolution and Comparative Genomics COSI** Continues
HitSeq COSI Continues	**3DSIG COSI** Continues	**BioVis COSI** Continues
MLCSB COSI Continues	**MICROBIOME COSI** Conttinues	**Bio-Ontologies COSI** Continues

3:30PM - 4:00PM	Coffee Break (Caffeinate and Connect with exhibitors) Room: Grand Terrace
4:00PM - 6:00PM	Sessions Continue

RegSys COSI Continues	**BOSC COSI** Continues	**Evolution and Comparative Genomics COSI** Continues
HitSeq COSI Continues	**3DSIG COSI** Continues	**BioVis COSI** Continues
MLCSB COSI Continues	**MICROBIOME COSI** Conttinues	**Bio-Ontologies COSI** Continues

6:15PM - 7:30PM	Birds of a Feather (BoF): Comparative Genomics Resource: a powerful tool for scientific discovery Room: KOPL Birds of a Feather (BoF): Cloud Computing and Bioinformatics Room: MQRN
6:15PM - 7:15PM	Virtual Poster Session (via Conference Platform)
6:15PM - 8:15PM	Protein Codeathon: Final Team Presentations

Schedule-at-a-glance
Thursday, July 14

ISCB
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JULY 10–14

All times in Central Time Zone

8:15AM-8:30AM	Morning Welcome and Conference updates, Room: Madison ABCD
8:30AM - 9:30AM	 ISCB Innovator Award Keynote: Núria López-Bigas, Institute for Research in Biomedicine Introduced by: Janet Kelso, ISCB Treasurer
9:30AM - 10:15AM	Caffeinate and Connect with exhibitors (Coffee Break) Room: Grand Terrace
10:15AM - 12:15PM	Sessions
	RegSys COSI: Regulatory and Systems Genomics (Room: Madison A) **MLCSB COSI: Machine Learning in Computational and Systems Biology** (Room: Madison CD) **BOSC COSI** (Room: Lecture Hall) **3DSIG COSI: Structural Bioinformatics and Computational Biophysics** (Room: EH) **MICROBIOME COSI** (Room: FI) **Evolution and Comparative Genomics COSI** (Room: GJ) **Special Session: COVID-19** (Room: KOPL) **Bio-Ontologies COSI** (Room: MQRN)
12:15PM - 1:15PM	Lunch and Ideation Hall (Poster Session A) Room: Exhibit Hall A (Level 1)
12:30PM - 2:00PM	Career Fair - Exhibition Area - Grand Terrace
12:15PM - 1:15PM	Protein Codeathon: Closing Project Discussions, Publication Timelines, and Suggestions
1:15PM - 3:15PM	Sessions Continue
	RegSys COSI Continues **MLCSB COSI** Continues **BOSC/Bio-Ontologies joint session** (Room EH) **3DSIG COSI** Continues **MICROBIOME COSI** Conttinues **Evolution and Comparative Genomics COSI** Continues **Equity-focused Research Track (1:15 - 2:15 pm)** (Room KOPL) **Bio-Ontologies COSI** Continues
3:15PM - 3:45PM	Refreshment Break Room: Grand Terrace
3:45PM - 4:45PM	Sessions Continue
	RegSys COSI Continues **MLCSB COSI** Continues **OBF: BOSC COSI Continues** **3DSIG COSI** Continues **MICROBIOME COSI** Conttinues
4:50PM - 5:15PM	 Awards Presentations & Conference Closing Room: Madison CD

Special Sessions

MONDAY, JULY 11 (10:30 AM – 6:00 PM CDT)

https://www.iscb.org/ismb2022-program/special-sessions

SPECIAL SESSION: COMPUTATIONAL IMMUNOLOGY

ORGANIZER(S):

Yuri Pritykin, *Princeton University*

10:30 - 11:00	**Shirley Liu,** GV20 Therapeutics *Integrated genomics and AI approach for IO target and drug discovery*
11:00 - 11:20	**Elham Azizi,** Columbia University *Machine Learning for Modeling Dynamics in the Tumor Microenvironment*
11:20 - 11:50	**Soumya Raychaudhuri,** Bigham and Women's Hospital, Harvard Medical School, Broad Institute *Single-cell eQTL models reveal dynamic T cell state dependence of disease loci*
11:50 - 12:10	**Ferhat Ay** *Studying the 3D organization of human immune cells to better interpret disease-associated variants*
14:30 - 14:50	**Duygu Ucar** *Sex differences in immune aging and vaccine responses*
16:00 - 16:30	**Christina Leslie** *Tumor immunity at single cell resolution*
16:50 - 17:10	**Yuri Pritykin** *Systems biology of T cells in cancer and infection*
17:10 - 17:25	**Linglin Huang,** Harvard T. H. Chan School of Public Health *Combined scRNA/TCR-seq reveals migratory phenotypes of tissue Th17 cells during autoimmunity*
17:25 - 17:40	**Chuan Xu,** Wellcome Sanger Institute *CellTypist: towards automated cell type annotation*
17:40 - 17:55	**Ken Hoehn** *Phylogenetic methods for understanding B cell migration, differentiation, and evolution over time*

Special Sessions

TUESDAY, JULY 12 (10:30 AM – 6:00 PM CDT)

https://www.iscb.org/ismb2022-program/special-sessions

SPECIAL SESSION: DIGITAL AGRICULTURE

ORGANIZER(S):

Jennifer L. Clarke, University of Nebraska-Lincoln, United States
Noah Fahlgren, The Donald Danforth Plant Science Center, United States
Camilo Valdes, University of Nebraska-Lincoln, United States

10:30 - 11:10
Joao Carlos Gomes Neto, UNL
Harnessing population-based patterns and inferring "ecological signal" from complex foodborne pathogen whole-genome datasets

11:10 - 11:50
Katie Summers, USDA
Cross-kingdom Interactions in the Porcine Gut: Implications in Health and Performance

11:50 - 12:10
Alexandra Crook, University of Nebraska
Combining Two Analytical Techniques with Chemometric Analysis to Characterize Wine by Vineyard, Region, and Vintage

12:20 - 12:30
Manoj Natarajan, Agri and Agri Food Canada
Developing a Low-Cost Digital Imaging System for Plant Phenotyping using Raspberry Pi Computers

14:30 - 15:30
Addie Thompson
Digital Agriculture at Scale

14:30 - 15:30
Keshav Singh
Digital Imaging Technology in Plant Phenotyping: Canadian Crops Perspective

14:30 - 15:30
Yijie Xiong, University of Nebraska-Lincoln
Precision Livestock Management: Sensing Technologies And Application

16:20 - 16:40
Guilherme J. M. Rosa, University of Wisconsin-Madison
Leveraging on High-throughput Phenotyping Technologies to Optimize Genetic Improvement in Livestock.

16:40 - 17:00
Chris Tuggle, Iowa State University
Integration of epigenomic and transcriptomic data to identify regulatory elements and networks controlling immune cell-type gene expression in the pig

17:00 - 17:20
Tobias Jores, University of Washington
Learning the grammar of plant regulatory DNA

17:20 - 17:40
Zhen Fan, University of Florida
Big data applications in strawberry breeding

17:40 - 18:00
Colleen Yanarella, Iowa State University
Speech-Based Genotype to Phenotype Analysis for Association Genetics in Maize: A Proof of Concept

Special Sessions

TUESDAY, JULY 12 (4:00 PM – 6:00 PM CDT)

https://www.iscb.org/ismb2022-program/special-sessions

SPECIAL SESSION: GENOME PRIVACY AND SECURITY

ORGANIZER(S):

Bonnie Berger, Massachusetts Institute of Technology, United States
Hyunghoon Cho, Broad Institute of MIT and Harvard, United States

16:10 - 16:45	**Yaniv Erlich** *Genetic privacy: a balanced view*
16:45 - 17:00	**Gamze Gürsoy** *Genome privacy in the era of multiomics*
17:00 - 17:15	**Alex Leighton,** Harvard Medical School **Yun William Yu**, University of Toronto *Secure Federated Aggregate-Count Queries on Medical Patient Databases Via Fully-Homomorphic Cryptography*
17:15 - 17:30	**David Froelicher** *Privacy-Preserving Federated Biomedical Analysis with Multiparty Homomorphic Encryption*
17:30 - 17:45	**Bradley Malin** *Sociotechical Controls for Genomic Data Privacy*
17:45 - 18:00	**Lucila Ohno-Machado** *Everyone is Unique: Individual and Group Preferences for Privacy*

Special Sessions

TUESDAY, JULY 14 (10:15 AM – 12:15 PM CDT)

https://www.iscb.org/ismb2022-program/special-sessions

SPECIAL SESSION: COVID-19

ORGANIZER(S):

Thomas Lengauer, Max Planck Institute for Informatics, Germany
Shoshana Wodak, VIB-VUB Center for Structural Biology, Belgium

10:15 - 10:55	**Andrea Ganna** *Mapping the human genetic architecture of COVID-19*
10:55 - 11:35	**Stephen MacKinnon,** Cyclica *Discovery of Broad Spectrum Coronavirus Drug Repurposing Candidates Via Computational Target Identification and Drug-Target Interaction Predictions*
11:35 - 12:15	**Artem Babaian** *Hacking Earth's Virome To Stop The Next Pandemic*

Birds of a Feather (BoF)

TUESDAY, JULY 12TH

https://www.iscb.org/ismb2022-program/bof

TUESDAY, JULY 12TH, 18:15-19:15

STRATEGIES FOR TEAM SCIENCE IN THE AGE OF HYBRID AND REMOTE WORK

ORGANIZER(S):

Brittany Lasseigne
Alejandra Rivera

FORMAT: LIVE FROM VENUE

TUESDAY, JULY 12TH, 18:15-19:15

BIOINFORMATICS IN THE CLOUD FOR NEWCOMERS

ORGANIZER(S):

Geraldine Auwera

FORMAT: LIVE FROM VENUE

Birds of a Feather (BoF)

WEDNESDAY, JULY 13TH

https://www.iscb.org/ismb2022-program/bof

WEDNESDAY, JULY 13TH, 18:15-19:15

COMPARATIVE GENOMICS RESOURCE: A POWERFUL TOOL FOR SCIENTIFIC DISCOVERY

ORGANIZER(S):

Tom Madden, National Library of Medicine, NIH

FORMAT: LIVE FROM VENUE

WEDNESDAY, JULY 13TH, 18:15-19:15

CLOUD COMPUTING AND BIOINFORMATICS

ORGANIZER(S):

Lee Pang, Amazon Web Services

FORMAT: LIVE FROM VENUE

ISCB TOWN HALL

MONDAY, JULY 11

6:15 - 7:30 CDT

Join us at the ISCB Town Hall meeting on Monday, July 11, 6:15 PM - 7:15 PM CDT 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.

The Town Hall will close with a celebration of achievement with the announcement of the Wikipedia Competition Award winners, Art in Science Award winners, Student Council Symposium award winners, celebration of the 2022 Class of Fellows, and announcement of the incoming Board of Directors.

Equity-focussed Research Presentations

THURSDAY, JULY 14TH

https://www.iscb.org/ismb2022-program/equity

1:15-1:35	***Aritra Bose,*** *IBM Research, United States* *Race versus Genetics in clinical decision-making: a perspective from cardiovascular disease*
1:35-1:55	***Zijun Zhang,*** *Flatiron Institute, Simons Foundation, United States* *CROTONdb identifies population-stratified genomic variations implicated in CRISPR/Cas9 editing outcomes*
1:55-2:05	***Leonardo Toshinobu Kimura,*** *University of Sao Paulo, Brazil* *Amazon Biobank: A collaborative genetic database for bioeconomy development.*
2:05-2:15	***Natalie Davidson,*** *University of Colorado Anschutz Medical Campus, United States* *Analysis of science journalism reveals gender and regional disparities in coverage*

Do your part to offset carbon emissions!
https://www.iscb.org/iscb-groves

Special Track:
NIH-NSF Smart Health Program

TUESDAY, JULY 12TH

https://www.iscb.org/ismb2022-program/nih-nsf

10:30-10:35	***Susan Gregurick*** *Keynote Presentation: Opening Remarks*
10:35-11:05	***Dana Wolff-Hughes*** *Keynote Presentation: The Smart Health Program*
11:05-11:15	***Guo-Qiang Zhang*** *Neurophysiological AI-Ready Data Resource*
11:15-11:25	***Christina Boucher*** *Enabling real time surveillance of antimicrobial resistance*
11:25-11:35	***Shandong Wu,*** *University of Pittsburgh, United States* *Leverage clinical knowledge to augment deep learning analysis of breast images*
11:35-11:45	***Amarda Shehu*** *Common Attributes of Responsive Proposals*
11:45-12:30	***Wendy Nilsen*** ***Dana Wolff-Hughes*** ***Natalia Komissarova*** ***Guo-Qiang Zhang*** ***Shandong Wu*** ***Christina Boucher*** ***Amarda Shehu*** *Panel: SCH Mock Review*
14:30-15:30	***Wendy Nilsen*** ***Dana Wolff-Hughes*** ***Natalia Komissarova*** ***Guo-Qiang Zhang,*** *The University of Texas Health Science Center at Houston, USA* ***Shandong Wu*** ***Christina Boucher*** ***Amarda Shehu*** *Panel: SCH Panel Discussion*

POSTERS

MONDAY, JULY 11 • TUESDAY, JULY 12 • WEDNESDAY JULY 13

https://www.iscb.org/ismb2022-program/posters

Poster Session A:
Monday, July 11 and Tuesday, July 12
between 12:30 PM CDT and 2:30 PM CDT

BioInfo-Core
CAMDA
CompMS
Education
Function
HiTSeq
iRNA
NetBio
Special Session: Computational Immunology
Special Session: Digital Agriculture
Special Session: Genome Privacy and Security
ssda
SysMod
Text Mining
TransMed
VarI
General Comp Bio

Poster Session B:
Wednesday July 13
between 12:30 PM CDT and 2:30 PM CDT

3DSIG
Bio-Ontologies
BioVis
BOSC
Equity-focussed Research
Presentations
EvolCompGen
HiTSeq
MICROBIOME
MLCSB
RegSys

Virtual Presentations:
All posters can be presented virtually
July 11 - 13, 7:30 AM CDT - 8:30 AM CDT and
6:15 PM CDT - 7:15 PM CDT.

3DSIG COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

3D-SIG: Structural Bioinformatics and Computational Biophysics

10:30- 11:10	**3DSIG Keynote** **Robert Jernigan** *Unprecedented Opportunities for Datamining of Protein Sequences and Structures*
11:10- 11:30	**3DSIG Keynote** **Robert Jernigan** *Unprecedented Opportunities for Careers in Protein Science*
11:30- 11:50	**Olivier Mailhot,** Université de Montréal, Canada *Sequence-sensitive elastic network captures dynamical elements necessary for human microRNA maturation*
11:50- 12:10	**Michał Denkiewicz,** Faculty of Mathematics and Information Science, Warsaw University of Technology, Warsaw, Poland *Intrinsic linking of chromatin in human cells*
12:10- 12:30	**Myungjin Lee,** National Institutes of Health, United States *GLYCO-2.0: a web-based server to quantify glycan shielding of glycosylated proteins with improved data processing and computational speed*
14:30- 14:40	**Elena Lilkova,** Institute of Information and Communication Technologies, Bulgarian Academy of Sciences, Bulgaria *Interaction between hIFNγ and HS oligosaccharides*
14:40- 14:50	**Seyedmohsen Hosseini,** University of Western Ontario, Canada *PITHIA: protein interaction site prediction using multiple sequence alignments and attention*
14:50- 15:00	**Md Hossain Shuvo,** Virginia Tech, United States *InterAccGAT: improved estimation of protein complex interfacial accuracy using geometry-integrated multi-head graph attention networks*
15:00- 15:10	**Kazuhiro Ikkyu,** University of Tsukuba, Riken, Japan *MTL4MHC2: MHC class II binding prediction by using multi-task learning*
15:10- 15:20	**Sandro Izidoro,** Universidade Federal de Itajubá - UNIFEI, Brazil *GASS platform: identifying active sites and binding sites on protein structures using parallel genetic algorithms*
15:20- 15:30	**Hugo Talibart,** Institut de Systématique, Evolution, Biodiversité (ISYEB), MNHN, Sorbonne Université, EPHE, UA, CNRS, France *PPalign: optimal alignment of Potts models representing proteins with direct coupling information*
16:00- 16:20	**Gabriel Tiago Galdino,** Universite de Montreal, Canada *Normal Mode Analysis Applied to GPCRs*
16:20- 16:40	**Tian Cai, Hunter College,** The City University of New York, United States *Structure-enhanced Deep Meta-learning Predicts Genome-Wide Uncharted Chemical-Protein Interactions*
16:40- 17:00	**Oliver Kohlbacher,** University of Tübingen, Germany *XLEC - Large-scale prediction of protein-protein complex structures from sequence co-evolution and cross-linking data*
17:00- 17:20	**Yasser Mohseni Behbahani,** Sorbonne Université, France *Deep Local Analysis evaluates protein docking conformations with locally oriented cubes*
17:20- 17:40	**Amar Singh, Computational Biology Program,** The University of Kansas, Lawrence, United States *Standing out in the crowd: Native protein partners are distinct from the non-native ones in protein-protein interactions*
17:40- 18:00	**Kapil Devkota,** Tufts University, United States *Proceedings Presentation: Topsy-Turvy: integrating a global view into sequence-based PPI prediction*

3DSIG COSI

COSI TRACK PRESENTATIONS

THURSDAY, JULY 14TH

3D-SIG: Structural Bioinformatics and Computational Biophysics

10:15- 11:15	**3DSIG Keynote** **David Baker,** University of Washington, United States *Protein design using deep learning*
11:15- 11:35	**Nicola Bordin,** University College London, United Kingdom *AlphaFold2 reveals commonalities and novelties in protein structure space for 21 model organisms*
11:35- 11:55	**Peter Røgen,** Technical University of Denmark, Denmark *ProteinAlignmentObstruction – an algorithm for detecting and quantifying steric and topological obstructions to structural alignments of proteins*
11:55- 12:15	**Rodrigo Gonzalo Parra,** Barcelona Supercomputing Center, Spain *FrustraEvo: Assessing Protein Families Divergence In The Light Of Sequence and Energetic Constraints*
12:15- 12:35	**Sandun Rajapaksa,** Monash University, Australia *Proceedings Presentation: On the reliability and the limits of inference of amino acid sequence alignments*
13:15- 13:35	**Paweł Szczerbiak,** Malopolska Centre of Biotechnology, Jagiellonian University, Krakow, Poland *Sequence-structure-function relationships in the microbial protein universe*
13:35- 13:55	**Sebastian Bittrich,** RCSB Protein Data Bank, United States *Scaling to Millions of Structures: Real-Time Protein Structure Motif Searching in the RCSB PDB & AlphaFold Databases*
13:55- 14:15	**Johannes Söding,** Max Planck Institute, Germany *Foldseek: fast and accurate protein structure search*
14:15- 14:35	**Neeladri Sen,** Institute of Structural and Molecular Biology, University College London, United Kingdom *Characterizing and explaining impact of disease-associated mutations in proteins without known structures or structural homologues*
14:35- 14:55	**Konstantin Weissenow, Technical University of Munich, Germany** *Opening the door for ultra-fast in-silico structure mutation*
14:55- 15:15	**Natalia Fagundes Borges Teruel,** UdeM: Université de Montreal, Canada *DYNAMICAL STUDY OF VIRAL GLYCOPROTEINS AND EVOLUTIONARY FITNESS SIMULATION*
15:45- 16:05	**Stuart A. MacGowan, University of Dundee, United Kingdom** *Population missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike: A case study in affinity predictions of interface variants*
16:05- 16:25	**Bruna Moreira da Silva,** The University of Melbourne, Australia *CSM-epitope: linear B-cell epitope prediction using graph-based signatures and interpretable machine learning*
16:25- 16:45	**Lewis Chinery,** University of Oxford, United Kingdom *Paragraph - Antibody paratope prediction using Graph Neural Networks with minimal feature vectors*

BIOINFO-CORE

COSI TRACK PRESENTATIONS

MONDAY, JULY 11TH

10:30- 10:37	**Scott Cain,** Adaptive Oncology, Ontario Institute for Cancer Research, United States *JBrowse 2: an open source genome browser for bioinfo cores*
10:39- 10:47	**Patricia Carvajal-López,** EMBL-EBI, United Kingdom *Bioinformatics core facility management training - availability and challenges*
10:49- 10:56	**Nikhil Kumar,** Memorial Sloan Kettering Cancer Center, United States *An open tech stack for the development of reproducible, portable, and robust bioinformatic pipelines.*
10:58- 11:06	**Fan Feng,** University of Michigan, United States *Connecting high-resolution 3D chromatin organization with epigenomics*
11:10- 11:40	**Jonathan Dursi,** Research Computing Teams, Canada ***Keynote Presentation:*** *Technology isn't the hardest part: What can bioinfo cores and research computing, software, and data teams teach each other?*
11:40- 12:10	**Shannan Ho Sui,** Harvard T.H. Chan School of Public Health, USA **George Bell** **Patricia Carvajal** **Ryan Dale,** National Institute of Child Health and Human Development, National Institutes of Health, USA **Jonathan Dursi,** Research Computing Teams, Canada ***Panel****: Bioinformatics Core Management*
12:10- 12:30	**Small discussions** ***Panel:*** *Small group discussions*

Bio-Ontologies COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

10:30-10:50 **Tiffany Callahan**
Keynote Presentation: *Bio-Ontologies COSI Opening Introductions*

10:50-11:50 **Maria Keet**
***Keynote Presentation**: Bio-Ontologies COSI Keynote: Encoding biases' influences on development and use of ontologies in the life sciences*

11:50-12:10 **Jiyu Chen,** The University of Melbourne, Australia
Proceedings Presentation: Exploring Automatic Inconsistency Detection for Literature-based Gene Ontology Annotation

12:10-12:30 **Sanya B. Taneja,** University of Pittsburgh, United States
Evaluation of Named Entity Recognition Systems to Improve Ontology Concept Annotation for Biomedical Knowledge Graphs

14:30-14:50 **Nirupama Benis,** University of Amsterdam, Netherlands
EJP RD meets OHDSI: enabling interoperability for rare disease research

14:50-15:10 **Liwei Wang,** Mayo Clinic, United States
Development of a general purpose cognitive-behavioral symptom taxonomy

15:10-15:20 **Michael Bradshaw,** University of Colorado Boulder, United States
Identification of clusters containing future gene-to-phenotype relations across heterogeneous data sources

16:00-16:20 **Martijn Kersloot,** Amsterdam UMC, Netherlands
Improving the FAIRness of vascular anomaly research data using the International Society for the Study of Vascular Anomalies (ISSVA) Ontology

16:20-16:40 **Xiaofeng Liao,** Radboud University Medical Center, Netherlands
Creating a FAIR data model for personalized risk-based breast cancer research: Findings from the PRISMA study

16:40-17:00 **José Luis Sánchez-Fernández,** BASF Group, Spain
Ontology Management in an Industrial Environment: The BASF Governance Operational Model for Ontologies (GOMO)

17:00-17:20 **Carsten Fortmann-Grote,** Max Planck Institute for Evolutionary Biology, Germany
From genome annotation to knowledge graph: The case of Pseudomonas fluorescens SBW25

17:20-17:40 **Yufei Shen,** Huazhong Agricultural University, China
RTO, A Specific Crop Ontology for Rice Trait Concepts

17:40-18:00 **Hervé Ménager,** Institut Pasteur, Paris, France
EDAM - The data analysis and management ontology (update 2022)

Bio-Ontologies COSI

COSI TRACK PRESENTATIONS

THURSDAY, JULY 14TH

10:15-10:45	**Maxat Kulmanov,** King Abdullah University of Science and Technology, Saudi Arabia *Proceedings Presentation: DeepGOZero: Improving protein function prediction from sequence and zero-shot learning based on ontology axioms*
10:45-10:55	**Tiffany Callahan,** Columbia University, United States *Assessing ontology fitness for use with the Harmonized Data Quality Framework*
10:55-11:05	**Irene Kyomugisha,** Division of Human Genetics, Faculty of Health Sciences, University of Cape Town, South Africa *Systematic Integration of Large-scale Clinical and Phenotype Datasets*
11:05-11:25	**Patrick Greaves,** Birkbeck, University of London, United Kingdom *Predicting the pro-longevity or anti-longevity effect of model organism genes with sub-graph embeddings of Gene Ontology*
11:25-11:45	**Nicole Vasilevsky,** University of Colorado Anschutz Medical Campus, United States *OBO Academy: Training materials for bio-ontologists*
11:45-12:05	**Frederic B. Bastian,** University of Lausanne, SIB Swiss Institute of Bioinformatics, Switzerland *Creation and unification of development and life stage ontologies for animals*
12:05-12:15	**Robert Hoehndorf** *Bio-Ontologies COSI Closing Remarks*
13:15-14:15	**Melissa Haendel,** University of Colorado Anschutz Medical Campus, USA ***Keynote Presentation:*** *The open data highway: turbo-boosting translational traffic with ontologies*
14:15-14:35	**James A. Overton,** Knocean, Inc., Canada *The OntoDev Suite of Ontology and Data Integration Tools*
14:35-14:55	**Hilmar Lapp,** Duke University, United States *RPhenoscape: Semantic computing with morphological traits and ontologies*
14:55-15:05	**Harry Caufield,** Berkeley Bioinformatics Open-source Projects, Lawrence Berkeley National Laboratory, Berkeley, CA *KG-OBO: Open Bio-Ontologies in Knowledge Graph Form*
15:05-15:15	**Tarcisio Mendes de Farias,** SIB Swiss Institute of Bioinformatics, Switzerland *Federating and querying heterogeneous and distributed Web APIs and triple stores*

BIOVIS COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

BioVis:
Biological Data
Visualizations

biovis

10:30-11:30	**Tatiana Landesberger** ***BioVis Keynote:*** *Once upon a time in Bio-Medical Data Visualization: Reflections on Research Before and During Pandem...*
11:30-11:50	**Mark Keller,** Harvard Medical School, United States Polyphony: an Interactive Transfer Learning Framework for Single-Cell Data Analysis
11:50-12:00	**Fritz Lekschas,** Ozette Technologies, United States *Data Transformations for Effective Visualization of Single-Cell Embeddings*
12:00-12:10	**Elzbieta Gralinska,** Max Planck Institute for Molecular Genetics, Germany *Visualizing Cluster-specific Genes from Single-cell Transcriptomics Data Using Association Plots*
12:10-12:20	**Jayaram Kancherla,** Genentech, Inc., United States *Kana: Interactive Single-Cell Analysis in the Browser*
12:20-12:30	**Zhiqian Zhai,** Department of Statistics, University of California Los Angeles, United States *Supervised capacity preserving mapping: a clustering guided visualization method for scRNA-seq data*
14:30-14:50	**Klaus Eckelt,** Johannes Kepler University Linz, Austria *Visual Exploration of Relationships and Structure in Low-Dimensional Embeddings*
14:50-15:10	**Patrick Adelberger,** Institute of Computer Graphics, Johannes Kepler University Linz, Linz, Austria *Coral: a web-based visual analysis tool for creating and characterizing cohorts*
15:10-15:20	**Tuğba Önal-Süzek,** Muğla Sıtkı Koçman University, Turkey *TCGAnalyzeR: A Web Portal for Visualization of Integrated Analysis Of Subcohorts of Pan-Cancer Patients With Molecular and Clinical Data*
15:20-15:30	**Charles Blatti,** University of Illinois at Urbana-Champaign, United States *PhyloDiver: A Visual Analytics Tool for Tumor Phylogenies*
16:00-16:20	**Camilo Valdes,** Lawrence Livermore National Laboratory, United States *Microbiome Maps: Hilbert Curve Visualizations of Metagenomic Profiles*
16:20-16:24	**Sarah Sandmann,** Institute of Medical Informatics, University of Münster, Germany *Plaice plots - an allele-aware visualization of clonal evolution*
16:24-16:27	**Tapsya Nayak,** Greehey Children's Cancer Research Institute, University of Texas Health San Antonio, United States *BioVis Highlights Talk: Insights From Experiments With Rigor in an EvoBio Design Study*
16:27-16:31	**Hanin Alzahrani,** Newcastle university, United Kingdom *INVESTIGATION AND IDENTIFICATION OF ESSENTIAL FACTORS FOR VISUALISATION TOOLS FOR COMPLEX BIOLOGICAL NETWORKS*
16:31-16:34	**Eliott Jacopin,** RIKEN, Center for Biosystems Dynamics Research, Japan *ECellDive: Exploring Biological Systems in Virtual Reality*
16:34-16:38	**Milton Yutaka Nishiyama-Jr,** Laboratório de Toxinologia Aplicada, Instituto Butantan, Brazil, Brazil *VenOmics and Cell Signaling Environment for Studies and BioDiscoveries*
16:38-16:41	**TBD** *SciViewer- An interactive browser for visualizing large single cell datasets*
16:41-16:45	**TBD** *Gos: a declarative (epi)genomics visualization library for Python*
16:45-16:48	**Anisha Haldar,** Heersink School of Medicine, The University of Alabama at Birmingham, United States *CoSIA: An R Package that Measures and Visualizes Transcriptome Diversity across Model Organisms and Their Tissues*

BIOVIS COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH CONTINUED...

BioVis:
Biological Data
Visualizations

biovis

16:48-16:52	**Nils Gehlenborg,** Harvard University, United States *Interactive Exploration of Tissues and Cells Guided by Visual Pattern Mining*
16:52-16:55	**Heba Sailem,** University of Oxford, United Kingdom *Effective visualisation of the tumour microenvironment using glyph-based approaches*
16:55-16:58	**Sarah Percival,** Michigan State University, United States *Using Mapper to Reveal Morphological Relationships in Passiflora Leaves*
17:00-18:00	**Lennart Martens,** VIB and Ghent University, Belgium ***Keynote Presentation**: Machine learning provides a new perspective on protein modification*

BOSC COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

BOSC:
Bioinformatics
Open Source
Conference

10:30- 10:50	**Nomi Harris** ***BOSC opening remarks***
10:50- 11:50	**Jason Williams,** Cold Spring Harbor Laboratory, US ***Keynote Presentation**: Riding the Bicycle: Including all Scientists on a Path to Excellence* *(BOSC/Education COSI joint keynote)*
11:50- 12:10	**Rachel Torchet,** Institut Pasteur, France *Gender-based disparities and biases in science: observational study of a virtual conference*
12:10- 12:20	**Halie Rando,** University of Colorado School of Medicine, Center for Health AI, Aurora, CO, USA *Adapting Manubot for Open Publishing in the COVID-19 Infodemic*
14:30- 14:35	**Xi Zhang,** Dalhousie University, Canada *Don't waste it: tidy up your bioinformatics work into appropriate publications*
14:35- 14:40	**Thomas Madden,** National Library of Medicine, NIH, United States *ElasticBLAST: accelerating alignments in the cloud*
14:40- 14:45	**Jeremy Arbesfeld,** The Ohio State University, United States *FUSOR and the VICC Fusion Curation Interface: Tools for the Structured Representation of Gene Fusions*
14:50- 15:10	**Christopher Mancuso,** Michigan State University, United States *GenePlexus: A web server and Python package for gene discovery using network-based machine learning*
15:10- 15:30	**Layne Sadler,** AIQC, United States *AI Quality Control (AIQC) open source API & UI for rigorous deep learning experiments*
16:00- 16:05	**Lauren Sanders,** NASA Ames, BMSIS, United States *Evaluation of batch effect correction methods for space biology RNA sequencing data*
16:05- 16:10	**Swati Gupta,** Iisc, India *INTERPIN- a database for INtrinsic transcription TERminator hairPINs in bacteria*
16:10- 16:15	**Paul Wighton,** Martinos Center for Biomedical Imaging at MGH, United States *Containers for increased accessibility and reproducibility of FreeSurfer's infant pipeline*
16:20- 16:30	**Scott Cain,** Adaptive Oncology, Ontario Institute for Cancer Research, Toronto, Canada, United States *Using JBrowse 2 for a model organism database: a WormBase case study*
16:30- 16:40	**Caroline Bridge,** Ontario Institute for Cancer Research, Canada *Using JBrowse 2 plugins to visualize genomics and other biological data.*
16:40- 17:00	**Yao Yao,** The Scripps Research Institute, United States *MyVariant.info: a high-performance biomedical data API for variant annotations*
17:00- 17:20	**Monica Munoz-Torres,** University of Colorado Anschutz Medical Campus, United States *The GA4GH Phenopacket schema: A computable representation of clinical data for precision medicine*
17:20- 17:25	**Bhavesh Patel,** FAIR Data Innovations Hub, California Medical Innovations Institute, United States *Making biomedical research software FAIR with FAIRshare*
17:25- 17:30	**Kathryn Stahl,** Nationwide Children's Hospital, United States *Creating Cloud-based Notebooks for Exploring the GA4GH VRS Standard*

BOSC COSI

COSI TRACK PRESENTATIONS

BOSC: Bioinformatics Open Source Conference

THURSDAY, JULY 14TH

10:15-10:35 **Hirotaka Suetake,** The University of Tokyo, Japan

Yevis: System to support building a workflow registry with automated quality control

10:35-10:55 **Peter Amstutz,** Curii Corporation, United States

Scientific Workflow and Data Management with the Arvados Platform

10:55-11:00 **Mikhail Lebedev,** GenX Global Ltd, United Kingdom

GRAPE: Genomic Relatedness Detection Pipeline

11:00-11:05 **Michael Bouzinier,** Harvard University Faculty of Arts and Sciences Research Computing, United States

Reproducible data engineering pipelines using Common Workflow Language and Apache Airflow

11:05-11:10 **Michael Kotliar,** Cincinnati Children's Hospital Medical Center, United States

CWL toolkit for single-cell sequencing data analysis

11:15-11:35 **Farica Zhuang,** University of Pennsylvania, United States

A cloud based international community effort for reproducible benchmarking of genomic tools

11:35-11:55 **Geraldine Van der Auwera, Broad Institute, United States**

Deciphering a mystery workflow written in WDL

11:55-12:05 **Michael Crusoe,** ELIXIR-NL; VU Amsterdam; CWL Project, Germany

wdl2cwl: Converting WDL workflows to CWL

13:15-14:15 **Melissa Haendel,** University of Colorado Anschutz Medical Campus, USA

Keynote Presentation: *The open data highway: turbo-boosting translational traffic with ontologies*

14:15-14:35 **James A. Overton,** Knocean, Inc., Canada

The OntoDev Suite of Ontology and Data Integration Tools

14:35-14:55 **Hilmar Lapp,** Duke University, United States

RPhenoscape: Semantic computing with morphological traits and ontologies

14:55-15:05 **Harry Caufield,** Berkeley Bioinformatics Open-source Projects, Lawrence Berkeley National Laboratory, Berkeley, United States

The OpenCGA genome-optimised data store: accessing a hundred thousand genomes, a billion variants, and a hundred trillion genotypes in real-time.

15:05-15:15 **Tarcisio Mendes de Farias,** SIB Swiss Institute of Bioinformatics, Switzerland

Federating and querying heterogeneous and distributed Web APIs and triple stores

15:45-16:40 **Jenea Adams**
Andrew Hasley
Gary McDowell
Monica Munoz-Torres
Rachel Torchet

Panel: Building and Sustaining Inclusive Open Science Communities

CAMDA COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 11TH

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

10:30-10:40	**David Kreil** *CAMDA Welcome*
10:40-11:40	**Lynn Schriml** ***Keynote Presentation:*** *Addressing standardization challenges through integrated approaches in biomedical and genomic data*
11:40-12:00	**Krista Ryon** *CAMDA Invited: MetaSUB, An initiative to characterize the global microbiome and establish planetary-scale metagenomic surveillance*
12:00-12:30	**Leonid Chindelevitch** *CAMDA Invited: Antimicrobial resistance prediction from whole-genome sequence and metagenomic data - challenges and opportunities*
14:30-14:50	**Tianqi Tang,** Department of Quantitative and Computational Biology, University of Southern California, United States *Proceedings Presentation: Phage-bacteria contig association prediction with a convolutional neural network*
14:50-15:00	**Serghei Mangul,** Department of Clinical Pharmacy, School of Pharmacy, University of Southern California, United States *The systematic assessment of completeness of public metadata accompanying omics studies*
15:00-15:10	**Yu-Ning Huang,** Department of Clinical Pharmacy, School of Pharmacy, University of Southern California, United States *Assessing the completeness of immunogenetics databases across diverse populations*
15:10-15:20	**Yu-Ning Huang,** Department of Clinical Pharmacy, School of Pharmacy, University of Southern California, United States *Data availability of open T-cell receptor repertoire data, a systematic assessment*
15:20-15:30	**Andrew Dickson,** University of California - Berkeley, United States *GO Bench: Shared-hub for Universal Benchmarking of Machine Learning-Based Protein Functional Annotations*
16:00-16:20	**Paweł Łabaj** *From Critical Assessment at CAMDA to real life applications - metagenomics in forensics*
16:20-16:40	**Deisy Gysi** *Network Medicine in Times of Pandemic: Can we repurpose drugs?*
16:40-17:00	**Mitsuhiro Odaka,** The Graduate University for Advanced Studies / National Institute of Informatics / Nantes Université, Centrale Nantes, Japan *Modeling of large biological knowledge graph augmented with COVID-19 casual network data for drug repurposing*
17:20-17:50	**Joaquin Dopazo** *History of CAMDA*
17:50-18:00	**Wenzhong Xiao** *CAMDA 1st day summary*

CAMDA COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY 12TH

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

10:30- 11:30	**Zhiyong Lu** ***Keynote Presentation: PubMed & Beyond: Biomedical Text Mining for Knowledge Discovery***
11:30- 11:50	**Jung Hun Oh,** Memorial Sloan Kettering Cancer Center, United States *Automatic identification of drug-induced liver injury literature using natural language processing and machine learning methods*
11:50- 12:10	**Malik Yousef,** Zefat College, Israel *The CAMDA Contest Challenges 2022: TextNetTopics Combined with Random Forest Applied on Drug-induced Liver Injury (DILI) Literature*
12:10- 12:30	**Ihor Stepanov, Institute of Molecular Biology and Genetics of NASU, Ukraine** *Ihor Stepanov, Institute of Molecular Biology and Genetics of NASU, Ukraine*
14:30- 14:50	**Eunyoung Kim,** School of Electrical Engineering and Computer Science, Gwangju Institute of Science and Technology (GIST), South Korea *Discovering relationship between bacteriophages and antimicrobial resistance*
14:50- 15:30	**Xianghao Zhan,** Stanford University, United States *AI-based Filter of Drug-induced Liver Injury Publications with Natural Language Processing and Conformal Prediction*
16:00- 16:20	**Andrew Ghazi,** Broad Institute, United States *Proceedings Presentation: High-sensitivity pattern discovery in large, paired multi-omic datasets*
16:20- 16:40	**David Kreil** ***CAMDA Trophy ceremony***
16:40- 17:40	**Wenzhong Xiao** *Panel: CAMDA Caffee*
17:40- 18:00	**Joaquin Dopazo** *CAMDA summary and closing remarks*

COMPMS COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 11TH

CompMS: Computational Mass Spectrometry

CompMS
Computational Mass Spectrometry

10:30-11:10 **Brian Searle,** The Ohio State University, United States
Keynote Presentation: Machine Learning Methods for Proteomics

11:10-11:30 **Martin Frejno,** MSAID GmbH, Germany
An AI-driven leap forward in peptide identification through deconvolution of chimeric spectra

11:30-11:40 **Andy Lin,** Pacific Northwest National Laboratory, United States
Detecting more peptides from bottom-up mass spectrometry data via peptide-level target-decoy competition

11:40-12:00 **Melih Yilmaz,** Paul G. Allen School of Computer Science and Engineering, University of Washington, United States
De novo mass spectrometry peptide sequencing with a transformer model

12:00-12:20 **Daniela Klaproth-Andrade,** Technical University of Munich, Germany
A genetic algorithm with deep learning-based guided mutations improves de novo peptide sequencing

12:20-12:30 **Thomas Mortier,** KERMIT, Department of Data Analysis and Mathematical Modelling, Ghent University, Belgium
Bacterial species identification using MALDI-TOF mass spectrometry and machine learning techniques: A large-scale benchmarking study

14:30-15:10 **Patti, Gary**
Keynote Presentation: Advancing Metabolomics for Precision Medicine

15:10-15:30 **Kai Dührkop,** Friedrich-Schiller-University Jena, Germany
Proceedings Presentation: Deep kernel learning improves molecular fingerprint prediction from tandem mass spectra

16:00-16:40 **Ying, Ge**
Keynote Presentation: Novel ComMS Approaches for Top-down Proteomics toward Precision Medicine

16:40-17:00 **Sean Colby,** Pacific Northwest National Laboratory, United States
DEIMoS: an open-source tool for processing high-dimensional mass spectrometry data

17:00-17:10 **Sean J. McIlwain,** University of Wisconsin-Madison, United States
MASH Native: A Universal and Comprehensive Software for Native Mass Spectrometry

17:10-17:20 **Marzieh Ayati,** University of Texas Rio Grande Valley, United States
Functional Characterization of Co-phosphorylation Networks and Its Application In Cancer Subtyping

17:20-18:00 **Michael Shortreed**
Keynote Presentation: Computer Vision – Unveiling the Hidden Proteome with Software

EDUCATION COSI

COSI TRACK PRESENTATIONS

TUESDAY, JULY 12TH

Education:
Computational Biology
and Bioinformatics
Education and Training

10:30-11:10	**Benjamin Moore,** EMBL-EBI, United Kingdom ***Keynote Presentation: Thoughts and experiences of organising and delivering bioinformatics training in low- and middle-income countries***
11:10-11:30	**Christopher Magnano,** University of Madison-Wisconsin, United States *Proceedings Presentation: An approachable, flexible, and practical machine learning workshop for biologists*
11:30-11:50	**Marta Lloret-Llinares,** EMBL-EBI, United Kingdom *The EMBL-EBI Competency Hub: a tool to support training design and professional development*
11:50-12:10	**Amanda M. Saravia-Butler, KBR, NASA Ames Research Center, Moffett Field, CA 94035, USA, United States** *GL4U: Bioinformatics training for students and educators using space omics data*
12:10-12:30	**Serghei Mangul,** University of Southern California, United States *Cultivating a data-driven computational culture within biomedical institutions by empowering graduate students with code-based data science skills*
14:30-15:30	***The Bioinformatics Education Summit 2022***
16:00-16:20	**Alastair M. Kilpatrick,** Centre for Regenerative Medicine, University of Edinburgh, UK, United Kingdom *Proceedings Presentation: Characterizing domain-specific open educational resources by linking ISCB Communities of Special Interest to Wikipedia*
16:30-16:40	**Anna Swan,** EMBL-EBI, United Kingdom *A blended approach to supporting learners through online bioinformatics training*
16:40-17:20	**Charla Lambert,** Cold Spring Harbor Laboratory/SACNAS, US *Inclusive training in computational biology*
17:20-18:00	***Panel: Inclusiveness in Bioinformatics Education***

EDUCATION COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

Education:
Computational Biology
and Bioinformatics
Education and Training

10:50-11:50	Jason Williams *Keynote Presentation: Riding the Bicycle: Including all Scientists on a Path to Excellence*

EVOLCOMPGEN COSI

COSI TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

10:30-11:00	**Mohammadamin Edrisi,** Rice University, United States *Proceedings Presentation: Phylovar: Towards scalable phylogeny-aware inference of single-nucleotide variations from single-cell DNA sequencing data*
11:00-11:20	**Luca Nesterenko,** CNRS, France *Phyloformer: fast and accurate phylogeny estimation with self-attention networks*
11:20-11:40	**Shadi Darvish Shafighi,** University of Warsaw, Poland *CACTUS: integrating clonal architecture with genomic clustering and transcriptome profiling of single tumor cells*
11:40-12:10	**Xuecong Fu,** Carnegie Mellon University, United States *Proceedings Presentation: Reconstructing tumor clonal lineage trees incorporating single nucleotide variants, copy number alterations, and structural variations*
12:10-12:30	**Giltae Song,** Pusan National University, South Korea *Multi-modal Transformer based deep neural network for determining false positive structural variation calls*
14:30-15:00	**Noa Ecker,** Tel Aviv University, Israel *Proceedings Presentation: A LASSO-based approach to sample sites for phylogenetic tree search*
15:00-15:20	**Alexey Markin,** National Animal Disease Center, USDA-ARS, United States *Sampling representative taxa on a phylogeny with PARNAS*
15:20-15:10	**Yongjun Tan,** Saint Louis University, United States *Comparative Phylogenomic Analysis of the Liberibacter Pathogens Associated with Huanglongbing and Zebra Chip*
16:00-16:30	**Siavash Mirarab,** University of California San Diego, United States *Proceedings Presentation: QuCo: Quartet-based Co-estimation of Species Trees and Gene Trees*
16:30-16:50	**Fritz Sedlazeck,** Baylor College of Medicine, United States *Read2Tree: scalable and accurate phylogenetic trees from raw reads*
16:50-17:20	**Yasamin Tabatabaee,** University of Illinois at Urbana-Champaign, United States *Proceedings Presentation: Quintet Rooting: Rooting Species Trees under the Multi-Species Coalescent Model*
17:20-17:40	**Mathieu Gascon,** Université de Montréal, Canada *Non-binary Tree Reconciliation with Endosymbiotic Gene Transfer*
17:40-18:00	**Joel Nitta,** The University of Tokyo, Japan *An Open and Continuously Updated Fern Tree of Life (FTOL)*

EVOLCOMPGEN COSI

COSI TRACK PRESENTATIONS

THURSDAY, JULY 14TH

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

10:15-10:25 **Ana Isabel Castillo Orozco,** McGill University Health Centre Research Institute, Canada
Comparative Genomic Analysis of Primary Medulloblastoma and Leptomeningeal Metastasis

10:25-10:55 **Xiaoyue Cui,** Carnegie Mellon University, United States
Proceedings Presentation: Simulating Domain Architecture Evolution

10:55-11:15 **Yuting Xiao,** Carnegie Mellon University, United States
Domain Promiscuity Correlates with Rates of Domain Gain and Loss

11:15-11:35 **Wend Yam Donald Davy Ouédraogo,** Université de Sherbrooke, Canada
TranscriptDB : A transcript-centric database to study transcript conservation and evolution within gene trees

11:35-11:45 **Aijing Feng,** University of Missouri, United States
Genomic Diversity and Associated Phenotyping of Escherichia coli Isolated from Poultry in the Southern United States

11:45-11:55 **Georgy Kurakin,** Pirogov Russian National Research Medical University, Russia
Bacterial lipoxygenases could facilitate cross-kingdom host jumps

11:55-12:15 **Yoann Anselmetti,** University of Sherbrooke, Canada
Studying the Evolution of CRISPR-Cas Systems using SuperDTL Reconciliation

13:15-13:45 **Dinithi Sumanaweera,** Wellcome Sanger Institute, United Kingdom
Proceedings Presentation: Bridging the gaps in statistical models of protein alignment

13:45-14:05 **Janani Ravi,** Michigan State University, United States
Cross-database integration using evolution and machine learning to identify multiscale molecular building blocks for antibiotic resistance

14:05-14:25 **Avery Selberg,** Temple University, United States
BUSTED-PH: distinguish adaptive innovation from reduced constraint

14:25-15:15 **Aida Ouangraoua**
Dannie Durand
Edward Braun
Panel: EvolCompGen panel discussion

FUNCTION COSI

COSI TRACK PRESENTATIONS

MONDAY, JULY 11TH

Function: Gene and Protein Function Annotation

Function

10:30- 10:40	**Kim Reynolds** **Dukka KC** *Introduction*
10:40- 11:20	**Lukasz Kurgan** *Keynote Presentation: Modern resources for the intrinsic disorder and disorder function prediction*
11:20- 11:30	**Maria Littmann,** Technical University of Munich, Germany *Protein embeddings and deep learning predict binding residues for various ligand classes*
11:30- 11:40	**Florian Boecker,** Crop Bioinformatics Uni Bonn, Germany *AHRD - Protein Function Transfer and Evaluation*
11:40- 11:50	**Yuval Tabach,** Hebrew university, Israel *Co-evolution based machine-learning for predicting functional interactions between human genes*
11:50- 12:00	**Peter Tonner,** National Institute of Standards and Technology, United States *Interpretable modeling of genotype-phenotype landscapes with state-of-the-art predictive accuracy*
12:00- 12:10	**Yan Chak Li,** Icahn School of Medicine at Mount Sinai, United States *Integrating multimodal data through interpretable heterogeneous ensembles*
12:10- 12:20	**Marcin Joachimiak,** Lawrence Berkeley National Laboratory, United States *Machine Learning to Uncover Microbial Function Indicators for Earth Biomes*
12:20- 12:30	**Mahdi Baghbanzadeh,** Computational Biology Institute, Milken Institute School of Public Health, The George Washington University, United States *Prioritizing important regions of sequencing data for function prediction*
14:30- 14:40	**Christine Chang,** Pacific Northwest National Laboratory, United States *Snekmer: A scalable pipeline for protein sequence fingerprinting based on amino acid recoding*
14:40- 14:50	**Vasilis Promponas,** Department of Biological Sciences, University of Cyprus, Cyprus *AlphaFold models can inform the prediction of functional LIR-motifs*
14:50- 15:00	**Michal Linial,** The Hebrew University of Jerusalem, Israel *Inferring MicroRNA Regulation from Inspecting the Proteome*
15:00- 15:10	**Henri Chung,** Iowa State University, United States *Network Based Analysis of Microbial Function Reveals Putative Bacterial Pathways*
15:10- 15:20	**Akshay Agarwal,** IBM Research, United States *Discovering Proteins: Function to Name*
15:20- 15:30	**Zeeshan Ahmed,** Institute for Health, Health Care Policy and Aging Research *Integrated gene expression and variant analysis to investigate CVD genes with associated phenotypes among high-risk Heart Failure patients.*
16:00- 16:10	**Ryo Ishibashi, Chuo University, Japan** *Tensor decomposition and principal component analysis based unsupervised feature extraction with optimized standard deviation applied to gene expression, DNA methylation and histone modification*
16:10- 16:20	**Tijana Milenkovic,** University of Notre Dame, United States *Protein functional prediction via multi-scale data integration*
16:20- 16:30	**Edoardo Sarti,** Inria Université Côte d'Azur, France *Paralog function annotation with ProfileView*
16:30- 16:40	**Predrag Radivojac,** Northeastern University, United States *The field of protein function prediction as viewed by different domain scientists*
16:40- 16:50	**Dan Ofer,** The Hebrew University of Jerusalem, Israel *ProteinBERT: a universal deep-learning model of protein sequence and function*
16:50- 17:00	**Joseph Szymborski,** McGill University, Canada *RAPPPID: Deep, Regularised Protein-Protein Interaction Prediction that Generalises to Unseen Proteins*
17:00- 17:10	**Constance Jeffery,** University of Illinois at Chicago, United States *The Expanding World of Metabolic Enzymes Moonlighting as RNA Binding Proteins*
17:10- 17:20	**Chan-Seok Jeong,** Korea Institute of Science and Technology Information, South Korea *Anti-CRISPR prediction by using Transformer Model*
17:20- 17:40	**Ronghui You,** Fudan University, China *Proceedings Presentation: DeepMHCII: A Novel Binding Core-Aware Deep Interaction Model for Accurate MHC II-peptide Binding Affinity Prediction*
17:40- 17:50	**Shur-Jen Wang,** Medical College of Wisconsin, United States *Ontological analysis of coronavirus associated human genes at the COVID-19 Disease Portal*

GENERAL COMP BIO

COSI TRACK PRESENTATIONS

MONDAY, JULY 11TH

10:40-11:00	**Yijia Li,** University of Minnesota, United States *CosTaL: An accurate and scalable graph-based clustering algorithm for high-dimensional single-cell data analysis*
11:00-11:20	**Sungwoo Bae,** Institute of Radiation Medicine, Medical Research Center, Seoul National University, South Korea *spSeudoMap: cell type mapping in spatial transcriptomics using unmatched single-cell RNA-seq data*
11:20-11:40	**Lin Zhang,** University Health Network, Canada *One Cell At A Time: a unified framework to integrate and analyze single-cell RNA-seq data*
11:40-12:00	**Adriano Martinelli,** ETH Zurich, Switzerland *ATHENA: Analysis of Tumor Heterogeneity from Spatial Omics Measurements*
12:00-12:20	**Jake Crawford,** University of Pennsylvania, United States *Widespread redundancy in -omics profiles of cancer mutation states*
14:30-14:50	**Matthew Smith,** Oden Institute, The University of Texas at Austin, United States *Amino acid sequence assignment from single molecule peptide sequencing data using a two-stage classifier*
14:50-15:10	Juexin Wang**, University of Missouri, United States** *Neural relational inference to learn long-range allosteric interactions in proteins from molecular dynamics simulations*
15:10-15:30	**Shaked Bergman,** Tel Aviv University, Israel *The effect of genomic 3D structure on CRISPR cleavage efficiency*
16:00-16:20	**Naoki Osato,** Waseda University, Japan *Systematic discovery of regulatory motifs associated with the insulator function of human enhancer-promoter interactions*
16:20-16:40	**Jing Li,** Case Western Reserve University, United States *High resolution chromatin loop mapping from sparse Hi-C data based on deep learning*

HITSeq COSI

TRACK PRESENTATIONS

HiTSeq: High Throughput Sequencing
Algorithms & Applications

HiTSeq

TUESDAY, JULY 12TH

10:30-11:30	**Yuzhen Ye** *Utilizing multi-omics, networks and bacterial immune systems to understand microbiome*
11:30-11:50	**Hector Roux de bezieux,** Pendulum Therapeutics, United States *Proceedings Presentation: CALDERA: Finding all significant de Bruijn subgraphs for bacterial GWAS*
11:50-12:10	**Xianglin Zhang,** Tsinghua University, China *Proceedings Presentation: MeConcord: a new metric to quantitatively characterize DNA methylation heterogeneity across reads and CpG sites*
12:10-12:30	**Jens-Uwe Ulrich,** Hasso Plattner Institute, Germany *Proceedings Presentation: ReadBouncer: Precise and Scalable Adaptive Sampling for Nanopore Sequencing*
14:30-14:50	**Serghei Mangul,** University of Southern California, United States *Rigorous benchmarking of T cell receptor repertoire profiling methods for cancer RNA sequencing*
14:50-15:10	**Shulan Tian, Division of Computational Biology, Department of Quantitative Health Sciences, Mayo Clinic, United States** *The statistics of \kmers from a sequence undergoing a simple mutation process without spurious matches*
15:10-15:30	**Lixing Yang,** University of Chicago, United States *Mutational signatures of complex genomic rearrangements in human cancer*
16:00-17:00	**Cole Trapnell** *Deep molecular- and cellular-phenotyping of zebrafish development at whole organism scale*
17:00-17:20	**Xiaoyan Guo,** Carnegie Mellon University, United States *Proceedings Presentation: Semi-deconvolution of bulk and single-cell RNA-seq data with application to metastatic progression in breast cancer*
17:20-17:40	**Yu Chen,** University of Alabama at Birmingham, United States *Gene fusion detection and characterization in long-read cancer transcriptomes with FusionSeeker*
17:40-18:00	**Qimin Zhang,** The Pennsylvania State University, United States *Accurate assembly of multi-end RNA-seq data with Scallop2*

HITSeq COSI

TRACK PRESENTATIONS

HiTSeq: High Throughput Sequencing Algorithms & Applications

HiTSeq

WEDNESDAY, JULY 13TH

10:30-11:30 **Benedict Paten**

TBD

11:30-11:50 **Yutong Qiu,** Carnegie Mellon University, United State

Proceedings Presentation: The Effect of Genome Graph Expressiveness on the Discrepancy Between Genome Graph Distance and String Set Distance

11:50-12:10 **Armaghan Sarvar,** Genome Sciences Centre, BC Cancer Agency, Canada

Stash: A data structure based on stochastic tile hashing

12:10-12:30 **Damla Senol Cali,** Bionano Genomics, United States

GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis

14:30-14:50 **Paul Medvedev,** The Pennsylvania State University, United States

Strobemers: an alternative to k-mers for sequence comparison

14:50-15:10 **Giulio Ermanno Pibiri,** ISTI-CNR, Italy

Proceedings Presentation: Sparse and Skew Hashing of K-Mers

15:10-15:30 **Jarno Alanko,** University of Helsinki, Finland

Matchtigs: minimum plain text representation of kmer sets

16:00-16:20 **Askar Gafurov,** Comenius University in Bratislava, Slovakia

Proceedings Presentation: Markov chains improve the significance computation of overlapping genome annotations

16:20-16:40 **Johnathan Wong,** BC Cancer, Genome Sciences Centre, Canada

GoldRush-Path: A de novo assembler for long reads with linear time complexity

16:40-17:00 **Kendell Clement,** Massachusetts General Hospital / Harvard Medical School, United States

Quantification of complex genome editing events including large insertions and translocations using CRISPRlungo

17:00-17:20 **Tianxi Ji,** Case Western Reserve Univeristy, United States

Proceedings Presentation: Robust Fingerprinting of Genomic Databases

17:20-17:40 **Rachael Aubin,** University of Pennsylvania, United States

ConDecon: a clustering-independent method for estimating single-cell abundance in bulk tissues using reference single-cell RNA-seq data

17:40-18:00 **Valérie Marot-Lassauzaie,** Berlin Institute for Medical Systems Biology, Max Delbrück Center in the Helmholtz Association, Berlin, Germany, Germany

κ-velo improves single-cell RNA-velocity estimation

iRNA COSI

TRACK PRESENTATIONS

MONDAY, JULY 11TH

iRNA:
Integrative
RNA Biology

IRB
Integrative RNA Biology
group

10:30-10:40	**Yoseph Barash** ***Keynote Presentation: Introduction to iRNA COSI***
10:40-11:20	**KinFai Au** *Keynote Presentation: How to model and investigate the information of long reads for gene isoform identification and quantification*
11:20-11:40	**Manolis Maragkakis,** National Institute on Aging, United States *Full-length direct RNA sequencing identifies differential RNA length upon cellular stress*
11:40-12:00	**Fairlie Reese,** University of California, Irvine, United States *Assessing the diversity of transcription from the ENCODE4 long-read RNA-seq dataset*
12:00-12:20	*Poster flash talks*
14:30-14:50	**Alexandra Sneddon,** Australian National University, EMBL Australia, Australia *RISER: Real-time in-silico enrichment of RNA species from Nanopore signals*
14:50-15:00	**Matthias Lienhard,** Max Planck Institute for molecular genetics, Germany *Long-read transcriptome sequencing analysis with IsoTools*
15:00-15:10	**Andre Sim,** Genome Institute Singapore, Singapore *Context-Specific Long-Read Transcriptomics with Bambu*
15:10-15:30	**Kevin Yang,** University of Pennsylvania, United States *LSV-Seq: A Novel Targeted Sequencing Method to Detect and Quantify Alternative Splicing Across Human Tissues*
16:00-16:20	**Anoushka Joglekar,** Weill Cornell Medicine, United States *A cell-type centric view of isoform expression reveals combination patterns of transcript elements across spatiotemporal axes of the brain*
16:20-16:30	**Catherine Zhou,** Lynbrook High School, United States *Using machine learning methods to explore significant alternative splicing events in murine melanoma with single cell RNA-seq data*
16:30-16:50	**Quentin Garrido,** Université Gustave Eiffel, ESIEE Paris, LIGM, France *Proceedings Presentation: Visualizing hierarchies in scRNA-seq data using a density tree-biased autoencoder*
16:50-17:10	**Kritika Karri,** Boston University, United States *Roles of mouse liver lncRNAs in non-alcoholic steatohepatitis (NASH) and liver fibrosis identified by single-cell transcriptomics-based gene co-expression regulatory network analysis*
17:10-17:30	**Shuze Wang,** University of Michigan, United States *Opposing gradients of retinoic acid and sonic hedgehog specify tonotopic identity in the murine cochlea*
17:30-17:50	**Faizy Ahsan,** McGill University, Canada *Proceedings Presentation: Visualizing hierarchies in scRNA-seq data using a density tree-biased autoencoder*
17:50-18:00	*Poster flash talks*

iRNA COSI

TRACK PRESENTATIONS

iRNA: Integrative RNA Biology

Integrative RNA Biology group

TUESDAY, JULY 12TH

10:30-11:10	**Liana Lareau** ***Keynote Presentation: Disentangling splicing regulation in single cells***
11:10-11:30	**Tamir Tuller,** Tel Aviv University, Israel *Modeling the ribosomal small subunit dynamic in Saccharomyces cerevisiae based on TCP-seq data*
11:30-11:50	**Étienne Fafard-Couture,** Université de Sherbrooke, Canada *A machine learning-based workflow to predict snoRNA abundance status across species*
11:50-12:10	**Joshua Fry,** University of Minnesota, United States *A pan-cancer transcriptome analysis of 3'UTR exitron splicing*
12:10-12:30	**Matthew Gazzara,** University of Pennsylvania Perelman School of Medicine, United States *Integrative analysis of hundreds of RNA binding proteins suggests known and novel regulators of 3'UTR diversity*
14:30-14:50	**Giulia Corsi,** University of Copenhagen, Denmark *CRISPRon: Enhanced CRISPR/Cas9 gRNA design by deep neural networks, data aggregation and interactive user interface*
14:50-15:10	**Shai Elkayam,** Ben-Gurion University, Israel *Proceedings Presentation: DeepCRISTL: Deep transfer learning to predictCRISPR/Cas9 functional and endogenous on-targetediting efficiency*
15:10-15:30	**Kathryn Monopoli,** University of Massachusetts Medical School | RNA Therapeutics Institute, United States *Trichotomous classification on small, limited datasets enables predictive model development for therapeutic small interfering RNA*
16:00-16:20	**Huaming Sun,** Worcester Polytechnic Institute, United States *Using machine learning to understand the determinants of mRNA stability in mycobacteria*
16:20-16:40	**Robert Ietswaart,** Department of Genetics, Blavatnik Institute, Harvard Medical School, Boston, United States *The kinetics of RNA flow across subcellular compartments*
16:40-17:20	**Chase Weidmann** *Keynote Presentation: Mapping protein interaction networks on RNA with live cell chemical probing*
17:20-17:40	**Yeon Choi,** Institute for Basic Science, Seoul National University, South Korea *The chronology of mRNP remodeling*
17:40-17:50	**Michelle Scott** *Closing remarks*

JPI COSI

TRACK PRESENTATIONS

MONDAY, JULY 11TH

JPI
Junior Principal
Investigators

10:30- 11:10	**Ivana Jelic** ***Keynote Presentation: Chan Zuckerberg Initiative***
11:10- 11:50	**TBD TBD** *Keynote Presentation: TBD*
11:50- 12:30	**Panel discussion** *Panel: How to build strong proposals for computational biology projects*

MICROBIOME COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

10:30-11:15	**Catherine Lozupone** *Keynote Presentation: Methods for integration and hypothesis generation from high dimensional biomedical microbiome datasets*
11:15-11:30	**Siddharth Uppal**, Division of Pharmaceutical Sciences, School of Pharmacy, University of Wisconsin—Madison, USA, United States *Lasonolide A is synthesized by a trans-AT PKS pathway present in an uncultured Verrucomicrobiota*
11:30-11:45	**Hao Zhou,** Cornell University, United States *Host-microbiome protein-protein interactions capture disease-relevant pathways*
11:45-12:00	**Wei-Hao Lee, Systems, Synthetic,** and Physical Biology Program, Rice University, United States *Pan-cancer characterization of microbiome signatures*
12:00-12:15	**Mohammed Muzamil Khan,** Boston University, United States *Characterization and integration of transcriptional and microbial profiles of oral lesions and cancer*
12:15-12:30	**Edwin Moses Appiah,** Department of biochemistry and Biotechnology, KNUST, Ghana *The Gastric Microbiome and Gastric Carcinogenesis: Bacteria diversity, Co-occurrence patterns and Predictive Models*
14:30-15:00	**Jarno Alanko,** University of Helsinki, Finland *Proceedings Presentation: Syotti: Scalable Bait Design for DNA Enrichment*
15:00-15:15	**Marco Oliva,** University of Florida, United States *Target-enriched long-read sequencing (TELSeq) contextualizes antimicrobial resistance risk in metagenomes.*
15:15-15:30	**Tu Luan,** University of Maryland, College Park, United States *SCRAPT: An Iterative Algorithm for Clustering Large 16S rRNA Data Sets*
16:00-16:15	**Deborah Chasman,** University of Wisconsin-Madison, United States *Breastfeeding and Farming Lifestyle Promotes Predominant Bifidobacterium in Infants*
16:15-16:30	**Aswathy K. Raghu,** Northwestern University, United States *A constraint-based method to identify function-specific minimal microbiomes from large microbial communities*
16:30-16:45	**Mary Maranga,** Małopolska Centre of Biotechnology, Jagiellonian University, Poland *Comprehensive functional annotation of metagenomes using a deep learning-based method (DeepFRI)*
16:45-17:00	**Gerald Friedland,** Department of EECS, University of California Berkeley, United States *Information-Measure Predicts the Generalizability of Machine Learning Models in Metagenomics Datasets*
17:00-17:15	**Samuel Ozminkowski,** University of Wisconsin-Madison, United States *Identifying microbial drivers in biological phenotypes with a Bayesian Network Regression model*
17:15-17:30	**Lance Lansing,** Agriculture and Agri-Food Canada, Canada *Resistome characterization of the honey bee gut microbiome via shotgun metagenomic sequencing*
17:30-17:45	**Ali Zomorrodi,** Massachusetts General Hospital - Harvard Medical School, United States *Metagenome-scale species-resolved functional profiling of the gut microbiota in Celiac Disease*
17:45-18:00	**Lan Zhao,** Stanford University, United States *A rat microbial BodyMap across 11 tissue types and 4 developmental stages*

MICROBIOME COSI

TRACK PRESENTATIONS

THURSDAY, JULY 14TH

10:15-11:00	**Chirag Jain** ***Keynote Presentation: Revisiting string graph model for long-read assembly of genomes and metagenomes***
11:00-11:15	**Zhong Wang,** DOE Joint Genome Institute, EGSB Lawrence Berkeley National Lab, UC Merced, United States *Persistent Memory as an Effective Alternative to Random Access Memory in Metagenome Assembly*
11:15-11:30	**Pau Piera Lindez,** University of Copenhagen, Novo Nordisk Foundation Center for Protein Research, Denmark *Adversarial and variational autoencoders improve metagenomics binning*
11:30-11:45	**Taylor Reiter,** University of Colorado Anschutz Medical Campus, United States ***Charcoal: filtering contamination in metagenome-assembled genome bins and other genomes***
11:45-12:00	**Ziye Wang,** Fudan University, China *MetaBinner: a high-performance and stand-alone ensemble binning method to recover individual genomes from complex microbial communities*
13:15-13:45	**Shaopeng Liu,** Pennsylvania State University, United States *Proceedings Presentation: CMash: fast, multi-resolution estimation of k-mer-based Jaccard and containment indices*
13:45-14:00	**N. Tessa Pierce-Ward,** University of California, Davis, United States *Average Nucleotide Identity estimation from FracMinHash sketches*
14:00-14:15	**Serghei Mangul,** University of California, Los Angeles, United States *TAMPA: interpretable analysis and visualization of metagenomics-based taxon abundance profiles*
14:15-14:30	**Yanbin Yin,** University of Nebraska - Lincoln, United States *Critical assessment of pan-genomics of metagenome-assembled genomes*
14:30-14:45	**Paweł P. Łabaj,** Małopolska Centre of Biotechnology of Jagiellonian University, Poland *Sample origin prediction in forensics with use of targeted metagenomic sequencing*
14:45-15:00	**Dinesh Kumar Kuppa Baskaran,** Indian Institute of Technology Madras, India *A protocol for studying metabolic interactions in a microbial community using graph-based approaches*

MLCSB: Machine Learning in Computational and Systems Biology

MLCSB COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

10:30-11:30	**Niko Beerenwinkel,** ETH Zurich, Switzerland ***Keynote Presentation: TBD***
11:30-11:50	**Manfred Claassen,** University of Tübingen, Germany *Proceedings Presentation: psupertime: supervised pseudotime analysis for time-series single cell RNA-seq data*
11:50-12:00	**Rossin Erbe,** Johns Hopkins School of Medicine, United States *Transcriptomic forecasting over short time periods using neural ODEs*
12:00-12:10	**Gaetan De Waele,** Ghent University, Belgium *CpG Transformer for imputation of single-cell methylomes*
12:10-12:20	**Florin Cornelius Walter,** German Cancer Research Center (DKFZ), European Molecular Biology Laboratory (EMBL), Germany *FISHFactor: A Probabilistic Factor Model for Spatial Transcriptomics Data with Subcellular Resolution*
12:20-12:30	**Evan Greene,** Ozette Technologies, United States *Unbiased discovery and annotation of cellular phenotypes in high-dimensional single-cell proteomic datasets*
14:30-15:30	**Casey Greene** **Florian Markowetz** **Gabriella Rusticci** *Panel: Reproducibility and transparency in ML: Training the next generation*
16:00-17:00	**Anne Carpenter** ***Keynote Presentation: Image-based profiling for drug discovery: Cell Painting***
17:00-17:20	**Philip Fradkin,** Univeristy of Toronto, Vector Institute, Canada *Proceedings Presentation: A Graph Neural Network Approach for Molecule Carcinogenicity Prediction*
17:20-17:30	**Yue Qin,** University of California San Diego, United States *Towards an in silico cell*
17:30-17:40	**Yuju Lee, University of Toronto, Canada** *Segmentation error aware probabilistic clustering for highly multiplexed imaging reveals densely packed tissue dynamics*
17:40-17:50	**Brian Clarke,** German Cancer Research Center (DKFZ), Germany *Joint modeling of rare variant genetic effects using deep learning and data-driven burden scores*
17:50-18:00	**Tareian Cazares,** University of Cincinnati, United States *maxATAC: Predicting Transcription Factor Binding at Disease Risk Loci from ATAC-seq and DNA Sequence with Convolutional Neural Networks*

MLCSB COSI

TRACK PRESENTATIONS

MLCSB: Machine Learning in Computational and Systems Biology

THURSDAY, JULY 14TH

10:15-11:15 **Søren Brunak,** University of Copenhagen, Denmark

Keynote Presentation: Machine learning for the analysis of multimorbidities, disease and prescription trajectories

11:15-11:35 **Lucia Saldana Barco,** Colorado School of Mines, United States

Proceedings Presentation: Scaling Multi-Instance Support Vector Machine to Breast Cancer Detection on the BreaKHis Dataset

11:35-11:45 **Maarten Larmuseau,** Ghent University, Belgium

The multifocal transcriptomic landscape of locally advanced prostate cancer

11:45-11:55 **Ziynet Nesibe Kesimoglu,** University of North Texas, United States

SUPREME: A cancer subtype prediction methodology integrating multiomics data using Graph Convolutional Neural Network

11:55-12:05 **Hao Xu,** Queen's University, Canada

Exploring the Mechanisms of Polypharmacy Side Effects via Two-stage Graph Neural Networks

12:05-12:15 **You Wu,** The City University of New York, United States

A Context-aware Deconfounding Autoencoder for Robust Prediction of Personalized in vivo Drug Response From Cell Line Compound Screening

13:15-14:15 **Su-In Lee**

TBD

14:15-14:35 **Stefan Schrod,** University Medical Center Göttingen, Germany

Proceedings Presentation: BITES: Balanced Individual Treatment Effect for Survival data

14:35-14:55 **Duc Anh Nguyen,** Kyoto University, Japan

Proceedings Presentation: SPARSE: a sparse hypergraph neural network for learning multiple types of latent combinations to accurately predict drug-drug interactions

14:55-15:05 **Mohamed Reda El Khili,** McGill University, Canada

Deep-Multitask learning framework to predict synergistic drug combinations

15:05-15:15 **Hannes Stärk,** Massachusetts Institute of Technology, Germany

EquiBind: Geometric Deep Learning for Drug Binding Structure Prediction

15:45-16:05 **An-Phi Nguyen,** IBM Research Europe, ETH Zurich, Switzerland

Proceedings Presentation: DECODE: a computational pipeline to discover T-cell receptor binding rules

16:05-16:25 **Mehmet Gönen,** Koç University, Turkey

Proceedings Presentation: Fast and interpretable genomic data analysis using multiple approximate kernel learning

16:25-16:35 **Jacob Schreiber,** Stanford University, United States

Accelerating in-silico saturation mutagenesis using compressed sensing

16:35-16:45 **Alex Lu,** Microsoft Research, United States

Discovering interpretable features of the intrinsically disordered dark proteome by using evolution for contrastive learning

NETBIO COSI

TRACK PRESENTATIONS

NetBio:
Network Biology

TUESDAY, JULY 12TH

10:30-11:10	**Teresa Przytycka** ***Keynote Presentation: Network-based approaches to study mutational processes in cancer***
11:10-11:30	**Zongliang Yue,** Informatics Institute, School of Medicine, University of Alabama at Birmingham, United States *Proceedings Presentation: DEMA: a distance-bounded energy-field mini-mization algorithm to model and layout bio-molecular networks with quantitative features*
11:30-11:50	**Lechuan Li,** Rice University, United States *Joint embedding of biological networks for cross-species functional alignment*
11:50-12:10	**Renming Liu,** Michigan State University, United States *Accurately identifying disease genes and relevant contexts using context-specific network embeddings*
12:10-12:30	**Tijana Milenkovic,** University of Notre Dame, United States *Multi-layer networks improve protein structural classification*
14:30-14:50	**Spencer Halberg-Spencer,** University of Wisconsin-Madison, Wisconsin Institute for Discovery, United States *Network-based data integration and visualization provides a global understanding of regulatory mechanisms in Aspergillus fumigatus*
14:50-15:10	**Kevin Drew,** University of Illinois at Chicago, United States *hu.MAP 2.0: integration of over 15,000 proteomic experiments builds a global compendium of human multiprotein assemblies*
15:10-15:30	**Yu Xia,** McGill University, Canada *Are Transient Protein-Protein Interactions More Dispensable?*
16:00-16:20	**Spencer Krieger,** University of Arizona, United States *Proceedings Presentation: Computing optimal factories in metabolic networks with negative regulation*
16:20-16:40	**Peter Karp,** SRI International, United States *The BioCyc Metabolic Network Explorer*
16:40-17:00	**Christian Arnold,** EMBL, Germany *GRaNIE and GRaNPA: Inference and evaluation of enhancer-mediated gene regulatory networks applied to study macrophages*
17:00-17:20	**Mikaela Koutrouli,** Novo Nordisk Foundation Center of Protein Research, Denmark *FAVA: High-quality functional association networks inferred from massive scRNA-seq and proteomics data*
17:20-18:00	**Chad Myers** ***Keynote Presentation: Mapping and analysis of a global reference genetic interaction network for human cells***

REGSYS COSI

TRACK PRESENTATIONS

WEDNESDAY, JULY 13TH

RegSys:
Regulatory &
Systems
Genomics

RegSys

10:30-11:10	**Julio Saez-Rodriguez,** Heidelberg University, Germany ***Keynote Presentation: Integrating prior knowledge and single-cell multi-omics to understand cellular regulation***
11:10-11:30	**Sara Mohammad Taheri,** Northeastern Univerusity, United States *Proceedings Presentation: Do-calculus enables estimation of causal effects in partially observed biomolecular pathways*
11:30-11:50	**Kevin Moyung,** Duke University, United States *Chromatin dynamics from genetic perturbations are associated with transcription and reveal a larger gene regulatory network*
11:50-12:10	**Lingfei Wang,** Massachusetts General Hospital, Harvard Medical School, United States *Dictys: dynamic gene regulatory network inference from single-cell multi-omics*
12:10-12:30	**Marcel Schulz,** Uniklinikum and Goethe University Frankfurt, Germany *GAZE: A single-cell gene regulatory inference framework from transcriptomics and epigenomics data*
14:30-15:10	**Lucia Peixoto** *Keynote Presentation: Understanding the interaction between sleep and chromatin regulation in Autism*
15:10-15:30	**Zidong Zhang,** Princeton University, United States *CREMA: Extracting Gene Regulation Mechanisms from Single Cell Multi-omics Assays*
16:00-16:40	**Rahul Satija** *Keynote Presentation: Integrated analysis of single cell data across technologies and modalities*
16:40-17:00	**Mingbo Cheng,** RWTH Aachen, Germany *Proceedings Presentation: MOJITOO: a fast and universal method for integration of multimodal single cell data*
17:00-17:20	**Pia Rautenstrauch,** Humboldt-Universität zu Berlin & Max-Delbrück-Center for Molecular Medicine in the Helmholtz Association, Germany *Liam tackles complex multimodal single-cell data integration challenges*
17:20-17:40	**Gerard Bouland,** Delft University of Technology, Netherlands *The rise of sparser single-cell RNAseq datasets: consequences and opportunities*
17:40-18:00	**Avi Srivastava,** New York Genome Center, United States *Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro and scChromHMM*

REGSYS COSI

TRACK PRESENTATIONS

THURSDAY, JULY 14TH

RegSys:
Regulatory &
Systems
Genomics

10:15-10:55	**Sushmita Roy** ***Keynote Presentation: Deciphering gene regulatory networks of cell fate***
10:55-11:15	**Ziqi Zhang,** Georgia Institute of Technology, United States *scMoMaT: mosaic integration of single cell multi-omics data using matrix trifactorization*
11:15-11:35	**Shamim Mollah,** Washington University in St. Louis School of Medicine, United States *HOCMO: A higher-order correlation model to deconvolute epigenetic microenvironment in breast cancer*
11:35-11:55	**Yaron Orenstein,** Ben-Gurion University, Israel *Computational modeling of mRNA degradation dynamics using deep neural networks*
11:55-12:15	**Trung Tran,** Duke University, United States *A Vision Transformer-based approach for identifying key markers in chromatin state associated with transcription*
13:15-13:55	**Mayra Furlan-Magaril,** Institute of Cellular Physiology, UNAM, Mexico City *Keynote Presentation: Chromatin spatial reorganization during erythroid differentiation*
13:55-14:15	**Da-Inn Lee,** University of Wisconsin-Madison, United States *Detecting higher-order structural changes in 3D genome organization with multi-task matrix factorization*
14:15-14:35	**Sourya Bhattacharyya,** La Jolla Institute for Immunology, United States *Identifying differential chromatin contacts from HiChIP data*
14:35-14:55	**Siqi Shen,** University of Wisconsin - Madison, United States *scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data*
14:55-15:15	**Anusri Pampari,** Stanford University, United States *Base-resolution deep learning models of chromatin accessibility reveal combinatorial sequence motif syntax and regulatory variation*
15:45-16:25	**Zhiping Weng** ***Keynote Presentation: Landscapes of Human cis-regulatory Elements and Transcription Factor Binding Sites Evolutionarily Constrained in the Mammalian Lineage***
16:25-16:45	**Meghana Kshirsagar, Microsoft, United States** *Dirichlet variational autoencoders for de novo motif discovery from accessible chromatin*

SYSMOD COSI

TRACK PRESENTATIONS

MONDAY, JULY 11TH

SysMod:
Computational
Modeling of
Biological Systems

SYSMOD

10:30-10:40	**Andreas Dräger** *Introduction to SysMod 2022*
10:40-11:20	**Reinhard Laubenbacher** ***Keynote Presentation: Multiscale computational models for lung immunity***
11:20-11:40	**Patrice Ravel,** Institut de Recherche en Cancérologie de Montpellier, France *Regressive Modular Response Analysis*
11:40-12:00	**Peter Karp,** SRI International, United States *Pathway Tools Visualization of Organism-Scale Metabolic Networks*
12:00-12:20	**Nathan Lewis,** University of California, San Diego, United States *Driving discovery in Human Milk Oligosaccharide biosynthesis through constraint-based modeling and multi-omics integration*
12:20-12:25	**Lavanya Raajaraam,** Indian Institute of Technology, Madras (IITM), India *Co-FSEOF: a computational framework to study the co-production of metabolites*
12:25-12:30	**Arda Halu,** Brigham and Women's Hospital, Harvard Medical School, United States *MuXTalk: Detecting and dissecting signaling crosstalk via multilayer networks*
14:30-14:50	**Nathan Manes,** National Institutes of Health, United States *Targeted Proteomics-Driven Computational Modeling of the Mouse Macrophage Toll-like Receptor Signaling Pathway*
14:50-15:10	**Aurelien Pelisiser,** IBM Research, Switzerland *Cell-type specific gene regulation in Rheumatoid Arthritis*
15:10-15:30	**Eric Bell,** University of Michigan, United States *Protein-protein interaction network analysis through consensus prediction and virtual reality visualization*
15:40-16:00	**Kang Jin, Cincinnati Children's Hospital Medical Center, United States** *CellDrift: Inferring Perturbation Responses in Temporally-Sampled Single Cell Data*
16:00-16:20	**Qian Qin,** Harvard Medical school and Massachusetts General Hospital, United States *Pyro-Velocity: Probabilistic and scalable RNA velocity inference from single-cell data*
16:20-16:40	**Shaimaa Bakr,** Stanford University, United States *Identifying key multifunctional components shared by critical cancer and normal liver pathways via sparseGMM*
16:40-17:00	**Joseph Wayman,** Cincinnati Children's Hospital, United States *An atlas of gene regulatory networks for IL 10-producing T memory cells in youth and old age*
17:00-17:40	**Surprise Surprise** ***Keynote talk 2***
17:40-18:00	**Puniya Puniya** *Closing Remarks and Poster Awards SysMod 2022*

Text Mining COSI

TRACK PRESENTATIONS

MONDAY, JULY 11TH

Text Mining for Healthcare and Biology

Mining

10:30-10:40	**COSI Chairs**	*Text Mining COSI Welcome*
10:40-11:30	**Andrey Rzhetsky**	*Keynote Presentation: Exploring semantic and genetic disease spaces*
11:30-11:50	**Katerina Nastou,** Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark	*Improving dictionary-based named entity recognition with deep learning*
11:50-12:10	**Witold Wydmański,** Małopolska Centre of Biotechnology, Jagiellonian University, Kraków, Poland, Poland	*Cosine similarity preserving compression of dense embedding vectors*
12:10-12:30	**Arman Edalatmand,** McMaster University, Canada	*A deep-learning approach for contextualizing antimicrobial resistance genes*
14:30-15:20	**Hongfang Liu**	***Keynote Presentation: A Context-aware Artificial Intelligence Framework for Biomedical Natural Language Processing***
15:20-15:30	**Posters authors**	*Poster Lightning Talks*
16:00-16:20	**Ling Luo,** NCBI, NLM, NIH, United States	*BioRED: A Comprehensive Biomedical Relation Extraction Dataset*
16:20-16:40	**Hosein Azarbonyad,** Elsevier, Netherlands	*Annotating and Indexing Scientific Articles with Rare Diseases*
16:40-17:00	**Arjun Krishnan,** Michigan State University, United States	*A general NLP approach to automatically interpret any gene list based on the literature*
17:00-18:00	**Katerina Nastou** **Robert Leaman** **etc etc**	*Panel: Disease analysis with NLP*

TRANSMED COSI

TRACK PRESENTATIONS

TUESDAY, JULY 12TH

TransMed:
Translational
Medicine
Informatics &
Applications

10:30-11:10	**Anthony Brookes,** University of Leicester, UK ***Keynote Presentation: "Data Science": A trendy name for conventional research using data, or a truly revolutionary new...***
11:10-11:30	**Bing-Xue Du, School of Life Sciences, Northwestern Polytechnical University, China** ***Proceedings Presentation: MLGL-MP: A Multi-Label Graph Learning Framework Enhanced by Pathway Interdependence for Metabolic Pathway Prediction***
11:30-11:40	**Heba Sailem,** University of Oxford, United Kingdom *Decoding tumour microenvironment heterogeneity using graph convolutional networks and multiplexed imaging*
11:40-11:50	**Yue Wang,** UNIVERSITY OF PITTSBURGH, United States *Perturbed Transcriptomic Analyses Identify Chemo-immunotherapy Synergisms to Shift Anti-PD1 Resistance in Cancer*
11:50-12:00	**Seffi Cohen,** Ben-Gurion University of the Negev, Israel *ICU Survival Prediction Incorporating Test-Time Augmentation to Improve the Accuracy of Ensemble-Based Models*
12:00-12:10	**David Gordon,** Institute for Genomic Medicine at Nationwide Children's Hospital, United States *Use of machine learning to classify high-risk variants of uncertain significance in lamin A/C cardiac disease*
12:10-12:20	**Meghana Pagadala,** UCSD, United States *PRState: Incorporating Genetic Ancestry in Prostate Cancer Risk Scores for African American Men*
12:20-12:30	**Madison Darmofal,** Memorial Sloan Kettering, Weill Cornell Graduate School, United States *Genome-Derived Diagnosis: Deep Learning Model for Tumor Type Prediction using MSK-IMPACT data*
14:30-14:50	**Satoko Namba,** Kyushu Institute of Technology, Japan *Proceedings Presentation: From drug repositioning to target repositioning: prediction of therapeutic targets using genetically perturbed transcriptomic signatures*
14:50-15:10	**Siyu Wang,** Tianjin University of Technology, China *Proceedings Presentation: Synthetic-to-Real: Instance Segmentation of Clinical Cluster Cells with Unlabelled Synthetic Training*
15:10-15:20	**Daniele Bizzarri,** Leiden University Medical Center, Netherlands *1H-NMR metabolomics-based models to impute common clinical variables and endpoints in epidemiological studies*
15:20-15:30	**Jishnu Das,** University of Pittsburgh, United States *A network-based approach to identify expression modules underlying rejection in pediatric liver transplantation*
16:00-16:40	**Elana Fertig,** Johns Hopkins University, USA ***Keynote Presentation: Learning cellular interactions from spatial transcriptomics with SpaceMarkers***
16:40-17:00	**Bowen Fan,** ETH Zurich, Switzerland *Proceedings Presentation: Prediction of Recovery from Multiple Organ Dysfunction Syndrome in Pediatric Sepsis Patients*
17:00-17:20	**Michael Murphy,** Massachusetts Institute of Technology, United States *Proceedings Presentation: Self-supervised learning of cell type specificity from immunohistochemical images*
17:20-17:30	**Michal Linial,** The Hebrew University of Jerusalem, Israel *Predictive Model for Endometriosis with Clinical, Lifestyle and Genetic Information*
17:30-17:40	**Akram Yazdani,** Division of Pharmacotherapy and Experimental Therapeutics, Eshelman School of Pharmacy, University of North Carolina at Chapel Hill, Chapel Hill, NC, United States ***Immune response-related gene regulatory pathways perturbed by targeted therapies in colorectal cancer: CALGB/SWOG 80405***
17:40-17:50	**Mykhaylo Slobodyanyuk,** University of Toronto, Canada *Direction-aware data fusion techniques for multi-omics pathway enrichment analysis and biomarker discovery*
17:50-18:00	**Peter White,** Nationwide Children's Hospital, United States *Solving the Puzzle of Genetic Disease with Bits and Bytes*
18:00-18:05	*Closing*

VarI COSI

TRACK PRESENTATIONS

TUESDAY, JULY 12TH

VarI: Variant Interpretation

10:30-10:40	**Hannah Carter** *Opening Remarks*
10:40-11:20	**Nicole Soranzo** ***Keynote Presentation: High-resolution genomic analyses in human populations***
11:20-11:30	**Leonardo Pellegrina,** University of Padova, Italy *Discovering Significant Evolutionary Trajectories in Cancer Phylogenies*
11:30-11:40	**Xiaolei Zhang,** Imperial College London, United Kingdom *Genetic constraint at single amino acid resolution improves missense variant prioritisation and gene discovery*
11:40-11:50	**Shaolei Teng,** Howard University, United States *Systematic Investigation of Missense Mutations of Coronavirus Spike and Human Receptor Proteins*
11:50-12:30	**David Robertson** ***Keynote Presentation: Evolution of SARS-CoV-2 variants: past, present and future***
14:30-14:40	**John Moult,** University of Maryland, United States *Lessons learned from 10 years of CAGI experiments*
14:40-14:50	**Alessia David,** Imperial College London, United Kingdom *Missense3D-PPI: a structure-based prediction algorithm of the impact of missense variants at protein interfaces*
14:50-15:00	**Kivilcim Ozturk,** UCSD, United States *Predicting functional consequences of mutations using molecular interaction network features*
15:00-15:10	**Emidio Capriotti,** University of Bologna, Italy *Evaluating the relevance of sequence conservation in the prediction of pathogenic missense variants*
15:10-15:30	**Shane Hussey,** Variantyx Inc *Keynote Presentation: Validation of WGS for clinical use down to 50 ng of DNA using tagmentation PCR-Free protocol*
16:00-16:20	**Joanna von Berg,** University Medical Center Utrecht, Netherlands *Proceedings Presentation: PolarMorphism enables discovery of shared genetic variants across multiple traits from GWAS summary statistics*
16:20-17:00	**Nathaniel Sharp** ***Keynote Presentation: Yeast experiments provide insight into the molecular causes and phenotypic consequences of spontaneous mutations***
17:00-17:10	**Vikas Pejaver,** Icahn School of Medicine at Mount Sinai, United States *Evidence-based calibration of computational tools for missense variant pathogenicity classification and ClinGen recommendations for their clinical use*
17:10-17:30	**Michal Linial,** The Hebrew University of Jerusalem, Israel *KHypertension Genetics is Sex-dependent*
17:30-17:40	**Blythe Moreland,** The Institute for Genomic Medicine, Nationwide Children's Hospital, United States *Information theoretic analysis of synonymous codon usage offers context-dependent metric to assess constraint on synonymous variants*
17:40-18:00	**Farica Zhuang,** University of Pennsylvania, United States *Mapping the human RNA G-Quadruplexes and genetic variants that affect them using Transformer based modeling*
18:00-18:05	**Hannah Carter** *Closing Remarks*

TECHNOLOGY TALK

PRESENTATIONS

MONDAY, JULY 11TH

14:30-14:50 **Yue Li,** MemVerge, United States
Big Memory Computing for Genomics

14:50-15:10 **Aaron Watters,** Flatiron Institute, United States
H5Gizmo visualizations of mouse embryos

15:10-15:30 **Nils Gehlenborg,** Gehlenborg Lab, United States
Vitessce: framework for integrative visualization of multi-modal and spatially-resolved single-cell data

16:00-17:00 **Ben Busby,** DNAnexus, United States
How to make bioinformatics tools you've developed easily accessible for Researchers using the UKBioBank Dataset

TECHNOLOGY TALK

PRESENTATIONS

TUESDAY, JULY 12TH

10:30-10:50	**Teodoro Laino,** IBM Research, Switzerland *A Cloud-based AI-driven Autonomous Lab*
10:50-11:10	**Mona Mona,** Google, United States **Michelle Holko,** Google, United States *Google Cloud's RAD Lab for Research*
11:10-11:30	**Jiaji Chen,** Boston University, United States *Vitessce: framework for integrative visualization of multi-modal and spatially-resolved single-cell dataGiotto Suite: An R Spatial Biology Framework for Subcellular and Multimodal Data*
11:30-11:50	**Ryan Looney,** Overleaf, United Kingdom *Overleaf - Collaborative LaTeX Authoring Platform*
11:50-12:10	**Tom Sinden,** F1000, United Kingdom *Holistic approaches to publishing Open Research*
14:30-14:50	**Bajuna Salehe,** University of Reading, United Kingdom *IntFOLD: A Webserver for Predicting 3D Protein Structures and Their Functions*
14:50-15:10	**Michael Sternberg,** Imperial College London, United Kingdom *Phyre2, Missense3D and GWYRE: Protein structure prediction and missense variant analysis*
15:10-15:30	**Nicola Bordin,** University College London, United Kingdom *Expanding CATH with AlphaFold2 data*

iSCB Green Pledge

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___ Power down before leaving home and office
___ Use low carbon travel options when possible
___ Use paperless boarding passes when possible
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___ Pack lightly to reduce fuel consumption
___ Bring a reusable BPA-free beverage container
___ Fill my own reusable travel sized amenity bottles
___ Turn off lights and heating/cooling in the hotel before leaving for the day
___ Take part in the towel and linen reuse program at the hotels; decline room service
___ Reduce shower time when possible
___ Make drought and carbon friendly food choices (vegetarian over beef, tea over coffee)
___ Sort garbage into appropriate bins - recycling, composable, landfill
___ Opt for the electronic version of the on-site programme

Sign the pledge and stop by the ISCB booth to get a ribbon

TECHNOLOGY TALK

PRESENTATIONS

WEDNESDAY, JULY 13TH

10:30-10:50 **Agata Kolomanska,** MDPI AG, Spain

Life - Journal Presentation

WEB 2022: REDUCE YOUR IMPACT - BECOME MORE GREEN!

MONDAY, JULY 11TH

This session is open to anyone with an interest in green computing practices for bioinformatics, especially those who deliver courses / programmes of computational training or are trainees attending such programmes.

14:30-14:35	**Sarah Morgan** *Introduction to WEB session*
14:35-15:05	**Loic Lannelongue** ***Keynote Presentation: Green computing***
15:05-15:30	**Loic Lannelongue** **Michael Inouye** **Alex Bateman** *Panel: Greener practices*
16:00-16:15	**Anna Swan** *Introduction to group discussions*
16:15-16:45	*Group discussion 1: Identifying elements of training that can be modified to reduce impact and actio...*
16:45-17:00	*Reporting back on discussion 1*
17:00-17:30	*Group discussion 2: Advice for individuals attending training on reducing their environmental impact*
17:30-17:45	**Reporting back on discussion 2** *Experiences from the SIB Swiss Institute of Bioinformatics*
17:45-18:00	**Sarah Morgan** *Closing remarks*

ISMB/ECCB2023

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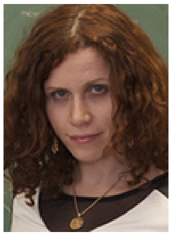

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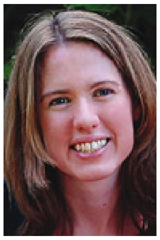

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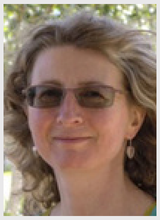

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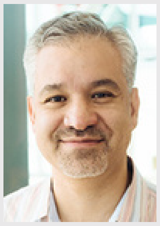

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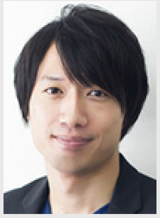

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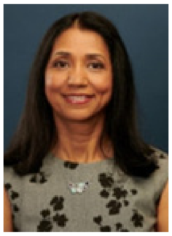

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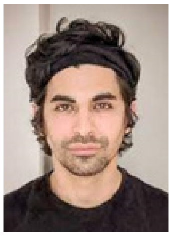

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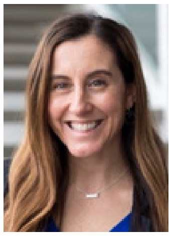

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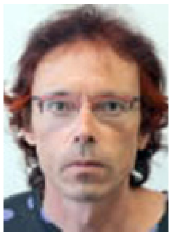

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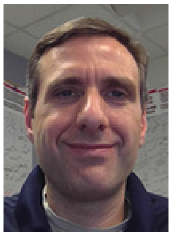

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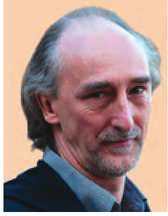

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