ISMB
2024
Montréal
July 12–16

CONFERENCE PROGRAMME

and

ISCB July Newsletter

ISMB 2024 • JULY 12-16
iSCB MONTREAL CANADA

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NEWSLETTER

CONFERENCE PROGRAMME

A Vision for the Future of ISCB

PRESIDENT PREDRAG RADIVOJAC

As we embark on a new chapter in the history of the International Society for Computational Biology (ISCB), “it is imperative that we chart a course that not only meets the evolving needs of our community but also anticipates future challenges and opportunities,” notes President Predrag Radivojac. The Society developed and implemented a long-range strategic plan under the leadership of Christine Orengo. That plan is assessed and evaluated each year by the ISCB Board of Directors to ensure the Society is serving its members at the highest levels and delivering upon its mission.

At the heart of our mission is the need to maintain financial stability while promoting the field of computational biology and supporting our members. The recent global events have highlighted the necessity for creative and flexible approaches. Our flagship event, the ISMB conference, has been a cornerstone of our success, but we must diversify our initiatives to reduce reliance on a single event. Encouraging the development of small and medium-sized local events, which offer organizational flexibility and reduce travel demands, will be key. These events will not only attract students and junior researchers but also foster a more inclusive and connected community. A pivotal aspect of our growth strategy involves the promotion of our new journal, Bioinformatics Advances. This platform will support the expansion of our Society scientifically, geographically, and socially.

Promoting scientific rigor remains a top priority. ISCB must create opportunities to recognize and award rigorous, impactful science, particularly in methodology development, and evaluation, which often have delayed, yet significant, impacts. Supporting education and our Student Council, as well as upholding high ethical standards, are essential components of this commitment. These values must be encouraged at every level.

While ISCB has historically been driven by science in North America and Europe, we must continue to engage with scientists globally. By investing in and partnering with researchers in Asia, South America, Africa, and Australia, we can foster a more unified and impactful scientific community. Science has the power to unite, and ISCB has the opportunity to contribute to this global unification. Along those lines, maintaining a welcoming and inclusive environment is essential, and we must continue to invest here. A diverse field is a stronger field, and promoting diversity is not only the right thing to do but also a strategic advantage.

Computational biology intersects with several other disciplines, including genetics, molecular evolution, structural biology, medical informatics, and machine learning. By engaging with these communities through joint initiatives and co-localized meetings, both locally and internationally, we can enrich our Society and provide greater value to our members. It is crucial that researchers from these overlapping fields see ISCB as their home and benefit from our resources and community.

A Vision for the Future of ISCB, President Predrag Radivojac

As we move forward, let us embrace the challenges and opportunities with strategic thinking, vision, and dedication. Together, we can ensure that ISCB remains at the forefront of computational biology, empowering our members and advancing our field for the betterment of society.

HOW YOU CAN SUPPORT ISCB

Donate Now!

ANNA TRAMONTANO FUND

The goal of the Anna Tramontano Fellowship Fund is to help reduce the financial burden to the students who are offered internships by providing travel support. We hope that by providing financial support and 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 travel 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 provides an influential voice on government and scientific policies that are important to our members and that 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.

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

ISMB AWARD WINNERS

As part of the ISMB 2024 conference in Montréal, the International Society for Computational Biology will be presenting its four annual awards to very deserving recipients! Each awardee has a full-length article that can be found in the ISMB 2024 Proceedings Supplement in *Bioinformatics*, but you don't have to wait; you can read a short summary of each article below!

2024 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD: DR. TANDY WARNOW

ISCB is proud to present the 2024 Accomplishments By a Senior Scientist Award to Dr. Tandy Warnow for her significant impact on and valuable additions to the field of computational biology. Dr. Warnow's journey in mathematics and science began in her early school days, inspired by her teachers. These early subject interests are what led her to research pursuits in computational biology. Now, working in the field, her research focuses on combining theoretical frameworks with data-driven approaches, significantly impacting phylogenetic tree estimation and evolutionary studies.

As a Principal Investigator, Dr. Warnow emphasizes the importance of trust in mentoring relationships and supports her students' intellectual growth, encouraging them to ask meaningful questions and develop coping strategies for research setbacks. Although surprised by being named the recipient of the Accomplishments By a Senior Scientist Award, Dr. Warnow is honored by the recognition.

Read the full article here: https://doi.org/10.1093/bioinformatics/btae289

2024 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD: DR. SCOTT MARKEL

Dr. Scott Markel is honored with the 2024 Outstanding Contributions to ISCB Award for his exemplary leadership, education, and service to the International Society for Computational Biology (ISCB). Markel's involvement with ISCB began in the early 2000s, participating in committees and eventually serving as Secretary of the Board of Directors for a decade. His contributions include establishing governance structures, leading the search for the current CEO, and introducing term limits for officers and board members.

Dr. Markel encourages junior scientists to seek service opportunities by being curious and sharing experiences. He advises involvement in technical, service, and educational aspects of the society, such as reviewing papers, joining committees, and mentoring others. He emphasizes the importance of commitment and follow-through in service roles. Looking ahead, Markel envisions ISCB continuing to support the computational biology community by bridging academia and industry, providing infrastructure for academic support, and promoting cutting-edge research.

Read the full article here: https://doi.org/10.1093/bioinformatics/btae285

2024 ISCB INNOVATOR AWARD: DR. SU-IN LEE

Dr. Su-In Lee is honored with the 2024 ISCB Innovator Award for her progressive contributions to computational biology and her pursuit of unexplored directions in the field. From a young age, influenced by her father's engineering background, Lee developed a strong affinity for math and science. Her journey in computational biology began with her interest in AI during her undergraduate studies in Korea, where she developed a deep neural network for handwritten digit recognition. This led her to the Stanford AI Lab, where her focus shifted to computational biology, and later, to a faculty position at the University of Washington, where her research now intersects AI, biology, and clinical medicine.

One of Lee's notable contributions to the field is the development of the SHAP framework for explainable AI, emphasizing the importance of model interpretability in clinical AI applications. Her current research focuses on AI auditing frameworks to uncover flaws in existing models driven by findings from COVID-19 prediction models. As a Principal Investigator, Lee prioritizes mentoring students and encourages them to embrace new challenges and explore interdisciplinary research. Reflecting on her award, Lee expressed gratitude and humility, acknowledging the many outstanding researchers in the field.

Read the full article here: https://doi.org/10.1093/bioinformatics/btae287

2024 ISCB OVERTON PRIZE AWARD: DR. MARTIN STEINEGGER

ISCB is delighted to award the 2024 Overton Prize to Dr. Martin Steinegger for his significant contributions to computational biology. Dr. Steinegger's path to the field was an unconventional one, fueled by an early interest in computers and a desire to overcome the limitations of a non-traditional educational background. Overcoming his hurdles, he has accomplished much in the field of computational biology. One such accomplishment includes the development of Linclust, an algorithm that has significantly improved the speed of clustering metagenomic data. Dr. Steinegger's research remains focused on protein structures, leveraging high-quality predictions to explore the structural universe on an unprecedented scale.

In his role as a Principal Investigator, he emphasizes the importance of optimistic support and flexibility in mentoring young scientists, encouraging exploration and scientific discovery over perfection. When asked how he felt being the Overton Prize winner, Dr. Steineggr said it feels surreal, but he was honored to have been chosen as the award recipient.

Read the full article here: https://doi.org/10.1093/bioinformatics/btae288

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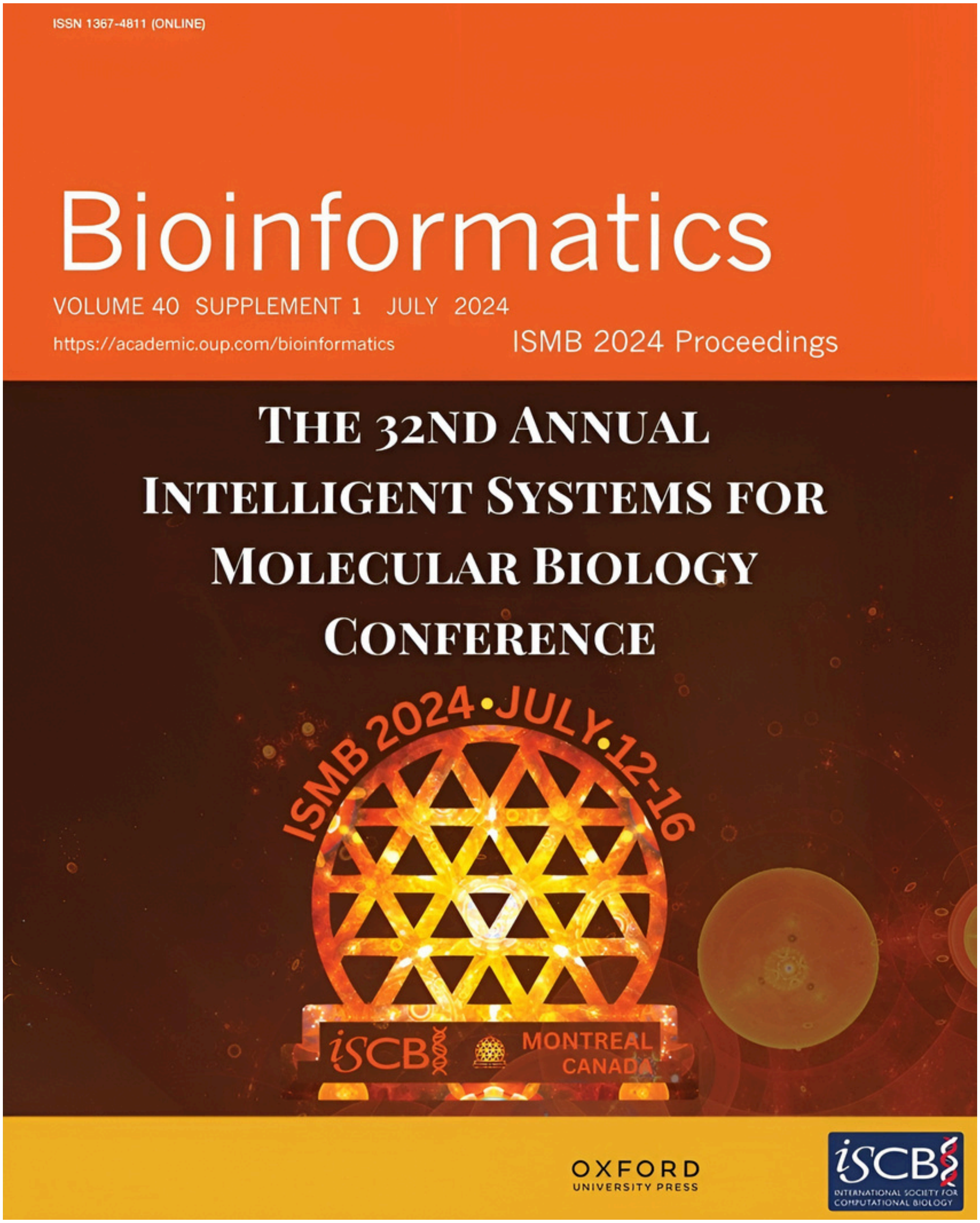
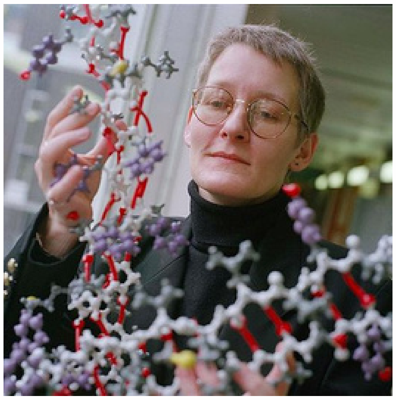


THE 2024 CLASS OF FELLOWS

The ISCB Fellows program is a prestigious recognition within the field of computational biology, honoring individuals who have made outstanding contributions to the discipline. These distinguished scientists and professionals have demonstrated exceptional leadership, research, and service, advancing the frontiers of computational biology and bioinformatics. Induction as an ISCB Fellow signifies a career of significant impact and a commitment to advancing the field.

CONGRATULATIONS 2024 CLASS OF FELLOWS!



Teresa Attwood, Emeritus Professor, Computer Science, University of Manchester

Teresa Attwood stands as a luminary in the realm of bioinformatics education, carving her legacy through unwavering commitment and innovative initiatives. Recognizing the pivotal role of education in propelling scientific advancement, Attwood embarked on a mission to democratize bioinformatics knowledge. Attwood's impact transcends mere publications. As a member of the ISCB Education Committee and later as an esteemed Board Member, she championed transformative educational strategies.

Niko Beerenwinkel, Professor, Computational Biology, Department of Biosystems Science and Engineering ETH Zurich; Swiss Institute of Bioinformatics

Niko Beerenwinkel has made groundbreaking contributions to cancer research and viral genomics. His innovative methods in cancer phylogenetics unveil deep insights into tumor dynamics, progression, and heterogeneity. In viral genomics, his development of ShoRAH and COJAC demonstrates excellence in quantifying genetic diversity and monitoring SARS-CoV-2 variants. Beerenwinkel's impactful work in integrating multi-omics data, exemplified by NetICS, enhances our understanding of cancer molecular mechanisms. His rigorous methods address complex biological problems, contributing significantly to medical and public health.

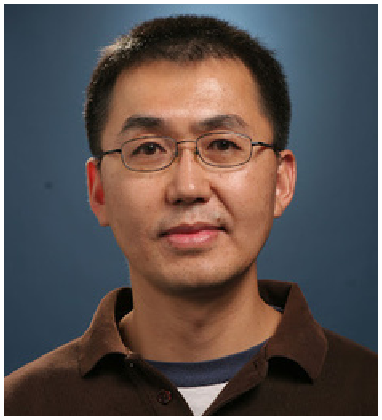
Doron Lancet, Dept. Molecular Genetics, Weizmann Institute of Science

Doron Lancet made outstanding contributions to genomics and computational biology. Notably, in 1993, he developed a molecular recognition model for olfaction and immunity, forming the basis for his novel quantitative model for life's origin. Lancet's creation of GeneCards in 1996, a comprehensive human gene compendium, has since evolved into the GeneCards Suite, serving 5 million users worldwide. Lancet's pioneering work in olfaction, genomics, and the GeneCards project exemplifies his significant impact on computational biology.

THE 2024 CLASS OF FELLOWS

Barbara Engelhardt, Senior Investigator, Gladstone Institutes; Professor (Research) of Biomedical Data Science, Department of Biomedical Data Science Stanford University

Barbara Engelhardt is globally acclaimed for advancing hierarchical Bayesian statistical and machine learning models for dimension reduction in biomedical data. Recognized with the 2020 Overton Prize, her impactful contributions span experimental design, exploratory data analysis, and predictive modeling in genomics, imaging, and hospital data. Engelhardt's emphasis on interpretable, robust, and computationally efficient methods has led to crucial discoveries in genetics, genomics, and epidemiology. As a leader and mentor, she promotes diversity and inclusion, making her an exemplary choice for ISCB Fellow.



Tao Jiang, Distinguished Professor, Computer Science & Engineering Dept, University of California Riverside

Tao Jiang is a pioneering figure in computational biology and bioinformatics, contributing significantly to algorithmic research. His seminal work spans multiple areas, including multiple sequence alignment, DNA fragment assembly, RNA secondary structure comparison, phylogenetic tree reconstruction, haplotype inference, ortholog assignment, and isoform quantification. His efficient combinatorial algorithms, recognized for their impact and citation frequency, have helped shape the field.

Carl Kingsford, Herbert A. Simon Professor of Computer Science, Ray and Stephanie Lane Computational Biology Department, School of Computer Science, Carnegie Mellon University

Carl Kingsford is a trailblazer in computational molecular biology, showcasing sustained innovation in scalable algorithmic approaches. His foundational contributions include transformative methods for gene expression quantification, k-mer-based computational methodologies, and efficient algorithms for searching unassembled sequence data. Notably, his software, Salmon and Jellyfish, are widely used in the field, with Salmon widely downloaded. Kingsford's theoretical understanding of algorithmic challenges and leadership in conferences further solidify his impactful role in shaping computational biology.

Eugene V Koonin, Evolutionary Genomics Group Leader, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health

Eugene Koonin is a distinguished figure in bioinformatics, comparative genomics, and evolutionary biology, with significant contributions recognized globally. Transitioning from experimental biology to bioinformatics, he contributed to viral genome analysis, leading to deep evolutionary insights. His work on COGs and genome evolution models advanced functional annotation and understanding of microbial evolution and cellular life origins. Koonin's research also encompasses metagenomics, antivirus defense systems, in particular, CRISPR, cancer evolution, and general theory of evolution.

THE 2024 CLASS OF FELLOWS

Philippe Lemey, Professor, Rega Institute, KU Leuven

Philippe Lemey, a leader in computational phylogenetics, has made outstanding contributions to understanding viral evolution and epidemiology. Renowned for his work in Bayesian statistics, he pioneered phylogeographic reconstruction in the widely used BEAST software, receiving the prestigious Mitchell Prize. Lemey's models, extended for pathogens like influenza and SARS-CoV-2, underpin diverse comparative analyses. Notably, he quantified measles' ancient origin and assessed intervention impact. In SARS-CoV-2 research, he reconstructed viral spread and contributed to origin studies, advising the WHO. Lemey's multidisciplinary collaborations emphasize innovative methods, making him a global asset in pathogen spread understanding.

Scott Markel, BIOVIA R&D Software Engineering Director, Biosciences & Scientific Informatics, Dassault Systèmes

Scott Markel's decade-long leadership within ISCB has been invaluable, notably as Secretary for 10 years. His governance expertise and commitment, evident in roles across committees like Nominations and Finance, have steered ISCB's strategic direction. Markel's contributions extend beyond official duties, supporting initiatives, mentoring, and advocating for computational biology's advancement. His outstanding service enriched ISCB's mission

Peter Park, Professor of Biomedical Informatics, Director, Bioinformatics and Integrative Genomics (BIG) PhD Track, Harvard Medical School

Peter Park is recognized for his seminal contributions in human genome and epigenome analysis. He led pioneering studies of structural alteration in cancer genomes, unveiling the landscape of somatic retrotransposition, microsatellite instability, chromothripsis, and other complex rearrangements. His work had clinical applications, such as a method for detecting homologous recombination deficiency to guide PARP inhibitor use in cancer patients. Dr. Park also explored mutational processes in the brain, utilizing single-cell whole-genome sequencing to study neuronal mutations and early human development. As a mentor, he shaped future leaders as the director of the Bioinformatics and Integrative Genomics Ph.D. program at Harvard Medical School for more than a decade.

Natasa Przulj, Leading Researcher, Life Sciences - ICREA Research Professor, Barcelona Supercomputing Center

Nataša Pržulj is a leader in biological network analysis, pioneering network biology geometry. She introduced graphlets to extract biomedical knowledge from omics networks, revolutionizing the field. Her recent research focus is artificial intelligence algorithms for multi-omics data fusion to improve precision medicine. Prof. Pržulj's scientific excellence is evident in her numerous awards, including election to ELLIS and Academia Europaea. She has provided exceptional service to ISCB, chairing ISMB's Systems Biology and Networks Area, NetBio COSI and contributing to editorial boards, advisory boards, and teaching, showcasing her commitment to advancing bioinformatics.

THE 2024 CLASS OF FELLOWS

Torsten Schwede, Professor, Structural Bioinformatics, Biozentrum, Vice President for Research, University of Basel; Swiss Institute of Bioinformatics

Torsten Schwede has made substantial contributions to computational biology through SWISS-MODEL, the first automated protein homology-modeling server, advancing our understanding of protein structure and fostering the use of computational models in life science research. Schwede's commitment to benchmarking and model quality assessment, with QMEAN and CAMEO, contributed to measuring progress in protein structure prediction. These developments formed groundwork for transformative technologies such as AlphaFold.

Michael J E Sternberg, Director Centre for Integrative Systems Biology and Bioinformatics (CISBIO), Imperial College London

Michael Sternberg, a structural bioinformatics pioneer since the 1970s, has made foundational contributions to understanding protein structure and function. His analyses of protein structures uncovered key principles, and he developed widely used resources like the Phyre web server, software for protein docking, and 3D-LigandSite for ligand binding prediction. These user-friendly tools have been crucial for researchers worldwide. His recent work on predicting the impact of missense variants vis the Missense3D portal and several collaborations, including COVID-19-related studies, showcase his ongoing impact in bioinformatics.

Fengzhu Sun, Professor, Quantitative and Computational Biology and Mathematics, University of Southern California

Fengzhu Sun is recognized for foundational contributions in computational biology, notably in protein-protein interaction network analysis, alignment-free sequence analysis, and metagenomic data analysis. A pioneer, Sun developed a probabilistically grounded model for predicting protein functional labels and introduced diffusion kernels for protein-protein interaction networks. His work, ahead of its time, laid the foundation for current diffusion-based methods. His contributions extend to error correction in PCR, statistical tools for metagenomics, and revolutionary alignment-free sequence analysis with applications in virus identification. His expertise, mathematical insights, and method development make him a standout in computational biology.

Mihaela Zavolan, Head of Research Group, Professor in Computational Biology/Genomics, Biozentrum, University of Basel; Swiss Institute of Bioinformatics

Mihaela Zavolan pioneered computational research into miRNAs, revealing their broad expression, and quantitatively prediction their interactions with target mRNAs. With a medical degree and a Ph.D. in Computer Science, her interdisciplinary background uniquely contributes to advancing computational biology. Her work includes algorithm development for miRNA gene and target prediction, innovations in CLIP methods for mapping RNA-protein interactions, as well as methods for unveiling the functions of RNA isoforms resulting from alternative polyadenylation. Zavolan's dedication to advancing both methodology and biological insights makes her a significant figure in the computational biology community.

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WELCOME THE INCOMING CO-EXECUTIVE EDITOR OF *BIOINFORMATICS*: INANC BIROL

From Oxford University Press and the *Bioinformatics* team:

The *Bioinformatics* team is proud to announce the appointment of Inanc Birol to the position of co-Executive Editor. Inanc has a strong background in computational molecular biology and genome bioinformatics, significant editorial experience, and compelling leadership qualities, which all position him well to lead *Bioinformatics* alongside Janet Kelso.

Inanc is a Distinguished Scientist of Genome Sciences at BC Cancer, a Professor of Medical Genetics at the University of British Columbia, and an associate faculty member at the Department of Pathology and Laboratory Medicine. He is the Head of the Bioinformatics Technology Lab at Canada's Michael Smith Genome Sciences Centre, and the Antimicrobial Research Lab at the UBC Centre for Disease Control.

Birol received his BSc and MSc in Electrical Engineering, and PhD in Physics from Bogazici University in Istanbul. His research interests are wide-ranging, from high performance computing for scalable sequence analysis to antimicrobial drug discovery.

He is a co-founder and the Chief Scientific Officer of Amphoraxe Life Sciences Inc., an R&D company that develops alternatives to conventional antibiotics.

MEET THE EDITOR

Inanc will be at the OUP booth in the ISMB 2024 Exhibitors' Hall from **1–2pm on Sunday, July 14th**.

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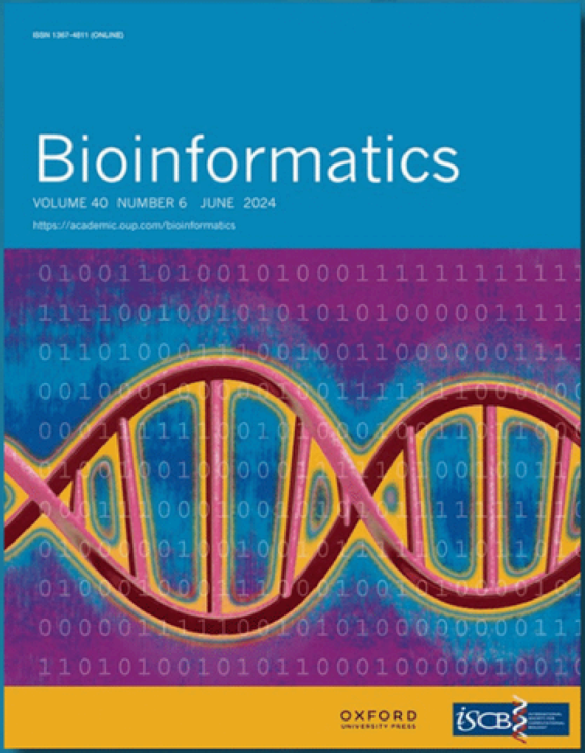
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Publishing with the journal helps to support the ISCB and its contributions to the field.

ISCB members receive a 15% discount on the open access charge.

WELCOME TO ISMB 2024!

On behalf of the ISMB 2024 organising committee, we wish you a warm welcome to this year's conference! If you're joining us in person, we want to welcome you to the vibrant city of Montréal, and if you're joining us virtually, we welcome you to the hybrid conference experience!

With ISMB taking place in Montréal this year, we respectfully acknowledge that this event is being held on the traditional territory of the Kanien'kehà:ka (Mohawk) Nation. This area has long been a site of meeting and exchange among First Nations, including the Kanien'kehà:ka of the Haudenosaunee Confederacy, Huron/Wendat, Abenaki, and Anishinaabeg. The Kanien'kehà:ka are recognised as the traditional custodians of the lands and waters of this region. We honour their elders, past and present, and their ongoing stewardship of these lands[1].

We hope you have an excellent time while in Montréal and attending ISMB. We encourage you to take full advantage of the conference and enjoy an amazing five days of science, networking, and collaboration!

The scientific programme features exceptional keynote talks and research, and technical talks organised thematically across Communities of Special Interest (COSI) tracks. Additionally, participants can attend workshops, special sessions, the hybrid Student Council Symposium, the Youth Bioinformatics Symposium, and poster sessions. Also, don't miss our Exhibit Hall in room 517c, where you can engage with our 17 conference exhibitors while enjoying coffee during breaks. This year's exhibition highlights bioinformatics tools and technologies, product-to-market advisors, and open-access and traditional publishers.

For those joining us virtually through ISCB's Nucleus platform, you can interact with all ISMB 2024 participants within the Collaboration Hub, including our exhibitors. In the Forums section, you can chat with your colleagues or start a conversation by launching an open meeting room at any time with another attendee. To start an open meeting room, simply set a time and join the room through the link sent to your email.

While viewing a live session, you can get involved by chatting and asking questions in the stream's live chat and Q&A sections. When not attending a session or viewing posters in the Virtual Poster Hall, you can look around the online Exhibit Hall to learn about each exhibitor at ISMB.

Highlights of the ISMB 2024 Programme include:

- 5 Distinguished Keynote presentations, including our three 2024 ISCB Award Winners
- 22 community-led COSI Tracks and workshops
- 4 Special Sessions, including Visualizing Protein Function, Equity and Diversity in Computational Biology, Demystifying Scientific Publishing, and Digital Agriculture
- a Special Track from the US National Institutes of Health Office of Data Science Strategy (NIH/ODSS)
- 16 Technology Track presentations
- 12 pre-conference Tutorials (7 in person, 5 virtual)
- the Career Fair
- the Success Circles networking event
- 700+ posters

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[1] https://www.mcgill.ca/circ/land-acknowledgement

WELCOME TO ISMB 2024!

There's a lot of science being shared throughout the conference, but don't worry if you miss something live; everything will be available via Nucleus as on-demand viewing!

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

We also want to acknowledge all the chairs of the Proceedings, COSI, Special Session, Technology Track, Travel Fellowship, Tutorial, Student Council Symposium, and the Youth Bioinformatics Symposium committees, as well as those who supported the committees. Their dedication and leadership have been invaluable in bringing these five days of exceptional and innovative science to life!

Before we close, we want to take this opportunity to thank our conference funders, sponsors, and exhibitors for their ongoing support.

Finally, as many of you know, without the highly skilled ISCB staff—especially Bel Hanson, ISCB's Operations and Programs Director, and Seth Munholland, ISCB's Lead Technologist, and Diane Kovats, CEO of the ISCB—there would be no ISMB meeting! We are immensely grateful to the ISCB team for the dedication and effort that they put into organizing the logistics of this very complex meeting while enabling a hybrid experience for those unable to attend in person.

We hope you take advantage of everything the conference offers, especially the endless opportunities to meet, network, and connect with your fellow computational biologists!

Wishing you all a wonderful ISMB 2024!

Bienvenue à Montréal!

Yours sincerely,

Aïda

Aïda Ouangraoua,
Conference Co-Chair

Karin Verspoor

Karin Verspoor,
Conference Co-Chair

BF Francis Ouellette,
Honorary Chair

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Kana Shimizu, Waseda University, Japan

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Patricia M. Palagi, SIB Swiss Institute of Bioinformatics, Switzerland

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R. Gonzalo Parra, Barceolna Supercomputing Center, Spain

BIO-ONTOLOGIES

Tiffany Callahan, University of Colorado Denver, USA

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

BIOINFO-CORE

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Shannan Ho Sui, Harvard School of Public Health, USA

Alberto Riva, Human Technopole, Italy

Brent Richter, Harbinger Health, USA

BIOINFORMATICS IN CANADA

Aïda Ouangraoua, University of Sherbrooke, Canada

Francis Ouellette, Origin Bioinformatics, Canada

BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Jan Byška, Masaryk University, Czech Republic

Qianwen Wang, Harvard Medical School, USA

BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE

Nomi L. Harris (Chair), Lawrence Berkeley National Laboratory, USA

Karsten Hokamp, Trinity College Dublin, Ireland

Deepak Unni, SIB Swiss Institute of Bioinformatics, Switzerland

Hervé Ménager, Institut Pasteur, France

Jason Williams, Cold Spring Harbor Laboratory, USA

Monica Munoz-Torres, University of Colorado Anschutz Medical Campus, USA

Swapnil Sawant, Phoenix Bioinformatics, USA

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COSI TRACK AND ABSTRACT CHAIRS

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

Joaquin Dopazo, Fundación Progreso y Salud, Spain

David P Kreil, Boku University Vienna, Austria

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

Wenzhong Xiao, Harvard Medical School, USA

COMPUTATIONAL AND SYSTEMS IMMUNOLOGY

Ferhat Ay, La Jolla Institute for Immunology, USA

Jishnu Das, University of Pittsburgh School of Medicine, USA

Hatice Ulku Osmanbeyoglu, University of Pittsburgh, USA

Yuri Pritykin, Princeton University, USA

COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Wout Bittremieux, University of Antwerp, Belgium

Timo Sachsenberg, University of Tübingen, Germany

Isabell Bludau, Max Planck Institute of Biochemistry, Germany

Lindsay Pino, University of Pennsylvania, United States

Marie Brunet, Shrebrooke University, Canada

EDUCATION: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS EDUCATION AND TRAINING

Russell Schwartz, Carnegie Mellon University, USA

Patricia M. Palagi, SIB Swiss Institute of Bioinformatics, Switzerland

Wai Keat Yam, International Medical University, Malaysia

EQUITY AND DIVERSITY IN COMPUTATIONAL BIOLOGY RESEARCH

Casey Greene, University of Colorado's Anschutz Medical Campus, USA

Alejandra Medina Rivera, Universidad Nacional Autonoma de Mexico, Mexico

EVOLCOMPGEN: EVOLUTION & COMPARATIVE GENOMICS

Nadia El-Mabrouk, University of Montreal, Canada

Janani Ravi, University of Colorado Anschutz Medical Campus, USA

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SCIENTIFIC ORGANIZING COMMITTEE

COSI TRACK AND ABSTRACT CHAIRS

FUNCTION: GENE AND PROTEIN FUNCTION ANNOTATION

Iddo Friedberg, Iowa State University, USA
Mark Wass, University of Kent, United Kingdom
Ana M. Rojas Mendoza, Centro Andauz de Biologica del Dessarrolo, Spain
Dukka KC, Michigan Technological University, USA

HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

Can Alkan, Bilkent University, Turkey
Ana Conesa, Spanish National Research Council, Spain; and University of Florida, Gainesville, USA
Francisco M. De La Vega, Stanford University; and Tempus Genomics, USA
Dirk Evers, Dr. Dirk Evers Consulting, Germany
Kjong Lehmann, Centre of Medical Technology, Germany
Christina Boucher, University of Florida, Gainesville, United States

IRNA: INTEGRATIVE RNA BIOLOGY

Michelle Scott, University of Sherbrooke, Canada
Athma Pai, University of Massachusetts Medical School, USA
Hagen Tilgner, Weill Cornell Medicine, USA
Maayan Salton, Hebrew University of Jerusalem in Israel, Israel

MICROBIOME

Alice McHardy, Helmholtz Centre for Infection Research, Germany
Alexander Sczyrba, Bielefeld University, Germany

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Yvan Saeys, Ghent University, Belgium
Maria Brbic, EPFL, Switzerland

NETBIO: NETWORK BIOLOGY

Chad Myers, Department of Computer Science and Engineering, University of Minnesota, USA
Deisy Morselli Gysi, Federal University of Paraná, Curitiba - Paraná, Brazil
Anaïs Baudot, CNRS - INSERM - AMU, France
Scooter Morris, University of California, San Francisco, USA
Martina Summer-Kutmon, Maastricht University, Netherlands

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SCIENTIFIC ORGANIZING COMMITTEE

COSI TRACK AND ABSTRACT CHAIRS

REGSYS: REGULATORY AND SYSTEMS GENOMICS

Shaun Mahony, Penn State University, USA

Anthony Mathelier, University of Oslo, Norway

Lonnie Welch (Ex Officio), Ohio University, USA

Alejandra Medina-Rivera, National Autonomous University of Mexico, Mexico

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Shaimaa Bakr, Stanford University, USA

Matteo Barberis, University of Surrey, United Kingdom

Chiara Damiani, Università degli Studi di Milano-Bicocca, Italy

Reihaneh Mostolizadeh, University of Tübingen, Germany

Bhanwar Lal Puniya, University of Nebraska-Lincoln, USA

Meghna Verma, AstraZeneca, USA

TEXT MINING

Robert Leaman, NCBI/NLM/NIH, USA

Lars Juhl Jensen, University of Copenhagen, Denmark

Zhiyong Lu, NCBI/NLM/NIH, USA

TRANSMED: TRANSLATIONAL MEDICINE INFORMATICS & APPLICATIONS

Venkata Satagopam, University of Luxembourg, Luxembourg

Maria Secrier, University College London, United Kingdom

Irina Balaur, University of Luxembourg, Luxembourg

Irene Ong, Universtiyt of Wisconsin-Madison, USA

Bosdriesz Evert, VU Amsterdamn, Netherlands

Heba Sailem, University of Oxford, United Kingdom

Mansoor Saqi, Institute of Cancer Research, United Kingdom

VARI: VARIANT INTERPRETATION

Emidio Capriotti, University of Bologna, Italy

Hannah Carter, University of California, San Diego, USA

Antonio Rausell, Imagine Institute for Genetic Diseases, France

GENERAL COMPUTATIONAL BIOLOGY

Gary Bader, University of Toronto, Canada

Iman Hajirasouliha, Cornell University, USA

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DISTINGUISHED KEYNOTES

Room 517d

Day	Time	Title and Speaker
Friday, July 12	18:30	*Sensitive Sustainable Science* **Fiona S. L. Brinkman**
Saturday, July 13	9:00	*Progress in Large-Scale Phylogenomic Estimation Methods* **Tandy Warnow**
Sunday, July 14	9:00	*Human genome 2.0 : why a pangenome graph is better for genetic and epigenetic analyses* **Guillaume Bourque**
Monday, July 15	9:00	*Supercharged Protein Analysis in the Era of Accurate Structure Prediction* **Martin Steinegger**
Tuesday, July 16	16:00	*Explainable AI for health: where we are and how to move forward* **Su-In Lee**

*Click the schedule to go to the Distinguished Keynotes page

FIONA S. L. BRINKMAN

Time: Friday, July 12, 2024 at 6:30pm

Sensitive Sustainable Science

How do we sustainably maintain and further develop bioinformatics and computational biology (BCB) software, databases and tools, in the face of short <5 year periods of funding support? How do we promote open data and open science in a way that best effects positive change and avoids causing unwitting harm on communities? Using some historical data and also my recent research as examples, I'll review how open science is evolving, building on FAIR (findable, accessible, interoperable, reusable) with also, for example, CARE (Collective Benefit, Authority to Control, Responsibility, Ethics) as Principles for Indigenous Data Governance. I'll review this and other principles in the context of both microbial data, as well as human cohort data, presenting some approaches to research that can support more sustainable, inclusive science that can potentially better lead to positive change. While there is no one size fits all solution, there are some common themes and considerations that we as a BCB community should discuss - and ideally incorporate into BCB training programs.

TANDY WARNOW

Time: Saturday, July 13, 2024 at 9am

Progress in Large-Scale Phylogenomic Estimation Methods

Over the last several years, interest in computing and then using large-scale phylogenies has increased for multiple reasons, including basic science (how did life evolve on earth) and applications in biomedicine and public health (e.g., understanding the evolution of SARS-Cov-2). The estimation of these large phylogenies, wiith potentially millions of leaves, presents fascinating mathmetical, statistical, and computational challenges, ranging from computing multiple-sequence alignments, developing effective heuristics to NP-hard optimization problems (e.g., maximum likelihood tree estimation) on large datasets), estimating species trees from genome- scale data while addressing biological causes for heterogeneity (e.g., gene duplication and loss and incomplete lineage sorting) across the genome). There are also many fascinating and difficult problems that have to do with “post-tree” analyses, such as rooting gene trees and species trees, or estimating branch lengths in species trees and dates at internal nodes, that are needed for many down-stream analyses. In this talk I will describe progress on these questions, and I will also present some open problems where new techniques are needed.

GUILLAUME BOURQUE

Time: Sunday, July 14, 2024 at 9am

Human genome 2.0: why a pangenome graph is better for genetic and epigenetic analyses

Genomic analyses often start by mapping reads to a reference genome. But, in every individual, there are DNA variants and sequences that are unique to that individual and reads coming from those regions will often be ignored. Thankfully, progress in long-read technologies and assembly can now efficiently deliver telomere-to-telomere genomes. Applying such approaches to a diverse panel of individuals combined with the development of graph-based genomic tools, the Human Pangenome Reference Consortium has just released the first human pangenome reference graph. This new resource is meant to alleviate the limitations of relying on a single linear human genome as the first step of most genetic and epigenetic analyses. In this talk, I will summarize some of the benefits of using the pangenome reference. In particular, I will show how this new reference can be used to extract missing signal when looking for genetic variants in a rare disease cohort called Genomic Answers for Kids. I will also describe the results of a new study using a genome-graph looking at epigenetic changes before and after influenza infection in monocyte-derived macrophages extracted from more than 30 individuals of different ancestry. Finally, considering the importance of data sharing in genomics, I will introduce a project called the Pan-Canadian Genome Library, which will establish the framework for Canada’s management and sharing of human genomic data.

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DISTINGUISHED KEYNOTES

MARTIN STEINEGGER

Time: Monday, July 15, 2024 at 9am

Supercharged Protein Analysis in the Era of Accurate Structure Prediction

Protein analysis has witnessed a revolution through machine-learning methods. At the forefront are highly accurate structure prediction methods such as AlphaFold2 and ESMFold. These have generated an avalanche of publicly available protein structures. The AlphaFold database and ESMatlas contain over 214 and 620 million predicted structures, respectively, covering nearly every protein sequence in our largest protein reference databases. This unprecedented access to structural information is not just critical for structural biology but impacts most fields of biology. In this talk, I will discuss how this data is revolutionizing genomic and proteomic annotations and introduce fast and sensitive methods to search and cluster this data to extract new biological insights.

SU-IN LEE

Time: Tuesday, July 16, 2024 at 4pm

Explainable AI for health: where we are and how to move forward

The first part of my talk delves into various research endeavors conducted by my lab, focusing on explainable AI's application across diverse biomedical domains. I will demonstrate how explainable AI can elucidate novel scientific inquiries, with a primary emphasis on understanding neurodegenerative diseases and biological age.

In the second part, we will explore the evolving landscape of explainable AI, uncovering its potential to chart new scientific directions in biomedicine, exemplified by our recent work in dermatology, emergency medicine, and precision cancer medicine. This discussion aims to shed light on the necessary enhancements for explainable AI to effectively tackle a wide array of real-world challenges in biomedicine.

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ISMB 2024 Montréal

July 12–16

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EXHIBITORS

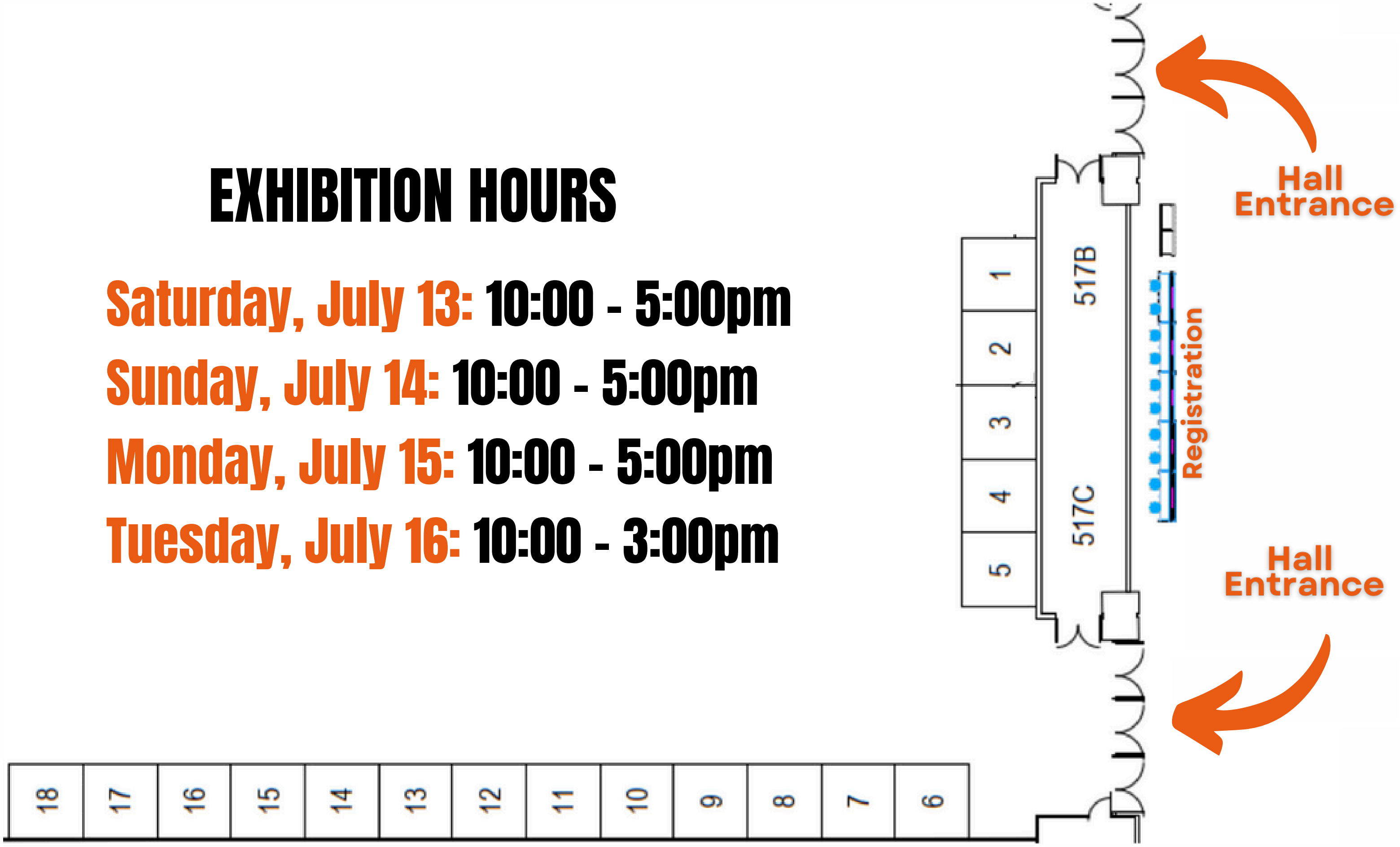
EXHIBITION HOURS

Saturday, July 13: 10:00 - 5:00pm

Sunday, July 14: 10:00 - 5:00pm

Monday, July 15: 10:00 - 5:00pm

Tuesday, July 16: 10:00 - 3:00pm



1	ISCB	2	ISCB-SC
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7	Alagia AI, Inc.	8	Illumina
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11	The Jackson Laboratory	12	Fulgent Genetics
13	Royal Society Publishing	14	St. Jud Children's Research Hospital
15	Seqera	16	Harvard Medical School
17	University of Southern California	18	Borderlands Science

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ABRIDGED AGENDA

Friday, July 12, 2024

Start	End	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
9:00	10:45		Tutorial IP1	Tutorial IP6	Tutorial IP5	Tutorial IP4	SCS	SCS Posters			Tutorial IP3	Tutorial IP2
10:45	11:00	**Coffee Break**										
11:00	13:00		Tutorial IP1	Tutorial IP6	Tutorial IP5	Tutorial IP4	SCS	SCS Posters	YBS		Tutorial IP3	Tutorial IP2
13:00	14:00	**Lunch Break**										
14:00	16:00		Tutorial IP1	Tutorial IP7	Tutorial IP5	Tutorial IP4	SCS	SCS Posters	YBS		Tutorial IP3	Tutorial IP2
16:00	16:15	**Coffee Break**										
16:00	18:00	Career Fair in 517c (pre-registration required)										
16:15	18:00		Tutorial IP1	Tutorial IP7	Tutorial IP5	Tutorial IP4	SCS	SCS Posters	YBS		Tutorial IP3	Tutorial IP2
18:15	18:30	Welcome										
18:30	19:30	Keynote: Fiona Brinkman										
19:30	21:00	Welcome Reception (517c)										

Saturday, July 13, 2024

Start	End	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
7:30	8:00	Serene Stretch Symposium - Yoga										
8:40	9:00	Welcome										
9:00	10:00	Keynote: Tandy Warnow										
10:00	10:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
10:40	12:20	HitSeq	RegSys	iRNA	Education	Bio-Ontologies	NIH/ ODSS	Function	MICROBIOME	Comp MS		Tech Track
12:20	14:20	**Poster Session with Lunch**										
14:20	16:00	HitSeq	RegSys	iRNA	Education	Bio-Ontologies	NIH/ ODSS	Function	MICROBIOME	Comp MS		Tech Track
16:00	16:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
16:40	18:00	HitSeq	RegSys	iRNA	Education	Bio-Ontologies	NIH/ ODSS	Function	MICROBIOME	Comp MS		
18:00	20:00	Celebrating 25 Years of Bioinformatics.ca										
18:00	22:00	Explore Montréal										

ABRIDGED AGENDA

Sunday, July 14, 2024

Start	End	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
7:30	8:00	Serene Stretch Symposium - Yoga										
8:40	9:00	Welcome										
9:00	10:00	Keynote: Guillaume Bourque										
10:00	10:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
10:40	12:20	HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function	MICROBIOME	BioInfo-Core	Text Mining	iCn3D
12:20	14:20	• **Poster Session with Lunch** • Fellows Workshop in 523b, lunch provided – **INVITE ONLY**										
14:20	15:00	HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function	MICROBIOME	BioInfo-Core	Text Mining	iCn3D
15:00	15:20	HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function		BioInfo-Core	Text Mining	iCn3D
15:20	16:00	HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function	NetBio	BioInfo-Core	Text Mining	iCn3D
16:00	16:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
16:40	18:00	HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function	NetBio	BioInfo-Core	Text Mining	iCn3D
18:00	19:30	Success Circles – Ticketed Event (517c)										
19:30	23:00	President's Reception, room 720a – **INVITE ONLY**										

Monday, July 15, 2024

Start	End	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
7:30	8:00	• Serene Stretch Symposium – Yoga • Green Task Force Meeting (523b)										
8:40	9:00	Welcome										
9:00	10:00	Keynote: Martin Steinegger										
10:00	10:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
10:40	12:20	MLCSB	EvolCompGen	General CompBio	VarI	Equity and Diversity in Computational Bio Research	3DSIG	CAMDA	NetBio	Web	BOSC	Tech Track
12:20	14:20	• **Poster Session with Lunch** • Bioinformatics Editorial Board Meeting in 523b, lunch provided – **INVITE ONLY** • Education Committee Meeting in 523b, lunch provided – **INVITE ONLY**										
14:20	16:00	MLCSB	EvolCompGen	General CompBio	VarI		3DSIG	CAMDA	NetBio	Web	BOSC	Tech Track
16:00	16:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
16:40	18:00	MLCSB	EvolCompGen	General CompBio	VarI	TransMed	3DSIG	CAMDA	NetBio		BOSC	
18:15	19:15		ISCB Town Hall									
Varying		COSI Dinners – **RSVP in advance required**										

ABRIDGED AGENDA

Tuesday, July 16, 2024

Start	End	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
7:30	8:00	Serene Stretch Symposium - Yoga										
8:40	10:00	MLCSB	EvolCompGen	TransMed	SysMod	Computational and Systems Immunology	3DSIG	CAMDA	Digital Agriculture		BOSC	
10:00	10:40	**Caffeinate and Connect with Exhibitors – Coffee Break**										
10:40	12:20	MLCSB	EvolCompGen	TransMed	SysMod	Computational and Systems Immunology	3DSIG	CAMDA	Digital Agriculture		BOSC	Demystifying the World of Scientific Publishing
12:20	14:20	**Poster Session with Lunch**										
14:20	15:40	MLCSB	EvolCompGen	TransMed	SysMod	Computational and Systems Immunology	3DSIG	CAMDA	Digital Agriculture		BOSC	
15:40	16:00	**Grab and Go – Quick Coffee Break**										
16:00	17:00	Keynote: Su-In Lee										
17:00	17:30	Awards Presentation										

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VIRTUAL
AND
IN-PERSON
TUTORIAL
SCHEDULES

TUTORIALS

TUTORIAL VT1: A PRACTICAL INTRODUCTION TO LARGE LANGUAGE MODELS IN BIOMEDICAL DATA SCIENCE RESEARCH

Part 1 – Monday, July 8	
Time	Title
14:00	*Overview and Welcome*
14:10	*Introduction to LLMs with a focus on Biomedical Data Science*
14:40	*How to use GPT-3.5 and GPT-4 with Python*
15:10	*How to use Open-source LLMs with Python*
15:30	**Break**
15:45	*Database Query Generation with LLMs*
16:10	*Retrieval-augmented Generation with Large Language Models*
16:35	*Code generation in Bioinformatics*

Part 2 – Tuesday, July 9	
Time	**Title**
14:00	*Large Language Models for Biomedicine: from PubMed Search to Gene Set Analysis*
14:45	*AI in Biomedicine: Developing Representations of Disease-Relevant Molecules*
15:30	**Break**
15:45	*Integrating Biomedical Data Database Development with LLMs*
16:10	*Querying PubMed with RAG to answer biomedical questions with GPT-4*
16:35	*Code generation in Bioinformatics with Opensource LLMs*
16:55	*Closing Remarks*

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TUTORIAL VT2: BIOVIZ: INTERACTIVE DATA VISUALISATION AND ML FOR OMICS DATA

Part 1 – Monday, July 8	
Time	**Title**
14:00	Lecture: *Introduction to Data Visualisation: Importance and Basic principles of data visualization in scientific research* **Jean-Christophe Nebel**
15:00	Hands-on: *Python Libraries for Visualization: Matplotlib, Seaborn, Plotly and others* **Farzana Rahman, Ragothaman Yennamalli, Shashank Ravichandran, and Megha Hegde**
15:45	**Break**
16:00	Lecture: *Colour theory in Visualization: Colour palettes, Accessible and Inclusive Visualisations* **Ragothaman Yennamalli**
17:00	Hands-on: *Creating various types of charts, plots for clarity and aesthetics. Case studies with real world datasets* **Farzana Rahman, Ragothaman Yennamalli, Shashank Ravichandran, and Megha Hegde**

Part 2 – Tuesday, July 9	
Time	**Title**
14:00	Lecture: *Fundamentals of Machine Learning: Types of ML, Data preprocessing and feature selection, model selection and training* **Ragothaman Yennamalli and Farzana Rahman**
15:00	Hands on: *Python libraries for Machine Learning: Scikit-learn, Pandas, NumPy, TensorFlow/Keras. Building models using real-world biological data* **Shashank Ravichandran, and Megha Hegde**
16:00	**Break**
16:15	Hands on: *Integrating Data Viz and ML: Yellowbrick, Bokeh, Tensorboard, Scikit-plot, etc.* **Farzana Rahman and Megha Hegde**
17:15	*Question and Answer session (Identify and highlight blocks of hands-on content in your submission)*

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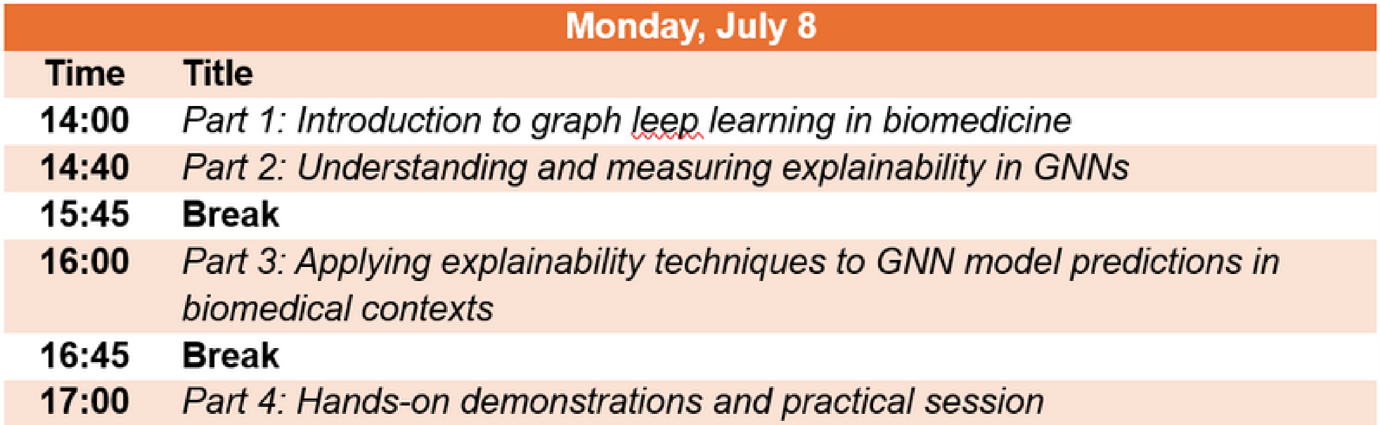
TUTORIAL VT3: USING LINKML (LINKED DATA MODELING LANGUAGE) TO MODEL YOUR DATA

Monday, July 8	
Time	**Title**
14:00	*Introduction* **Sierra Moxon**
14:20	*Section 1: Set up a LinkML repository* **Patrick Kalita**
14:50	*Section 2: Authoring a LinkML Model* **Sierra Moxon**
15:10	**Break**
15:25	*Section 2: Authoring a LinkML Model (cont.)* **Sierra Moxon**
15:40	*Section 3: Schema best practices, including linting* **Patrick Kalita**
15:55	*Section 4: Generating code from your model* **Kevin Schaper**
16:35	**Break**
15:45	*Section 5: LinkML Validate* **Patrick Kalita**
17:05	*Section 6 (Time permitting): Schema Automator (LLM + LinkML)* **Sierra Moxon**
17:35	*Wrap up/Questions*

TUTORIAL VT4: COMPUTATIONAL APPROACHES FOR IDENTIFYING CONTEXT-SPECIFIC TRANSCRIPTION FACTORS USING SINGLE-CELL MULTI-OMICS DATASETS

Tuesday, July 9	
Time	**Title**
14:00	*Welcome remarks and tutorial overview* **Hatice**
14:05	*Basic principles behind TF activity inference methods* **Hatice**
14:45	*Overview of computational TF inference methods based on single cell omics* **Hatice and Merve**
15:45	**Break**
16:00	*Hands-on experience in applying tools and interpreting results using multiple TF activity inference methods using public scRNA-seq* **Linan and Merve**
16:45	*Hands-on experience in applying tools and interpreting results using multiple TF activity inference methods using public scATAC-seq and multiome* **Parham and Merve**
17:30	*Hands-on experience in applying tools and interpreting results using TF activity inference methods using public CITE-seq* **Parham and Hatice**
15:55	*Discuss current bottlenecks, gaps in the field, and opportunities for future work* **Hatice**

TUTORIAL VT5: EXPLAINABILITY IN GRAPH DEEP LEARNING FOR BIOMEDICINE



Monday, July 8	
Time	**Title**
14:00	*Part 1: Introduction to graph leep learning in biomedicine*
14:40	*Part 2: Understanding and measuring explainability in GNNs*
15:45	**Break**
16:00	*Part 3: Applying explainability techniques to GNN model predictions in biomedical contexts*
16:45	**Break**
17:00	*Part 4: Hands-on demonstrations and practical session*

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TUTORIALS

TUTORIAL IP1: ADVANCED MACHINE LEARNING METHODS FOR MODELING, ANALYZING, AND INTERPRETING SINGLE-CELL OMICS AND SPATIAL TRANSCRIPTOMICS DATA

Friday, July 12; Room 518

Time	Title
9:00	Part 1: Overview: Introduction to single-cell multi-omics and spatial transcriptomics and corresponding challenges.
9:45	Part 2: Introduction to biological analyzing methods.
10:45	Coffee Break
11:00	Part 3: Clustering-based single-cell analysis and scGNN.
11:30	Part 4: Applications #1: Single-cell RNA-seq dataset acquisition, model training, and analysis.
13:00	Lunch break
14:00	Part 5: Network analysis on single-cell multi-omics and DeepMAPS.
14:30	Part 6: Applications #2: Single-cell multi-omics dataset acquisition, model training, and analysis.
16:00	Break
16:15	Part 7: Marker analysis on spatial transcriptomics and BSP.
16:45	Part 8: Applications #3: Spatial transcriptomics dataset acquisition, model fitting, and analysis.

TUTORIAL IP2: JUST-IN-TIME COMPILED PYTHON FOR BIOINFORMATICS RESEARCH

Friday, July 12; Room 524c

Time	Title
9:00	Introduction to the numba just-in-time compiler for Python; small examples, possibilities, limitations, how the compilation works. *Last 30 minutes are short hands-on exercises (timing iterated execution of a small function in pure vs. compiled Python).*
10:45	Coffee Break
11:00	Introduction to DNA motif search and a “motif description” mini-language, with examples from the literature. Automaton-based pattern search and a bit-parallel algorithm. *Hands-on: Implementation in pure Python (45 min, 15-20 lines).*
13:00	Lunch break
14:00	Transforming a Python implementation to a numba-compiled implementation; separation of high-level and low-level code parts; managing memory allocations; introduction of type annotations *(1 hour principles, 1 hour supervised coding).*
16:00	Coffee Break
16:15	Parallelization: Using threads to parallelize the application (e.g. parallel search across chromosomes); Replacing the command-line interface by a simple but effective GUI using streamlit. *Hands-on coding: Splitting the task, collecting and visualizing the results.*

TUTORIAL IP3: MULTI-OMIC DATA INTEGRATION FOR MICROBIOME RESEARCH USING SCIKIT-BIO

Friday, July 12; Room 524a	
Time	**Title**
9:00	**Introduction and software setup** Lecture: Current trends in microbiome research Exercise: Setting up the software environment
10:00	**Working with various omic data types** Lecture: Omic data types in microbiome research Exercise: A real-world multi-omic dataset
10:45	Coffee Break
11:00	**Working with sparse, high-dimensional data tables** Lecture: Nuances of omic data tables Exercise: Working with omic data tables
12:00	**Analyzing microbial community structures** Lecture: Microbial community ecology Exercise: Community diversity analyses
13:00	Lunch Break
14:00	**Inferring and associating critical features** Lecture: Microbial signatures and their biological roles Exercise: Statistical modeling and tests
15:00	**Predicting host and environmental traits** Lecture: Microbiomes are predictive of biology Exercise: Constructing predictive models
16:00	Coffee Break
16:15	**Developing an analytical protocol for publication** Lecture: Good practices in scientific data analysis Exercise: Assembling an analytical protocol
17:15	**Debugging, wrapping-up and open questions** Exercise: Troubleshooting and expansion Lecture: Looking beyond

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TUTORIAL IP4: QUANTUM-ENABLED MULTI-OMICS ANALYSIS

Friday, July 12; Room 522	
Time	**Title**
9:00	Session I: Quantum Information and Fundamentals
10:45	Coffee Break
11:00	Session II: Hello Qiskit!: Writing your first program in Qiskit
12:30	Session III: Processing multi-omics data with classical ML algorithms
13:00	Lunch Break
14:00	Session IV, Part I: Design and implement QML algorithm for single-cell data in Qiskit.
16:00	Coffee Break
16:15	Session IV, Part II: Analyze QML algorithm and compare with classical ML
17:00	Session V: Interactive Q&A session with the participants.

TUTORIAL IP5: MODELLING MULTI-MODAL BIOMEDICAL DATA USING NETWORKS

Friday, July 12; Room 521	
Time	**Title**
9:00	Welcome and Introduction
9:10	“An Introduction to Networks”
9:40	Practical Session 1
10:45	Coffee Break
11:00	“The Do’s and Don’ts of Biomedical Network Construction”
11:30	Practical Session 2
13:00	Lunch Break
14:00	“Common Approaches to the Analysis of Biomedical Networks”
14:30	Practical Session 3
16:00	Coffee Break
16:15	“An Introduction to Network Inference Using Graph Neural Networks”
16:45	Practical Session 4
17:50	Closing Remarks

TUTORIAL IP6: CREATING AND RUNNING CLOUD-NATIVE PIPELINES WITH WDL, DOCKSTORE, AND TERRA

Friday, July 12; Room 519	
Time	**Title**
9:00	Welcome, Opening Remarks, Review Agenda, and Learning Goals
9:05	Introduction to Docker
9:15	Building and Using Dockers
9:45	Introduction to WDL
10:00	Basic WDL Scripting
10:45	Coffee Break
11:00	Introduction to Dockstore
11:30	Integrate Your GitHub With Dockstore
12:00	Real Genomics Example: Modify, Export, and Run a WDL
12:30	Wrap-Up and Q&A

TUTORIAL IP7: FEDERATED ENSEMBLE LEARNING FOR BIOMEDICAL DATA

Friday, July 12; Room 519	
Time	**Title**
14:00	Lecture: *Federated ensemble learning in biomedical health data* **Anne-Christin Hauschild**
14:30	Hands-on tutorial: *How to develop and implement a federated random forest* **Hryhorii Chereda, Maryam Moradpour, Younjun Park**
15:45	Coffee Break
16:00	Continuation of hand-on tutorial: *How to develop and implement a federated random forest* **Maryam Moradpour, Youngjun Park**
16:15	Lecture: *Federated ensemble learning with graph neural networks* **Hryhorii Chereda**
16:30	Hands-on tutorial: *How to train an apply federated Ensemble-GNN* **Hryhorii Chereda, Maryam Moradpour, Youngjun Park**

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POSTER SESSIONS

There will be **four** poster presentation sessions at ISMB 2024:

- **Session A:** Posters on display Saturday, July 13 and Sunday, July 14, with posters being presented by the author on Saturday, July 13
- **Session B:** Posters on display Saturday, July 13 and Sunday, July 14, with posters being presented by the author on Sunday, July 14
- **Session C:** Posters on display Monday, July 15 and Tuesday, July 15, with posters being presented on Monday, July 15
- **Session D:** Posters on display Monday, July 15 and Tuesday, July 15, with posters being presented on Tuesday, July 16

Please review the schedule below for poster set up, poster presentation, and poster removal times.

If you can't find your poster please contact submissions@iscb.org IMMEDIATELY and provide either your submission ID or presentation title.

Poster space is limited and we may not be able to accommodate adding posters on site.

DISPLAY SCHEDULE

Session A/B: (July 13 and July 14)

Set up time: Saturday, July 13 between 8:00 – 10:00am,
Location: Palais des Congrés de Montréal, Room 517bc

Session A/B Posters should be removed at 4:40pm, Sunday, July 14.

Session C/D: (July 15 and July 16)

Set up time: Monday, July 15 between 8:00 – 10:00am,
Location: Palais des Congrés de Montréal, Room 517bc

Session C/D Posters should be removed at 4:40pm, Tuesday, July 16.

POSTER SESSIONS

AUTHORS WITH POSTERS

- **Session A:** Odd Numbered Posters will present on Saturday, July 13 from 12:30 – 2:20pm
- **Session B:** Even Numbered Posters will present on Sunday, July 14 from 12:30 – 2:20pm
- **Session C:** Odd Numbered Posters will present on Monday, July 15 from 12:30 – 2:20pm
- **Session D:** Even Numbered Posters will present on Tuesday, July 16 from 12:30 – 2:20pm

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

DID YOU KNOW?

- YOUR BADGE IS RECYCLABLE
  - If you don't save your badges, please recycle it
- YOUR LANYARD IS MADE FROM 100% RECYCLED SODA BOTTLE
  - We encourage you to save your lanyard and use it for future conferences

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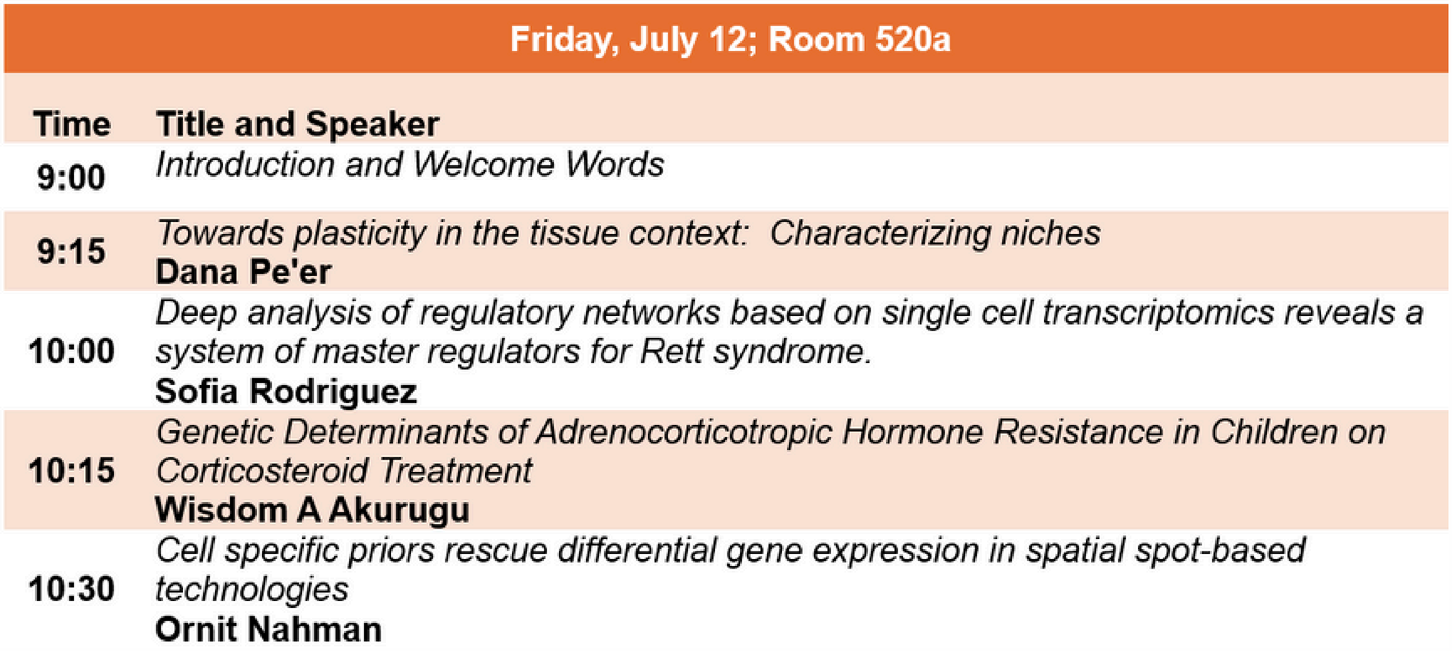
STUDENT COUNCIL SYMPOSIUM

The ISCB Student Council and its Regional Student Groups are organizing the 20th Student Council Symposium (SCS), preceding ISMB 2024 in Montreal, Canada.

The Student Council Symposium is a forum for students and young researchers in the fields of Computational Biology and Bioinformatics. Participants will have the opportunity to present their work to an international audience, build a network within the computational biology community and develop important soft skills in an environment that fosters the exchange of ideas and knowledge.

Date: Friday, July 12
Time: 9:00 – 18:00
Location: Room 520a, Palais des Congrés de Montréal



Friday, July 12; Room 520a

Time	Title and Speaker
9:00	*Introduction and Welcome Words*
9:15	*Towards plasticity in the tissue context: Characterizing niches* **Dana Pe'er**
10:00	*Deep analysis of regulatory networks based on single cell transcriptomics reveals a system of master regulators for Rett syndrome.* **Sofia Rodriguez**
10:15	*Genetic Determinants of Adrenocorticotropic Hormone Resistance in Children on Corticosteroid Treatment* **Wisdom A Akurugu**
10:30	*Cell specific priors rescue differential gene expression in spatial spot-based technologies* **Ornit Nahman**

SCS SCHEDULE CONTINUED

Time	Title and Speaker
10:45	*First Draft Assembly and Annotation of the Genome of the Cadmium-Resistant Fungus Talaromyces santanderensis using Oxford Nanopore sequencing: First Molecular Insights into its Cadmium Resistance.*
10:45	*Constructing representative sequence models for evolutionary analysis of protein superfamilies*
10:45	*Characterization of Non-Equilibrium Phase-Separated Biomolecular Condensates*
10:45	*Multiomics analysis highlighted the role of senescence in regulating trophoblast differentiation: a promising target for early preeclampsia prediction.*
11:25	*Unraveling patient heterogeneity through explainable AI and network-based strategies* **Iria Pose Lagoa**
11:40	*Interpretable deep generative ensemble learning of cell identity paired with automated annotation for single-cell multi-omics* **Manoj M Wagle**
11:55	*Exploring the biophysical boundaries of protein families with deep learning methods* **Miriam Poley-Gil**
12:10	*Utilizing a Novel VAE Pipeline for Tau Inhibitor Screening Validated in Drosophila Melanogaster Alzheimer's Models*
12:15	*Keynote: TBD*
13:00	*Lunch with Poster Session & Networking*
14:55	*FinaleToolkit: Accelerating Cell-Free DNA Fragmentation Analysis with a High-Speed Computational Toolkit*
14:55	*Development and Application of the MultiSEp R Package to Identify Multiple Myeloma Achilles' Heels for Drug Discovery*
14:55	*Bridging Education and Research: Data Hunters Workshop Empowering Bioinformatics Education via Microbiome Studies*
14:55	*Seven Domain Topics in Bioinformatics Education - Refining the ISCB Core Competencies to Access Diversity in Training*
15:15	*The impact of Student Council in your personal and scientific trajectory*
16:30	*Metagenomic sequence analysis: from protein sequences to structures* **Martin Steinegger**
17:30	*Introducing ISCB Student Council activities*
17:35	*Closing remarks*
17:55	*All on stage for picture/photo of the event*

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OPEN SCIENCE SESSIONS

BIOINFORMATICS IN CANADA

Sunday, July 14; Room 520a

Time	Title and Speaker
10:40	*The Silent Genomes Project: Building the path to equitable genomic care for Indigenous patients, one variant at a time.* **Laura Arbour**
11:20	*From Sequences to Reports: A Controlled Approach to Pipeline Validation in Cancer Genomics* **Beatriz Lujan Toro**
11:40	*The Canadian Genomic Data Commons (CGDC): A Platform for National Genomic Data Sharing* **Erika Frangione**
12:00	*Binomify: Unified normalization of ChIP-seq data through negative binomial regression* **Abdul Rahman Diab**
14:20	*About Ag and AI*
15:00	*UseGalaxy Canada now in production* **Pierre-Étienne Jacques**
15:20	*Apollo: A comprehensive GPU-powered Within-host Viral simulator with tissue and cellular hierarchies for studying viral evolutionary and infection dynamics.* **Deshan Perera**
15:40	*Utanos: A general-purpose shallow whole genome sequencing analysis toolkit identifies interpretable copy number signatures* **J Maxwell Douglas**
16:40	*The Quebec Genomic Data Center* **Vincent Ferretti**
17:20	*FraGNNet: A Deep Probabilistic Model for Mass Spectrum Prediction* **Fei Wang**
17:40	*Formation of the Canadian Artificial Intelligence and Mass Spectrometry Consortium (CAN-AIMS)* **Jennifer Geddes-McAlister**

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COMPUTATIONAL AND SYSTEMS IMMUNOLOGY

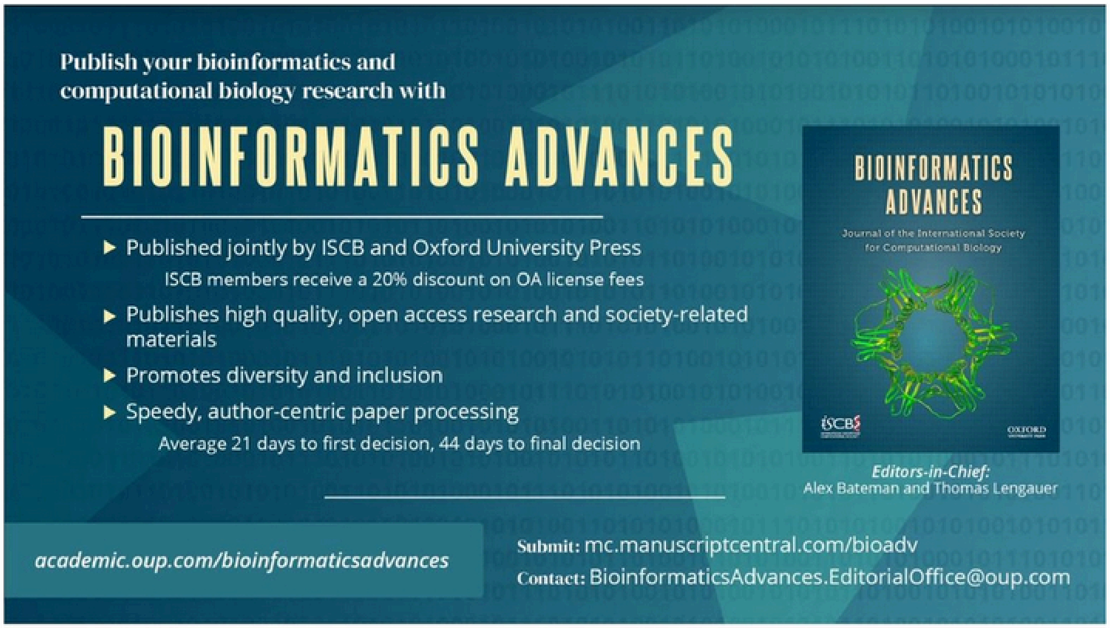
Tuesday, July 16; Room 522	
Time	**Title and Speaker**
9:00	*Building models of CAR-T signal integration, using automatized/dynamic high-dimensional dynamic profiling* **Gregoire Altan-Bonnet**
9:20	*TBD*
9:40	*Inferring B cell phylogenies from single cell and bulk BCR sequence data with Dowser* **Kenneth Hoehn**
10:40	*TBD*
11:00	*Learning multiomic velocities of dynamic germinal center B cells using single-cell multiome* **Alireza Karbalayghareh**
11:20	*Sliding Window INteraction Grammar (SWING): a generalized interaction language model for peptide and protein interactions* **Jane Siwek**
11:40	*Improved Peptide-MHC Interaction Predictions through Deep Generative Adversarial Networks and a Unified MHC Class I and Class II Representation* **Michael Klausen**
11:40	*TSpred: a robust prediction framework for TCR-epitope interactions using paired chain TCR sequence data* **Ha Young Kim**
11:40	*Comprehensive neoantigen identification and prioritization using pVACtools and pVACview* **Susanna Kiwala**
11:40	*Immune checkpoint molecule Tim-3 regulates microglial function and the development of Alzheimerâ€™s disease pathology.* **Ayshwarya Subramanian**
11:40	*Single-cell multi-omics reveals similarity between progenitor stem-cell-like CD8+ T cells and CD4+ follicular helper T cells in viral infection* **Sarah Walker**
11:40	*Optimizing CAR T cell design using quantum convolutional neural networks* **Sara Capponi**
11:40	*A Computational Approach to Auto-Immunity Risk Assessment: Use Cases of Molecular Mimicry Hypothesis for Viral Infections and Vaccines-Associated Adverse Events* **Seda Arat**
14:20	*TBD*
14:40	*sciCSR infers B cell state transition and predicts class-switch recombination dynamics using single-cell transcriptomic data* **Joseph Ng**
15:00	*FineST: Super resolved ligand-receptor interaction discovery by fusing spatial RNA-seq and histology images* **Lingyu Li**
15:20	*Computational integration of cellular circuits and immune repertoires based on multilayer network community association* **Chang Lu**

OPEN SCIENCE SESSIONS

DEMYSTIFYING THE WORLD OF SCIENTIFIC PUBLISHING

Tuesday, July 16; Room 524c

Time	Title and Speaker
10:40	*Welcome & Introductions*
10:40	*Publishing reproducibility, FAIR, and using best practices* **Patricia Palagi**
10:40	*Use of LLMs in writing, plagiarism and text recycling* **Alex Bateman**
11:00	*Open Access Publishing: pros and cons* **David Landsman**
11:00	*Strategies for managing expectations for submission, review, and publication timeline* **Thomas Lengauer**
11:20	*Challenges with reviewers: reviewing fatigue, acknowledgement, and dealing with delays and rejections.* **Scott Edmunds**
11:20	*Emerging Trends in Publishing Computational Biology Research* **Jason Papin**
11:40	*Panel Discussion*
12:15	*Closing*



DIGITAL AGRICULTURE

Tuesday, July; Room 525	
Time	**Title and Speaker**
8:40	*Introductory remarks*
8:41	*Current and new development in Digital Agriculture – Implication of deep learning and robotics in this new data science* **Etienne Lord**
9:20	*Single-plant omics : profiling individual plants in a field to identify processes affecting yield* **Steven Maere**
9:40	*Biomarker-based learning for disease prediction in precision dairy farming* **Hayda Almeida**
10:40	*Empowering Dairy Farmers: A Transformer-Based Framework for Informed Decision Making in Dairy Agriculture* **Vahid Naghashi**
11:00	*Anomaly Detection for Smart Aquaculture: Predicting Water Color Changes in Grouper Ponds* **Kuan Y. Chang**
11:20	*Extracting meaningful video segments using a movement detection algorithm applied to dairy cow behavior study and welfare monitoring.* **Thomas Gisiger**
11:40	*Precision Farming for Profit: Leveraging Profitability Maps and ILPMZ to Optimize Return on Investment and Soil Conservation of Agricultural Fields* **Amanda Ashley Boatswain Jacques**
12:00	*Revolutionizing Livestock Monitoring: AI-Powered Cow Detection in Farm Environments* **Voncarlos Marcelo De Araujo**
14:20	*Temporal Synchronization of Multi-View Video for Cattle Movement Analysis in Dynamic Farm Settings* **Houda Orchi**
14:40	*TBD*
15:20	*HaloClass: State-of-the-art salt tolerant protein classification with natural language models*
15:40	*Final remarks*

OPEN SCIENCE SESSIONS

EQUITY AND DIVERSITY IN COMPUTATIONAL BIOLOGY RESEARCH

Monday, July 15; Room 522

Time	Title and Speaker
10:40	*Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions* **Aritra Bose**
11:00	*Disparate radiomic imaging features are predictive of recurrence events and molecular subtype in Black and White breast cancer patients* **George Acquaah-Mensah**
11:20	*Towards Equitable MHC Binding Predictions: Computational Strategies to Assess and Reduce Data Bias* **Mona Singh**
11:40	*From CABANA to CABANAnet — Building bioinformatics and knowledge exchange capacity in Latin America.* **Selene L Fernandez-Valverde**
12:00	*Closing the computational biology knowledge gap: Spanish Wikipedia as a case study* **Nelly Sélem-Mojica**

ISCB works to maintain an environment that allows science and scientific careers to flourish through respectful, inclusive, and equitable treatment of others and is committed to providing a safe place for its members and nonmember participants. As a statement of principle, ISCB rejects discrimination and harassment by any means, based on factors such as ethnic or national origin, race, religion, citizenship, language, political or other opinion, sex, gender identity, sexual orientation, disability, physical appearance, age, or economic class. In addition, ISCB opposes all forms of bullying including threatening, humiliating, coercive, or intimidating conduct that causes harm to, interferes with, or sabotages scientific activity and careers. Discrimination, harassment (in any form), and bullying create a hostile environment that reduces the quality, integrity, and pace of the advancement of science by marginalizing individuals and communities. It also damages productivity and career advancement and prevents the healthy exchange of ideas.

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All conference delegates are expected to adhere to the ISCB Code of Ethics and Professional Conduct.

ISCB SAFE

iCn3D: VISUALIZING PROTEIN FUNCTION FROM GENES TO BIOLOGY: BACK TO THE FUTURE

Sunday, July 13; Room 524c

Time	Title and Speaker
10:40	*Introduction*
10:50	*Predicting Protein-Protein Interactions* **Barry Honig**
11:20	*Critical assessment in Computational Structural Biology* **John Moult**
11:50	*Protein Structure Accuracy Estimation Using Geometry-Complete Graph Neural Networks* **Jianlin Cheng**
12:10	*The NSF funded iCn3D POSE project*
14:20	*The impact of comparative structure analysis on protein classification at NCBI*
14:35	*From Immersive Visualization to Interdisciplinary Communication*
14:50	*Visualizing Immune Epitope Data: The Innovations of IEDB-3D 2.0* **Marcus De Almeida Mendes**
15:00	*New iCn3D tools for educators: color keys and collections* **Sandra Porter**
15:10	*iCn3D: visualization, analysis & sharing of protein structures and interactions* **Jiyao Wang**
15:25	*Using iCn3D to address molecular structure/function and to bridge the biology and chemistry educational communities* **Henry Jakubowski**
15:40	*RCSB.org: a one-stop shop to explore biology in 3D* **Jose Duarte**
15:50	*Advancing Molecular Graphics: MolviewSpec and Recent Enhancements in Molstar* **Marcelo Querino Lima Afonso**
16:40	*Envisioning the OSE for Biology Research and Education*
16:50	*Community Hackathons*
17:00	*Round Table Discussion*
18:00	*iCn3D Workshop*

NIH/ODSS

Saturday, July 13; 520a

Time	Title and Speaker
10:40	*Opening Remarks*
10:50	*AI/ML to Identify and Stratify Non-Clinical Factors Contributing to Cancer Health Disparity in Rural Appalachia* **Aisha Montgomery**
10:50	*Estimating and Controlling for Fairness in Radiology with Missing Sensitive Information* **Jeremias Sulam**
11:10	*Ethical Development of Imaging Biomarkers for Colorectal Biomarkers* **Rina Khan**
11:10	*Examining how social and behavioral determiants affect the prevalence, severity, and outcomes of Long-COVID-19 and health disparity* **Deborah Mudali**
11:30	*An Ethical Framework-Guided Tool for Assessing Bias in EHR based Big Data Studies* **Bankole Olatosi**
11:30	*Modern, Intuitive Tools for Managing AI/ML Data in Health Equity-Focused Multiomic and Population Studies* **Victor Nwankwo**
11:50	*Use Explainable AI to Improve the Trust of and Detect the Bias of AI Models* **Senait Tekle**
12:00	*Discussion*
14:20	*Deep LTMLE: Scalable Causal Survival Analysis with Transformer* **Toru Shirakawa**
14:20	*Cloud exploration and AI/ML-readiness of CAZyme annotation in human gut microbiome* **Yanbin Yin**
14:20	*Wearable Biosensing to Predict Imminent Aggressive Behavior in Psychiatric Inpatient Youths with Autism* **Matthew Goodwin**
14:20	*Improve speed, scalability, inter-operability of core C++ modules for Stan - a tool doing Bayesian modeling and statistical inference* **Mitzi Morris**
14:40	*LinkML: A FAIR data modeling framework for the biosciences and beyond* **Nomi L Harris**
14:40	*PubTator 3.0: an AI-powered Literature Resource for Unlocking Biomedical Knowledge* **Robert Leaman**
14:40	*Leveraging Language Models for Enhanced Biocuration and User Interaction in Reactome: A Pathway Towards Community-Driven Knowledge Enrichment* **Nancy Li**

NIH/ODSS CONTINUED

Time	Title and Speaker
14:40	*ToxPipe: Harnessing AI and Cloud Computing for Toxicological Data Exploration and Interpretation* **Trey Saddler**
15:00	*Discussion*
16:40	*Multi-Context Graph Neural Networks for Enhanced Multivariate Time-Series Analysis in Healthcare* **Luciano Nocera**
16:40	*Clustering-Informed Shared-Structure Variational Autoencoder for Missing Data Imputation in Large-Scale Healthcare Data* **Yasin Khadem Charvadeh**
17:00	*Predicting and Preventing Adverse Pregnancy Outcomes in Nulliparous Women*
17:00	*SCH: Graph-based Spatial Transcriptomics Computational Methods in Kidney Diseases* **Juexin Wang**
17:20	*AI/ML Ready mHealth and Wearable Data for Dyadic HCT* **Bengie L Ortiz**
17:20	*Enhancing the AI-readiness of gnomAD with GA4GH Genomic Knowledge Standards* **Alex Wagner**
17:40	*Enhancing Imputation for Clinical Research: The Path for aÂ Flexible Toolkit* **Vida Abedi**
17:40	*Closing Remarks*

WEB: 2024: EXPERIENTIAL LEARNING ON HOW TO IMPLEMENT AI IN BIOINFORMATICS TRAINING

Monday, July 15; Room 525

Time	Title and Speaker
10:40	*WEB 2024: Experiential Learning on How to Implement AI in Bioinformatics Training*
14:20	*WEB 2024: Experiential Learning on How to Implement AI in Bioinformatics Training*

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TECHNOLOGY TRACK

Saturday, July 13; Room 524c

Time	Title and Speaker
10:40	*HPC-AI Support for Singapore's Bioinformaticians and Computational Biologists* **Shoba Ranganathan**
11:00	*Traversing the mouse-human interface with a knowledge graph of analytic and data services* **Robyn Ball**
11:20	*Network analyses for functional annotation with FunCoup tools* **Erik Sonnhammer**
11:40	*Advances towards comprehensive and accurate whole genome analysis at scale using DRAGEN accelerated algorithms* **Rami Mehio**
14:20	*Enhancing Clinical Trial Outcomes with AI-based Predictive Biomarker Discovery via Contrastive Learning* **Etai Jacob**
14:40	*Miqa: Automating bioinformatics testing, evaluation and validation for real-time performance data & instant bug detection on every code change* **Gwenn Berry**
15:00	*UniProt: The Universal Protein resource: new features, access and tools for protein data* **Aurélien Luciani**
15:40	*TBD*

Monday, July 15; Room 524c

Time	Title and Speaker
10:40	*Utilizing Pre-Treatment Lab Values & Whole-Lung Radiomics for Modeling Survival Risk for ICB in the mNSCLC Setting* **Kedar Patwardhan**
11:00	*Enhancing Genomic Research through National Collaboration: The Role of Canada's National Data Platform* **Felipe Pérez-Jvostov**
11:20	*The Missense3D portal: Structure-based evaluation of missense variants including protein complexes and transmembrane regions* **Alessia David**
11:40	*Integrated Pathway/Genome/Omics Informatics in Pathway Tools and BioCyc* **Suzanne Paley**
12:00	*CATH and TED: Protein structure classification in the age of AI* **Nicola Bordin**
14:20	*GPCRVS – a machine learning system for GPCR drug discovery* **Paulina Dragan**
14:40	*Modelling multi-omic, real-world data reveals immunogenomic drivers of resistance to cancer immunotherapy*
15:00	*Decoding the grammar of DNA using Natural Language Processing*
15:20	*Transform Healthcare and Life Sciencewith Biomedical Foundation modelsand Quantum computing* **Filippo Utro**

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COSI TRACK SCHEDULES

Monday, July 15; Room 520a

Time	Title and Speaker
10:40	*50 Years of Protein Structures & Structural Bioinformatics* **Janet M Thornton**
11:20	*Democratizing Protein Language Models with Parameter-Efficient Fine-Tuning* **Samuel Sledzieski**
11:40	*EquiPNAS: improved protein–nucleic acid binding site prediction using protein-language-model-informed equivariant deep graph neural networks* **Debswapna Bhattacharya**
12:00	*Accurate High-throughput Cryptic Binding Site Prediction Using Protein Language Model* **Shuo Zhang**
14:20	*Contrastive learning in protein language space predicts interactions between drugs and protein targets* **Rohit Singh**
14:40	*NRGDock: An open-source software for ultra-massive high-throughput virtual screening* **Thomas Descoteaux**
15:00	*Enhancing Generalizability and Performance in Drug-Target Interaction Identification by Integrating Pharmacophore and Pre-trained Models* **Zuolong Zhang**
15:20	*DOCKGROUND: a new release of the long-standing resource for studying protein recognition* **Petras Kundrotas**
15:40	*On finding the right match – a structural perspective* **Marian Novotny**
16:40	*Explaining Conformational Diversity in Protein Families through Molecular Motion* **Valentin Lombard**
16:40	*Pathway of transition for HIV-1 envelope trimer from prefusion-closed to CD4-bound open through an occluded-intermediate state* **Myungjin Lee**
17:00	*Analysis and prediction of RuBisCO kinetics using deep learning* **Aleksey Porollo**
17:20	*Understanding and predicting ligand efficacy in the mu-opioid receptor through quantitative dynamical analysis of complex structures* **Gabriel Galdino**
17:40	*Dynamic network analysis of protein structural change* **Aydin Wells**

Tuesday, July 16; Room 520a

Time	Title and Speaker
8:40	*Metallic origins of life* **Yana Bromberg**
9:20	*De Novo Atomic Protein Structure Modeling for Cryo-EM Density Maps Using 3D Transformer and Hidden Markov Model* **Jianlin Cheng**
9:40	*RiboDiffusion: Tertiary Structure-based RNA Inverse Folding with Generative Diffusion Models* **Han Huang**
10:40	*Positional Protein Bioinformatics: A universal residue numbering scheme for the Immunoglobulin (Ig) fold enables its systemic detection in the protein universe.* **Philippe Youkharibache**
10:50	*ImmunoMatch: Illuminating the design of antibody heavy and light chain pairs using deep learning approaches and structure analysis* **Dongjun Guo**
11:10	*Exploring the biophysical boundaries of protein families with deep learning methods* **Miriam Poley-Gil**
11:30	*Can proteins be represented through secondary structures?*
11:40	*SPfast: Highly efficient protein structure alignment with segment-level representations and block-sparse optimization* **Thomas Litfin**
11:40	*STRPsearch: fast detection of structured tandem repeat proteins* **Alexander Monzon**
12:00	*The Encyclopedia of Domains* **Nicola Bordin**
14:20	*EXPLORING THE IMPACT OF STRESS-RESISTANT MUTATIONS IN PLANTS USING ALPHAFOLD2 PROTEIN STRUCTURES*
14:40	*DDMut-PPI: predicting effects of mutations on protein-protein interactions using graph-based deep learning* **Yunzhuo Zhou**
15:00	*DDAffinity: Predicting the changes in binding affinity of multiple point mutations using protein three-dimensional structure* **Qichang Zhao**
15:20	*A multiscale functional map of somatic mutations in cancer integrating protein structure and network topology* **Yingying Zhang**

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BIO-ONTOLOGIES

Saturday, July 13; Room 522

Time	Title and Speaker
10:40	*COSI Opening Remarks*
10:50	*Learning from our collective scientific ignorance: How can ontologies help us determine what isn't yet?* **Mayla Boguslav**
11:55	*Poster Madness*
14:20	*Integration of Background Knowledge for Automatic Detection of Inconsistencies in Gene Ontology Annotation* **Jiyu Chen**
15:05	*The cyclic nature of biases against understudied genes and diseases in knowledge graph embedding link prediction models* **Michael Bradshaw**
15:30	*Prioritizing Causative Genomic Variants by Integrating Molecular and Functional Annotations from Multiple Biomedical Ontologies* **Azza Althagafi**
16:40	*Taking AIIM at antibiotic resistance: harmonizing the nomenclature for aminoglycoside inactivating enzymes* **Emily Bordeleau**
17:05	*Investigating Food Composition Components in Cancer Prevention and Therapy using Knowledge Graphs* **Hande McGinty**
17:30	*COSI Day 1 Wrap-up*

Sunday, July 14; Room 522

Time	Title and Speaker
10:40	*COSI Announcements*
10:50	*Exploring Multiple Perspectives for Associative Knowledgebases* **Karin Slater**
11:55	*Extracting Clinical Significance for Drug-Gene Interactions using FDA Label Packages* **Matthew Cannon**
14:20	*Predicting protein functions using positive-unlabeled ranking with ontology-based priors* **Fernando Zhapa-Camacho**
15:05	*Protein Function: how much do we know and how much do we care?* **An Phan**
15:30	*Harmonizing human and microbial datasets to explore mechanisms of the gut microbiome in disease* **Brook Santangelo**
16:40	*Using ontologies to make bioassay protocols machine readable* **Alex Clark**
17:05	*Knowledge graphs in Cancer Genomics: The Case of Mutational Signatures* **Ulrike Steindl**
17:30	*COSI Closing Remarks*

BIOINFO-CORE

Sunday, July 14; Room 525

Time	Title and Speaker
10:40	*Building a Future-Proof Resource: The Comprehensive Modernization of TAIR* **Swapnil Sawant**
11:15	*TBA*
11:45	*AI and LLMs in cores: How are we using them now?*
14:20	*Streamlining Bioinformatics Pipelines with Nextflow: A Scalable, Portable, Reproducible, and Collaborative Solution.* **Francesco Lescai**
14:50	*Leveraging the NF-Core Framework for sharable institutional Nextflow modules at Memorial Sloan Kettering Cancer Center* **Nikhil Kumar**
14:50	*UTAP2: User-friendly Transcriptome and Epigenome Analysis Pipeline* **Leshkowitz Dena**
15:10	*Managing Big Data in a High-Throughput Genomics Pipeline* **Grace Pigeau**
15:10	*Novel Linux-style code helps us all down the road* **George Bell**
15:30	*New technologies in cores: single-cell, spatial, etc.*
16:40	*Short Talks, Various topics*
17:10	*Breakout Groups*

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Sunday, July 14; Room 521

Time	Title and Speaker
10:40	*Opening*
10:40	*When Visualization Meets AI: Exploring Opportunities*
11:40	*PRIMAVO: Precision Immune Monitoring Assay Visualization Online* **Zeynep H. Gümüş**
12:00	*The Best of Both Worlds: Blending Mixed Reality and 2D displays in an Hybrid Approach for Visual analysis of 3D Tissue Maps* **Eric Mörth**
14:20	*Understanding Visualization Authoring for Genomics Data through User Interviews* **Sehi L'Yi**
14:20	*New BioCyc Visualization Tools for Genome Exploration and Comparison* **Suzanne Paley**
14:20	*Matreex: compact and interactive visualisation of large gene families* **Yannis Nevers**
14:20	*Interactive visualisation of raw nanopore signal data with Squigualiser* **Hiruna Samarakoon**
14:20	*Aggregate Annotated Single-Cell Heatmap Visualizations* **Devin Lange**
15:20	*Aardvark: Composite Visualizations of Trees, Time-Series, and Images* **Devin Lange**
15:40	*Boosting Data Interpretation with GIBOOST to Enhance Visualization of High-Dimensional Data* **Komlan Atitey**
16:40	*Unveil Cis-acting Combinatorial mRNA Motifs by Interpreting Deep Neural Network* **Xiaocheng Zeng**
17:00	*The Insight's in the Details: Challenges and Opportunities in Visually Exploring High-Dimensional BioMedical Data* **Fritz Lekschas**
17:00	*Award Ceremony and Closing*

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Monday, July 15; Room 524ab

Time	Title and Speaker
10:40	*Opening Remarks*
10:40	*Open Bioinformatics Foundation Update*
10:40	*CoFest Intro*
10:40	*Platinum and Gold Sponsor Videos*
11:00	*Gemma: Curation, re-analysis and dissemination of 18,000 gene expression studies* **Paul Pavlidis**
11:20	*EASTR: Identifying and eliminating systematic alignment errors in multi-exon genes* **Ida Shinder**
11:20	*ROC Picker: propagating statistical and systematic uncertainties in biological analyses* **Jeffrey Roskes**
11:20	*Djerba: Sharing and Updating a Modular System for Clinical Report Generation* **Iain Bancarz**
11:20	*Q&A For Flash Talks*
11:40	*Antimicrobial resistance prediction of nontuberculous mycobacteria from whole genome sequence data* **Idowu Olawoye**
12:00	*Open2C: Advancing 3D and functional genomics research* **Vedat Yilmaz**
12:00	*A Framework for DNA Binding Motifs Prediction for Nontraditional Model Organism Transcription Factors* **Stephanie Hao**
12:00	*Bioinformatics tools for comparative genomics analysis of highly similar duplicate genes in eukaryotic genomes* **Xi Zhang**
12:00	*Q&A For Flash Talks*
14:20	*The Data Shows We Need Better Data* **Mélanie Courtot**
15:20	*Creating an open-source data platform.* **Mitchell Shiell**

Time	Title and Speaker
15:40	*Going Viral: The Development of the VirusSeq Data Portal* **Justin Richardsson**
15:40	*intermine.bio2rdf.org : A QLever SPARQL endpoint for InterMine databases* **François Belleau**
15:40	*Organizing community curation to create an Open database on Thermodynamics of Enzyme-Catalyzed Reactions (openTECR)* **Robert T. Giessmann**
15:40	*Q&A For Flash Talks*
16:40	*Connecting Integrated Genome Browser to a huge genome database using its open API solves one problem and creates another* **Ann Loraine**
17:00	*Collaborating our way to optimal integration between Tripal 4 and JBrowse 2* **Carolyn T. Caron**
17:00	*An integrated environment for browsing 3-D protein structures and multiple sequence alignments in JBrowse 2* **Colin Diesh**
17:00	*iCn3D, a Platform to Integrate Structures with Functions and Genomics* **Jiyao Wang**
17:00	*Q&A For Flash Talks*
17:20	*Codefair: Make Biomedical Research Software FAIR Without Breaking a Sweat* **Bhavesh Patel**
17:20	*An Open-source Ecosystem For Scalable And Computationally Efficient Nanopore Data Processing* **Hasindu Gamaarachchi**
17:20	*GenomeKit, a Python library for fast and easy access to genomic resources* **Avishai Weissberg**
17:20	*Q&A For Flash Talks*
17:40	*Tataki: Enhancing the robustness of bioinformatics workflows with simple, tolerant file format detection* **Masaki Fukui**
17:40	*BiocPy: Facilitate Bioconductor Workflows in Python* **Jayaram Kancherla**
17:40	*Arvados Project Update* **Peter Amstutz**
17:40	*Q&A For Flash Talks*

Tuesday, July 16; Room 524ab

Time	Title and Speaker
8:40	*Enhancing Reproducibility in Immunogenetics: Leveraging Containerization Technology for Bioinformatics Workflows* **Rayo Suseno**
9:00	*Breaking the silo: composable bioinformatics through cross-disciplinary open standards* **Nezar Abdennur**
9:20	*For long-term sustainable software in bioinformatics: a manifesto* **Luis Pedro Coelho**
9:20	*BioCompute: A Descriptive Standard for Computable Metadata* **Jonathon Keeney**
9:20	*Breaking Down Research Silos and Fostering Radical Collaboration through Collective Intelligence* **Alberto Pepe**
9:20	*Q&A For Flash Talks*
9:40	*Tripal: a community-driven framework supporting open science, sustainable data web portals* **Lacey-Anne Sanderson**
10:40	*Open Data, Knowledge Graphs, and Large Language Models* **Andrew Su**
11:40	*Gene Set Summarization Using Large Language Models* **Marcin Joachimiak**
12:00	*FAIR, modular and reproducible image-based ML workflows for biologists: a template and case study from imageomics* **Hilmar Lapp**
14:20	*Trust and Transparency in Reporting Machine Learning: The DOME-GigaScience Press Trial* **Chris Armit**
14:40	*Open Approaches to AI/ML in Bioinformatics*

Monday, July 15; Room 520b

Time	Title and Speaker
10:40	*Welcome & Overview*
11:00	*CAMDA Keynote: Exploring drivers of gut microbiome compositional differences in disease and mechanistic pathways to recovery using big data* **Catherine Lozupone**
14:20	*The Gut Microbiome based Health Index Challenge - Introduction* **Kinga Zielińska**
14:50	*Integrating Taxonomic and Functional Features for Gut Microbiome Health Indexing* **Rafael Perez Estrada**
15:20	*Using Gradient Boosting to Predict Health States from Composition and Function of the Gut Microbiome* **Patrick Smyth**
15:40	*Microbiome time series data reveal predictable patterns of change* **Karwowska Zuzanna**
16:40	*Prediction in microbiome science* **Jesse Shapiro**
17:10	*The Elephant in the Room: Software and Hardware Security Vulnerabilities of Portable Sequencing Devices*
17:10	*Improving genomic epidemiology of Giardia intestinalis with a core genome gene-by-gene subtyping schema*
17:30	*Analysis of Inverted Repeats in Viral Genomes at a Large Scale*
17:30	*Intgration of Spatial Transcriptomics into Multimodal Imaging of Skin Aging*
17:50	*CAMDA 1st day summary*

Tuesday, July 16; Room 520b

Time	Title and Speaker
8:40	*Computational dissection of complex human disease* **Andrey Rzhetsky**
10:40	*The Synthetic Clinical Health Records Challenge - Introduction* **Joaquin Dopazo**
11:10	*Predicting Diabetes Complications from Electronic Health Record Visits Using Machine Learning Algorithms* **Daniel Voskergian**
11:30	*Cluster-based machine learning prediction of diabetes complications* **Daniel Santana-Quinteros**
11:50	*Statistical Measures for the Evaluation of Clustering Methods on Single Cell Data* **Owen Visser**
14:20	*The Anti-Microbial Resistance Prediction Challenge - Introduction*
14:25	*The Antimicrobial Resistance Prediction Challenge* **Alper Yurtseven**
14:55	*Machine learning models for AMR prediction* **Anton Pashkov**
15:15	*Biomarker identification by interpretable Maximum Mean Discrepancy* **Dexiong Chen**
15:35	*CAMDA Trophy ceremony*
15:45	*CAMDA summary and closing remarks*

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Saturday, July 13; Room 525

Time	Title and Speaker
10:40	*Disruption of ClpX reverses antifungal resistance* **Jennifer Geddes-McAlister**
11:20	*Perception and reality of FDR control, data completeness and quantitative precision in (single-cell proteomics) DIA data* **Martin Frejno**
11:20	*A novel supervised learning algorithm for real-time collision energy selection to optimize peptide fragmentation in mass spectrometry* **Mathieu Lavallée-Adam**
11:40	*A learned score function improves the power of mass spectrometry database search* **Varun Ananth**
12:00	*Multi-Omic Data Workflows for Drug Discovery and Development* **Matthew Glover**
14:20	*A unified LC-MS metabolomics framework for multi-omics and systems biology* **Jianguo Xia**
15:00	*waveome: characterizing temporal dynamics of metabolites in longitudinal studies* **Ali Rahnavard**
15:00	*AI-driven de novo structural candidate generation for mass spectra annotation* **Margaret Martin**
15:00	*A consensus serum metabolome by large-scale data mining reveals major gaps in metabolomic measurements and modeling* **Yuanye Chi**
15:00	*Transformers for MALDI-TOF MS-based antimicrobial drug recommendation* **Gaetan De Waele**
15:40	*The sky is the limit: a cloud-based proteomics platform for the masses* **Martin Frejno**
16:40	*SpecEncoder: Deep Metric Learning for Accurate Peptide Identification in Proteomics* **Haixu Tang**
17:00	*FLASHTagger: An open-source web application for ion type- and precursor mass-free protein identification in top-down mass spectrometry* **Kyowon Jeong**
17:00	*Imputation of cancer proteomics data with a deep model that learns jointly from many datasets* **Lincoln Harris**
17:00	*Proteogenomics analysis of human tissues using pangenomes* **Husen M. Umer**
17:00	*Optimising Thermal Proteome Profiling experimental design with GPMelt* **Cecile Le Sueur**
17:40	*An algorithm for decoy-free false discovery rate estimation in XL-MS/MS* **Shantanu Jain**

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Saturday, July 13; Room 521

Time	Title and Speaker
10:40	*Expanding data science training and health innovations in Africa: the DS-I Africa Consortium* **Rolanda Julius**
11:20	*Expanding the ISCB competency framework to describe professionals in bioinformatics core facilities* **Marta Lloret-Llinares**
11:40	*Seven Domain Topics in Bioinformatics Education - Refining the ISCB Core Competencies to Access Diversity in Training* **Nilson Coimbra**
12:00	*Support consistent, competent practice for data science in pathogen genomics: the development of an innovative competency framework* **Dusanka Nikolic**
14:20	*Bridging Education and Research: Data Hunters Workshop Empowering Bioinformatics Education via Microbiome Studies* **Sara Fumagalli**
14:40	*Increasing training access with a new Distributed workshop model* **Nia Hughes**
15:00	*Learning through play: using games in bioinformatics training* **Anna Swan**
15:20	*Empowering Global Genomic Innovation: The BioDev Network's Educational Blueprint for Cutting-Edge Science and Inclusion* **Priyanka Surana**
15:40	*Report from New York City: Bioinformatics Education Summit 2024*
16:40	*Teaching Bioinformatics through the Analysis of SARS-CoV-2: Project-Based Training for Computer Science Students* **Pavlin G. Poličar**
17:20	*Celebrating 25 Years of Bioinformatics.ca* **Francis Ouellette**

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Monday, July 15; Room 518

Time	Title and Speaker
10:40	*Median and Small Parsimony Problems on RNA trees* **Bertrand Marchand**
11:10	*Inferring transcript phylogenies based on precomputed groups of conserved transcripts* **Wend Yam Donald Davy Ouedraogo**
11:20	*A Representation for Phylogenetic Trees and Networks* **Louxin Zhang**
11:40	*Accurate, scalable, and fully automated inference of species trees from raw genome assemblies using ROADIES* **Anshu Gupta**
12:00	*Generalized c/μ Ratio Test for Detecting Molecular Adaptation: Beyond the conventional Ka/Ks Ratio test without Assuming Synonymous Site Neutrality or Limitation to Translated Regions* **Chun Wu**
12:00	*AlphaHOGs, a protein structure-based reference classification to improve orthology inference* **Christophe Dessimoz**
14:20	*Joint inference of cell lineage and mitochondrial evolution from single-cell sequencing data* **Viola Chen**
14:50	*Tracking tumorigenesis and the transition state through copy number variation-based pseudotime* **Jonghyun Lee**
15:00	*SPICE: Probabilistic reconstruction of copy-number evolution in cancer* **Abigail Bunkum**
15:20	*Uncovering Cancer's Fitness Landscape* **Meaghan Parks**
15:40	*Measuring pseudogenes' kinship to unravel overlooked evolutionary patterns* **Valeriia Vasylieva**
15:40	*Pseudogenes in plasmid genomes reveal past transitions in plasmid mobility* **Dustin Hanke**
16:40	*Long range segmentation of prokaryotic genomes by gene age and functionality* **Yuri Wolf**
17:00	*The evolution of antibiotic resistance islands occurs within the framework of plasmid lineages* **Yiqing Wang**
17:00	*Elucidating the Co-Evolution and Genetic Diversity of Acquired Phototrophy in Marine Worm Convolutriloba longifissura* **Adena Collens**
17:20	*Quality assessment of gene repertoires with OMArk* **Yannis Nevers**
17:40	*Leveraging machine learning to predict antimicrobial resistance in ESKAPE pathogens* **Ethan Wolfe**
17:40	*Predicting pathogen preferences and host adaptation by leveraging microbial genomics and machine learning* **Evan Brenner**

Tuesday, July 16; Room 518

Time	Title and Speaker
8:40	*Maximum Likelihood Phylogeographic Inference of Cell Motility and Cell Division from Spatial Lineage Tracing Data* **Gary Hu**
9:10	*Interpretable variational encoding of genotypes identifies comprehensive clonality and lineages in single cells geometrically* **Hoi Man Chung**
9:20	*PHALCON: Phylogeny-aware variant calling from large-scale single-cell panel sequencing datasets* **Priya**
9:40	*Genome streamlining: effect of mutation rate and population size on genome size reduction* **Juliette Luiselli**
9:40	*Evolutionary dynamics of microRNAs pinpoint innovations in the gene regulatory network of vertebrates* **Felix Langschied**
10:40	*A machine-learning based alternative to phylogenetic bootstrap* **Tal Pupko**
11:10	*Neutral variation in a protein interaction network limits predictability of protein evolution* **Soham Dibyachintan**
11:20	*Simultaneously Building and Reconciling a Synteny Tree* **Mathieu Gascon**
11:40	*ntSynt: multi-genome synteny detection using minimizer graph mappings* **Inanc Birol**
14:20	*Automated clade-level detection of Incomplete lineage sorting* **Maureen Stolzer**
14:40	*Sparse Neighbor Joining: rapid phylogenetic inference using a sparse distance matrix* **Semih Kurt**
15:00	*Scalable distance-based phylogeny inference using divide-and-conquer* **Lars Arvestad**
15:20	*Impact of Vaccination on SARS-CoV-2 Evolution and Immune Escape Variants*
15:40	*Panel session*

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FUNCTION

Saturday, July 13; Room 520b

Time	Title and Speaker
10:40	*Roll Call and Introduction to the Function COSI*
11:00	*Linking Gene and function in the post-genomic era: issues and opportunities* **Valerie de Crécy-Lagard**
11:40	*Unveiling the Functional Fate of Duplicated Genes Through Expression Profiling* **Alex Warwick Vesztrocy**
12:00	*Leveraging deep learning for characterization of malaria parasite PUFs – proteins of unknown function* **Harsh R. Srivastava**
14:20	*Crowdsoursing the Fifth Critical Assessment of Protein Function Annotation Algorithms (CAFA 5)* **M. Clara De Paolis Kaluza**
15:00	*StarFunc: interplaying template-based and deep learning approach for accurate protein function prediction* **Chengxin Zhang**
15:20	*ProtBoost: Prediction of functional properties of the proteins by Py-Boost and protein language models (CAFA5 top2)* **Alexander Chervov**
15:40	*GORetriever: Reranking protein-description-based GO candidates by literature-driven deep information retrieval for precise protein function annotation* **Huiying Yan**
16:40	*InterLabelGO+: Unraveling label correlations in protein function prediction* **Quancheng Liu**
17:00	*Discovery of PETases using a computational classification system* **Joel Roca Martinez**
17:20	*Plastic-Ml-Tool, a machine learning tool for discovering and optimising plastic degrading enzymes* **David Medina-Ortiz**
17:40	*A BLAST from the past: revisiting BLAST's E-value* **Yang Lu**

FUNCTION

Sunday, July 14; Room 520b

Time	Title and Speaker
10:40	*Fast, high-performance biophysics-based computational methods in function prediction* **Rafael Najmanovich**
11:20	*Energetic Local Frustration Through Time and Species* **R. Gonzalo Parra**
11:40	*Function Prediction of Intrinsically Disordered Proteins and Regions: A Graph Auto-Encoder Approach* **Mahta Mehdiabadi**
12:00	*Mapping the affinity of protein-protein interactions with multiple amino acid mutations using deep neural networks* **Yaron Orenstein**
14:20	*Utilising Large Language Models for GO Term Extraction in UniProt Annotation* **Vishal Joshi**
14:40	*ProstGOPred: Advancing Protein Function Prediction through Graph Contrastive Learning and Structure-Aware Protein Language Model Embeddings* **Weining Lin**
15:00	*Evaluation of large language models for discovery of gene set function* **Mengzhou Hu**
15:20	*Transformer based data mining for predicting moonlighting in proteins and comparison with first principle annotation* **Dana Varghese**
15:40	*Gene families of unknown function conserved across Fungi* **Asaf Salamov**
16:40	*Improved prediction of DNA and RNA binding proteins with deep learning models* **Jun-Tao Guo**
17:00	*Analysing multifunctional proteins with MultifacetedProtDB* **Giulia Babbi**
17:20	*Dynamic network analysis of multi-scale -omics data for protein function prediction* **Siyu Yang**
17:40	*Enhanced Functional Annotation for Genome-Scale Metabolic Models Using an Omics-Informed Integrated Pipeline* **Jason Mcdermott**

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Saturday, July 13; Room 519

Time	Title and Speaker
10:40	*Welcome*
10:45	*Unsupervised learning approaches for genomics to decipher structure and dynamics of 3D genome organization and gene regulatory networks* **Sushmita Roy**
11:40	*An Adaptive K-Nearest Neighbor Graph Optimized for Single-cell and Spatial Clustering* **Qi Liu**
12:00	*Forseti: A mechanistic and predictive model of the splicing status of scRNA-seq reads* **Yuan Gao**
14:20	*Sigmoni: classification of nanopore signal with a compressed pangenome index* **Vikram Shivakumar**
14:40	*Label-guided seed-chain-extend alignment on annotated De Bruijn graphs* **Harun Mustafa**
15:00	*Compressed Indexing for Pangenome Substring Queries* **Stephen Hwang**
15:20	*Sequence-to-graph alignment based copy number calling using a flow network formulation* **Hugo Magalhães**
15:40	*Targeted genotyping of complex polymorphic genes using short and long reads* **Timofey Prodanov**
16:40	*VISTA: An integrated framework for structural variant discovery* **Varuni Sarwal**
17:00	*Long-read sequencing and pangenome perspective of structural variation*

HITSEQ

HiTSeq

Sunday, July 14; Room 517d

Time	Title and Speaker
10:40	*Why and how long reads are used to improve gene isoform quantification*
11:40	*Telomere-to-telomere assembly by preserving contained reads* **Sudhanva Shyam Kamath**
12:00	*Rawsamble: Overlapping and Assembling Raw Nanopore Signals using a Hash-based Seeding Mechanism* **Can Firtina**
14:20	*Conway-Bromage-Lyndon (CBL): an exact, dynamic representation of k-mer sets* **Igor Martayan**
14:40	*Learning Locality-Sensitive Bucketing Functions* **Xin Yuan**
15:00	*Fast Multiple Sequence Alignment via Multi-Armed Bandits* **Kayvon Mazooji**
15:20	*Contrasting and Combining Transcriptome Complexity Captured by Short and Long RNA Sequencing Reads* **Seong Woo Han**
15:40	*Quantum Computing for Genomic Analysis* **Sergii Strelchuk**
16:40	*Adaptive Digital Tissue Deconvolution* **Franziska Görtler**
17:00	*Maximizing accuracy of cellular deconvolution. (ACeD)* **Jonathan Bard**
17:20	*Evolution of genomic and epigenomic heterogeneity in prostate cancer from tissue and liquid biopsy* **Marjorie Roskes**
17:40	*Accurate and robust bootstrap inference of single-cell phylogenies by integrating sequencing read counts* **Rija Zaidi**

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Saturday, July 13; Room 519

Time	Title and Speaker
10:40	*Introduction to iRNA track*
10:50	*SPLASH is a reference-free statistical algorithm, unifying biological discovery in RNA-seq, single cell sequencing and beyond*
11:30	*Hybrid exons build genome-wide proteomic complexity* **Zachary Wakefield**
11:50	*Splicing-derived neo-epitopes in pediatric high-grade glioma* **Priyanka Sehgal**
12:00	*Flash talks to advertise the posters*
14:20	*Accurate Assembly of Multiple RNA-seq Samples with Aletsch* **Qian Shi**
14:40	*Detecting differential transcript usage in heterogenous populations with SPIT* **Beril Erdogdu**
15:00	*Bias analysis for long-reads transcriptomics multi-sample datasets* **Ana Victoria Conesa Cegarra**
15:00	*RISE: Relative Impact of Splicing and Expression in RNA-seq studies* **Yu-Jen Lin**
15:00	*From Noise to Signal: Quantifying Stochasticity in mRNA Splicing* **Eraj Khokhar**
15:30	*Deciphering Transcriptional Bursting Using Single-Cell Metabolic Labeling Data* **Teresa Rummel**
15:50	*Coordinated regulation by lncRNAs results in tight lncRNA-target couplings* **Pavel Sumazin**
16:40	*SWARM: Single-molecule Workflow for Analysing RNA Modifications* **Stefan Prodic**
17:00	*Refinement of SARS-CoV-2 Intra-host Mutations Using Explainable Representations* **Fatima Mostefai**
17:20	*Tackling the genotype-to-phenotype problem in cancer evolution* **Ashley Laughney**

Sunday, July 14; Room 519

Time	Title and Speaker
10:40	*Interpretable models to understand regulation of RNA splicing* **Christopher Burge**
11:20	*IsoCLR: Contrastive learning for RNA foundation models* **Ruian Shi**
11:40	*Explaining Deep Neural Networks for the Prediction of Translation Initiation* **Uwe Ohler**
12:00	*Translational efficiency covariation across cell types is a conserved organizing principle of mammalian transcriptomes* **Can Cenik**
14:20	*CellRBP: Improving Protein-RNA Binding Prediction In Vivo Using Cell-Type-Specific Features* **Yaron Orenstein**
14:40	*Reconstructing the sequence specificities of RNA-binding proteins across eukaryotes* **Kaitlin Laverty**
15:00	*A novel NLP-based RBP binding motif and context discovery method using multiple-instance learning* **Shaimae Elhajjajy**
15:10	*snoFlake: Discovery of a snoRNA-guided splicing regulatory complex via the snoRNA-RBP interactome* **Kristina Sungeun Song**
15:30	*scTail: precise polyadenylation site detection and its alternative usage analysis from reads 1 preserved 3' scRNA-seq data* **Ruiyan Hou**
15:40	*G4mer: Transcriptome-wide prediction of RNA G-quadruplexes with a deep RNA language model* **Farica Zhuang**
16:40	*Fast and accurate RNA virtual screening using non-canonical RNA base pair interaction networks and graph machine learning* **Jérôme Waldispühl**
17:20	*Partial RNA Design* **Frederic Runge**
17:40	*High resolution deconvolution of RNA secondary structure via long read nanopore technology* **J. White Bear**
17:50	*Conclusion and awards*

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MICROBIOME

Saturday, July 13; Room 520c

Time	Title and Speaker
10:40	*Towards fully genome-resolved metagenomics* **Christopher Quince**
11:25	*Effective binning of metagenomic contigs using contrastive multi-view representation learning* **Shanfeng Zhu**
11:40	*Floria: Fast and accurate strain haplotyping in metagenomes* **Jim Shaw**
12:00	*The impact of transitive annotation on the training of taxonomic classifiers* **Mihai Pop**
12:00	*Sensitive, specific association of microbial functions with host phenotypes using Phylogenize2* **Patrick Bradley**
14:20	*Reference-free Structural Variant Detection in Microbiomes via Long-read Co-assembly Graphs* **Kristen Curry**
14:40	*Targeted Sequencing and Triplet Loss classification allow for microbiome-based inference of soil sample origin* **Paweł P. Łabaj**
14:55	*Integration and analysis of 168,000 human gut microbiome samples* **Samantha Graham**
15:10	*MC-Funcformer: A foundational model of microbial community metabolism* **Ananthan Nambiar**
15:10	*Assessing Microbial Genome Representation Across Various Reference Databases: A Comprehensive Evaluation* **Serghei Mangul**
15:30	*A rigorous benchmarking of methods for SARS-CoV-2 lineage abundance estimation in wastewater* **Victor Gordeev**
15:30	*MetaViz: Realistic assortment of novel metagenomics benchmarks with diverse biological and technological characteristics* **Nitesh Kumar Sharma**
15:30	*Phage Host Prediction Using Novel Global-Scale Phage-Host Interaction Atlas and Genomic Language Models* **Jonas Grove**
16:40	*Towards more accurate microbial source tracking via non-negative matrix factorization (NMF)* **Yanni Sun**
17:00	*Carbohydrate-active enzyme annotation in microbiomes using dbCAN3* Yanbin Yin
17:15	*NUTRIclock, NEURAL NETWORKS ANALYSIS OF MICROBIOME FOR IMPLEMENTING PRECISSION NUTRITION IN AGING.* **Adrian Martin-Segura**
17:30	*MIOSTONE: Modeling microbiome-trait associations with taxonomy-adaptive neural networks* **Yifan Jiang**
17:40	*Critical Assessment of Metagenome Interpretation - Updates and Future Benchmarking Challenges* **Alice McHardy**

Sunday, July 14; Room 520c

Time	Title and Speaker
10:40	*Sequence-based interrogation of soil microbiomes and their ecosystem benefits* **Susannah Tringe**
11:25	*Understanding the small proteins from the global microbiome* **Luis Pedro Coelho**
11:40	*Multi-level analysis of the gut–brain axis shows autism spectrum disorder-associated molecular and microbial profiles* **James Morton**
11:55	*Metagenomic Mining Reveals Niche-Specific Bilirubin Reductases in the Gut Microbiome* **Xiaofang Jiang**
14:20	*Scalable de novo Classification of Antimicrobial Resistance of Mycobacterium Tuberculosis* **Christina Boucher**
14:40	*Genomic analysis reveals dysregulation of the intratumor microbiome related to immune response in lung cancer* **Youping Deng**
14:40	*Bioinformatics exploration of bacterial communities and plastic-degrading laccase from the gut microbiomes of plastic degrading beetle larvae* **Jithin Sunny**

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Monday, July 15; Room 517d

Time	Title and Speaker
10:40	*How generative AI can transform biomedical research*
11:30	*SPRITE: improving spatial gene expression imputation with gene and cell networks* **Eric Sun**
11:40	*Deciphering High-order Structures in Spatial Transcriptomes with Graph-guided Tucker Decomposition* **Charles Broadbent**
12:00	*CellPie: a fast spatial transcriptomics factor discovery method via joint factorization of gene expression and imaging data*
12:10	*Integrating patients in time series clinical transcriptomics data* **Sachin Mathur**
14:20	*Learning the Language of Biology: Transforming Biomedical Discovery with Foundation Models and Causal Inference*
15:10	*Deep Reinforcement Learning for Controlled Traversing of the Attractor Landscape of Boolean Models in the Context of Cellular Reprogramming* **Jakub Zarzycki**
15:20	*AttentionPert: Accurately Modeling Multiplexed Genetic Perturbations with Multi-scale Effects* **Ding Bai**
15:40	*Predicting single-cell cellular responses to perturbations using cycle consistency learning* **Wei Huang**
16:40	*The role of chromatin state in intron retention: a case study in leveraging large scale deep learning models* **Asa Ben-Hur**
16:40	*Predicting interchromosomal Hi-C contacts from DNA sequence with TwinC* **Anupama Jha**
17:00	*MolPLA: A Molecular Pre-training Framework for Learning Cores, R-Groups and their Linker Joints* **Mogan Gim**
17:20	*Deep generative models for RNA splicing predictions and design* **Yoseph Barash**
17:20	*NEAR: Neural Embeddings for Amino acid Relationships* **Daniel Olson**
17:40	*Machine learning-enabled highly multiplexed monitoring of subcellular protein localization in live cells* **Jiri Reinis**
17:40	*PTM-Mamba: A PTM-Aware Protein Language Model with Bidirectional Gated Mamba Blocks* **Zhangzhi Peng**

Tuesday, July 16; Room 517d

Time	Title and Speaker
8:40	*Domain adaptation for cell-free DNA fragmentomics* **Natalie Davidson**
8:40	*DeepROCK: Error-controlled interaction detection in deep neural networks* **Yang Lu**
9:00	*CODEX: COunterfactual Deep learning for the in-silico EXploration of cancer cell line perturbations* **Stefan Schrod**
9:20	*A statistical method for migration history inference reveals alternative patterns of metastatic dissemination, clonality and phyleticity* **Divya Koyyalagunta**
9:20	*A deep learning model of tumor cell architecture elucidates response and resistance to CDK4/6 inhibitors* **Sungjoon Park**
9:40	*oncotree2vec â€“ A method for embedding and clustering of tumor mutation trees* **Monica-Andreea Baciu-Dragan**
10:40	*Deep learning of personal genomes* **Sara Mostafavi**
11:30	*ConfuseNN: Interpreting convolutional neural network inferences in population genomics with data shuffling* **Linh Tran**
11:40	*Trustworthy AI in the life sciences*
14:20	*Towards spatiotemporal design principles in multicellular systems*
15:10	*Probabilistic Pathway-based Multimodal Factor Analysis* **Alexander Immer**
15:30	*SLIDE: Significant Latent Factor Interaction Discovery and Exploration across biological domains* **Jishnu Das**

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NETBIO

Sunday, July 14; Room 520c

Time	Title and Speaker
15:10	*NetBio Opening*
15:20	*Towards semantic representation and causal inference in biomedicine. Challenges and applications* **Sergio Baranzini**
16:40	*Modeling metastatic progression from cross-sectional cancer genomics data* **Kevin Rupp**
17:00	*Multi-omics systems biology approach identifies novel signature genes for neuropsychiatric disorders*
17:20	*Improved community detection through signed graphs in single-cell co-expression networks* **Luis Augusto Eijy Nagai**
17:40	*Fast Gene Regulatory Network Inference in Single-cell RNA-Seq with RegDiffusion* **Hao Zhu**

Monday, July 15; Room 520c

Time	Title and Speaker
10:40	*Using proximity-dependent biotinylation to understand dynamic cell organization* **Anne-Claude Gingras**
11:20	*GraphCompass: Spatial metrics for differential analyses of cell organization across conditions* **Merel Kuijs**
11:40	*Functional analysis of MS-based proteomics data: from protein groups to networks* **Nadezhda T. Doncheva**
12:00	*Direct Contacts 2: identification of direct physical interactions from > 25,000 mass spectrometry experiments* **Kevin Drew**
14:20	*Identifying new cancer genes based on the integration of annotated gene sets via hypergraph neural networks* **Chao Deng**
14:40	*Are under-studied proteins under-represented? How to fairly evaluate link prediction algorithms in network biology* **Mehmet Koyutürk**
15:00	*Protein Large Language Models are Effective, Generalized Protein-Protein Interaction Predictors* **Joseph Szymborski**
15:20	*Addressing data scarcity in biomedical research using Multilayer Networks* **Iker Núñez Carpintero**
15:40	*Target repositioning using multi-layer networks and machine learning: the case of prostate cancer* **Milan Picard**
16:40	*Transfer Learning of Condition-Specific Perturbation in Gene Interactions Improves Drug Response Prediction* **Dongmin Bang**
17:00	*Draphnet: Learning the drug and phenotype network linking drug effects to disease genetics* **Rachel Melamed**
17:20	*Blending Biology, Chemistry and AI through network embeddings* **Patrick Aloy**

Saturday, July 13; Room 518

Time	Title and Speaker
10:40	*Continual improvement of cis-regulatory models* **Carl de Boer**
11:20	*Interpreting Cis-Regulatory Interactions from Large-Scale Deep Neural Networks for Genomics* **Peter Koo**
11:40	*Chromatin accessibility is driven by intra-nucleosomal pioneer cooperativity that includes low affinity motifs* **Melanie Weilert**
12:00	*Characterizing transcription factor binding with multi-omics sequence model*
12:00	*Protein Language Models improve the target prediction of nucleic acid-binding proteins*
12:00	*DNA language models reveal the architecture of nucleotide dependencies in genomes* **Pedro Tomaz da Silva**
12:00	*LoopHunter: Enhancing Chromatin Loop Annotation by Focusing on Larger Regions in Hi-C Data*
12:00	*A systematic comparison of Machine learning methods for the prediction of enhancer-gene interactions from epigenomic data*
12:00	*Q&A for Flash Talks*
14:20	*Integrative modeling of multiscale single-cell spatial epigenome* **Jian Ma**
15:00	*Enhancing Hi-C contact matrices for loop detection with Capricorn, a multi-view diffusion model* **William Noble**
15:20	*Ultra-long-range and interchromosomal loops link T cell superenhancers* **Gabriel Dolsten**
15:40	*scGrapHiC: Deep learning-based graph deconvolution for Hi-C using single cell gene expression* **Ghulam Murtaza**
16:40	*Cross-species and tissue imputation of species-level DNA methylation samples across mammalian species* **Emily Maciejewski**
17:00	*Ontology-aware prediction of tissue-specific DNA methylation* **Mirae Kim**
17:20	*Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome* **Michael Hoffman**

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Sunday, July 14; Room 518

Time	Title and Speaker
10:40	*Single-cell and single-molecule computational epigenomics* **Maria Colomé Tatché**
11:20	*REUNION: transcription factor binding prediction and regulatory association inference from single-cell multi-omics data* **Yang Yang**
11:40	*scHOCMO: Higher Order Correlation Model for Single-cell Multi-omics* **Reetika Ghag**
12:00	*Pan-cell type continuous chromatin state annotation of all IHEC epigenomes*
12:00	*Automated and genome-scale exploration of the cis-regulatory code involved in neuronal differentiation*
12:00	*Expanding GTEx dataset with brain ontology-based graph neural networks to investigate genetic impacts on brain diseases*
12:00	*Interpretable single-cell factor decomposition using sciRED*
12:00	*Accurate allocation of multi-mapped reads enables regulatory element analysis at repeats* **Shaun Mahony**
12:00	*Q&A for Flash Talks*
14:20	*A count-based model for delineating cell-cell interactions in spatial transcriptomics data* **Hirak Sarkar**
14:40	*Mapping lineage-resolved scRNA-seq data with spatial transcriptomics using TemSOMap* **Xinhai Pan**
15:00	*Enhancing spatial transcriptomics analysis using deep learning-based batch effect mitigation* **Rian Pratama**
15:20	*Gene Regulatory Networks analysis from single cell multi-omics data* **Zhana Duren**
15:40	*Dynamic Gene Regulatory Network Inference with Interpretable, Biophysically-Motivated Neural ODEs* **Maggie Beheler-Amass**
16:40	*Optimal sequencing budget allocation for trajectory reconstruction of single cells* **Noa Moriel**
17:00	*Charting the role of RNA binding proteins in tissue-specific alternative splicing using machine explanations* **Ayan Paul**
17:20	*Harnessing deep learning to amplify insights from GWAS* **Hae Kyung Im**

Tuesday, July 16; Room 525

Time	Title and Speaker
8:30	*Welcome and Introduction to SysMod!*
8:50	*Keynote Speaker Talk*
9:30	*Building high quality dynamical models of gene regulatory circuits driving cellular state transitions using scRNA-seq data* **Mingyang Lu**
9:50	*Deciphering epigenetic regulatory mechanisms of IFNg-induced Epithelial to Mesenchymal Transition in human breast cells using systems approach* **Humza Hemani**
10:40	*Mathematical Modeling suggests that Monocyte Activity may drive Sex Disparities during Influenza Infection* **Tatum Liparulo**
11:00	*Predictive Modeling and Experimental Control of Macrophage Pro-Inflammatory Dynamics* **Jennifer Riccio**
11:20	*Deciphering Cellular Fate Decisions: A Boolean Network Approach to Stress Response Network Tipping Points* **Imran Shah**
11:40	*Integrative Systems and Synthetic Biology identifies a Yeast Minimal Cell Cycle network that coordinates cell proliferation dynamics* **Matteo Barberis**
12:00	*Harnessing Agent-Based Modeling in CellAgentChat to Unravel Cell-Cell Interactions from Single-Cell Data* **Vishvak Raghavan**
14:20	*Metabolic Objectives and Trade-offs in Single-cells during Cellular Transitions* **Da-Wei Lin**
14:40	*Structural Systems Biology of Levan Biosynthesis in Bacillus subtilis* **Ragothaman Yennamalli**
14:50	*Simple rules of intercellular communication for modeling emergent multicellular organization* **Melissa Kemp**
15:30	*Closing Words*

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TEXT MINING

Sunday, July 14; Room 524ab

Time	Talk and Speaker
10:40	*Combining computational pipelines and text mining to build a cell type knowledge graph resource* **Richard Scheuermann**
11:20	*Enhancing Machine Learning Based Drug Response Prediction Models via Text Mining-Driven Feature Selection Approach* **Arvind Mer**
11:20	*Streamlining Drug Development with Conversational AI-Powered Knowledge Graphs: From Preclinical Discovery to Clinical Trials* **Maaly Nassar**
11:40	*eMIND: Enabling automatic collection of protein variation impacts in Alzheimer's disease from the literature* **Cathy Wu**
12:00	*Poster Flash Presentations*
14:20	*An informatic path to better understanding of cardiovascular biology and medicine* **Peipei Ping**
15:00	*The Netherlands Neurogenetics Database: Reveiling clinical, neuropathological and genetic heterogeneity of brain-disorders* **Inge Holtman**
15:00	*GeneAgent: Self-verification Language Agent for Gene Set Knowledge Discovery* **Zhiyong Lu**
15:20	*MolLM: A Unified Language Model for Integrating Biomedical Text with 2D and 3D Molecular Representations* **Andrew Tran**
15:40	*BioCoder: A Benchmark for Bioinformatics Code Generation with Large Language Models* **Xiangru Tang**
16:40	*Improving Medical Reasoning through Retrieval and Self-Reflection with Retrieval-Augmented Large Language Models* **Minbyul Jeong**
17:00	*Leveraging AI, text mining and large language models to advance biology and medicine*

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Monday, July 15; Room 519

Time	Title and Speaker
16:40	*Introduction*
16:40	*Quality Assurance, Semantic Enrichment and Integration of Multimodal Health Data for Phenotype and Cohort Discovery with Deep Learning* **Ian Overton**
17:00	*TA-RNN: an Attention-based Time-aware Recurrent Neural Network Architecture for Electronic Health Records* **Serdar Bozdag**
17:20	*Share genetics between breast cancer and its predisposing diseases identifies candidate drugs for repurposing for breast cancer* **Panagiotis Nikolaos Lalagkas**
17:20	*Prevalence and biological impact of clinically relevant gene fusions in head and neck cancer* **Emily Hoskins**
17:40	*PhiHER2: Phenotype-informed weakly supervised model for HER2 status prediction from pathological images* **Jian Liu**

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Tuesday, July 16; Room 519

Time	Title and Speaker
8:40	*Advancing Genomic Medicine through Clinical and Research Strategies* **Heidi Rehm**
9:20	*Transcriptional modulation unique to vulnerable motor neurons predict ALS across species and SOD1 gene mutations* **Irene Mei**
9:20	*Multi-dimensional Integration of PPI Network with Genetic and Molecular Data to Decipher the Genetic Underpinnings of RA Endotypes* **Javad Rahimikollu**
9:40	*AI Epilepsy: Software solution to aid in the diagnosis of epilepsy using machine learning algorithms* **Juan Carvajal**
9:40	*HTJ2K as a Default Storage Format for Medical Images* **Utkarsh Rai**
10:40	*The challenges of clinical deployment of automated cancer type classification for routine use* **Quaid Morris**
11:20	*CIViC - an open-access knowledgebase for community driven curation of clinical variants in cancer* **Mariam Khanfar**
11:20	*Timing the development of chemoresistance in relapsed pediatric cancer* **Sasha Blay**
11:40	*PHENO-DEX: Phenotypic Mapping of Dexamethasone Response in Breast Cancer Cells using Single-cell Transcriptomics* **Jiaqi Li**
11:40	*Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment* **Hatice Osmanbeyoglu**
12:00	*Integrative transcriptomic analysis and predictive modeling for immunotherapy response in melanoma* **Yamil Damian Mahmoud**
12:00	*A computational approach for the high-throughput identification of cancer-specific antigens for immunotherapeutic development* **Rawan Shraim**
14:20	*Leveraging a Single-Cell Language Model for Precise EMT Status Prediction and Gene Signature Identification in Cancer* **Shi Pan**
14:20	*Streamlining Clinical Trial Matching Using a Two-Stage Zero-Shot LLM with Advanced Prompting* **Mozhgan Saeidi**
15:00	*Multi-Omics Integration with High-Resolution AI-Derived Retinal Thickness: Unraveling Spatial Patterns of Retinal Susceptibility to Systemic Influences* **Roberto Bonelli**
15:20	*New methods to discover drug combinations impacting cancer incidence* **Rachel Melamed**
15:20	*Closing Remarks*

VARI

Monday, July 15; Room 521

Time	Title and Speaker
10:40	*Opening Remarks*
10:40	*Exploring the landscape of regulatory uORFs in BMPR2 and their potential as therapeutic targets* **Danielle Gutman**
11:00	*Beyond the sequence: interpreting missense variants with structure context* **Jun Cheng**
11:40	*Capturing biophysical and protein language model constraints for an improved assessment of the impact of mutations on protein function and stability* **Wim Vranken**
12:00	*VespaG: Expert-guided protein Language Models enable accurate and blazingly fast fitness prediction* **Burkhard Rost**
12:00	*Addressing biases in large language models for variant impact prediction in macro proteins* **Oriol Gracia I Carmona**
14:20	*Clinical classification of variation for disease causality* **Heidi Rehm**
15:00	*Ensemble Prediction of the Clinical Impact of Missense Variants Substantially Decreases VUS Rate in Genetic Testing*
15:00	*MAJIQ-CLIN: A novel tool for the identification of Mendelian disease-causing variants from RNA-seq data* **Dina Issakova**
15:20	*Reclassifying variants of uncertain significance with transcriptional profiling* **Kivilcim Ozturk**
15:40	*Metacell burden: A method to quantify the effects on neurodevelopmental disorders of rare genomic variants aggregated across brain cells.* **Thomas Renne**
16:40	*Representing Mutations for Predicting Cancer Drug Response* **Patrick Wall**
17:00	*Assessing lethal missense mutations and polymorphism in Drosophila melanogaster with an evolutionary-informed model* **Marina Abakarova**
17:00	*A phylogenetic mutation-selection model predicts fitness effects of mutations in extant mammals* **Thibault Latrille**
17:20	*Functional variomics for decoding variant effects*

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Monday, July 15; Room 519

Time	Title and Speaker
10:40	*An Empirical Study on KDIGO-Defined Acute Kidney Injury Prediction in the Intensive Care Unit* **Xinrui Lyu**
11:00	*Mapping spatial omics when tissue architecture doesn’t match.* **Patrick Martin**
11:20	*MALAT1 expression consistently indicates cell quality in single-cell RNA and single-nucleus RNA sequencing* **Zoe Clarke**
11:40	*Combining DNA and protein alignments to improve genome annotation with LiftOn* **Kuan-Hao Chao**
12:00	*Optimal Phylogenetic Reconstruction of Insertion and Deletion Events.* **Sanjana Tule**
14:20	*Approximating facial expression effects on diagnostic accuracy via generative AI* **Tanviben Patel**
14:40	*Using Relation Equivariant Graph Neural Networks to Explore the Mosaic-like Tissue Architecture of Kidney Diseases with Spatially Resolved Transcriptomics* **Mauminah Raina**
15:00	*scResolve: Recovering single cell expression profiles from multi-cellular spatial transcriptomics* **Young Je Lee**
15:20	*Multiview factorization for joint modeling of spatial multi-omics and histology images via NMF* **William Bowie**
15:40	*Predicting gene functional associations from coevolutionary signals with EvoWeaver* **Erik Wright**
16:40	*Efficient parameter estimation for ODE models of cellular processes using semi-quantitative data* **Domagoj Doresic**
17:00	*NCBIâ€™s RNA-seq analysis pipeline produces millions of pre-computed gene expression counts to accelerate data reuse and discovery* **Emily Clough**
17:20	*Enabling Affordable Single-Cell Data in Large Cohort Studies via Deep Generative Neural Networks and Active Learning* **Jingtao Wang**
17:40	*HINN: A Novel Neural Network Architecture to Integrate Multi-Omics Data based on their Biological Relationships* **Yashu Vashishath**

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SOCIAL EVENTS

Opening Reception with Exhibitors

Date: Friday, July 12, 2024

Time: 19:30 - 21:00

Location: 517c (Level 5) Palais des Congrés de Montréal

Success Circles

Date: Sunday, July 14, 2024

Time: 18:00 - 19:30

Location: 517c (Level 5) Palais des Congrés de Montréal

Cost: $10

More info: https://www.iscb.org/ismb2024/programme-schedule/success-circles

Serene Stretch Symposium

Time: 7:30 - 08:00

Location: Palais des Congrés de Montréal, Level 2, Hall Viger

Cost: $20

Note: You may also join complimentary, but please ensure you bring your own yoga mat or towel.

Celebrating 25 years of Bioinformatics.ca

Date: Saturday, July 13, 2024	**Time:** 18:00
Location: 710a	**Cost:** $50

Register: https://t.ly/jctIB

JOIN US IN *Celebrating* 25 YEARS OF BIOINFORMATICS IN CANADA!
SATURDAY, JULY 13TH AT 6PM

bioinformatics.ca

SOCIAL EVENTS

BioInfo-Core Social Event

Date: Monday, July 15
Time: 19:30
Location: 3 Brasseurs,
732 Ste-Catherine Ouest,
Montréal, QC, H3B 1B9
Cost: Pay your own way

BioVis Informal Dinner

Date: Sunday July 14
Time: TBD
Location: TBD
Cost: pay your own way

CAMDA Dinner & Drinks

Date: Monday, July 15
Time: 18:30
Location: Marché des Éclusiers
Cost: $79
Capacity: 95 people
Meet at the main conference entrance at 18:15

CompMS Social Event

Date: Monday, July 15
Time: 7 pm
Location: 3 Brasseurs
1255A Crescent St, Montreal,
Quebec, H3G 2B1
Cost: $15

SOCIAL EVENTS

iRNA Dinner

Date: Saturday, July 13th
Time: 19:00
Location: Bistro-Brasserie Les Soeurs Grises
Cost: $65 USD
Capacity: 50 people

SysMod Social Event

Date: Monday, July 15
Time: 18:30
Location: Tiradito, 1076 Rue de Bleury, Centre-Ville, Montréal, QC H2Z 1N2

Women in Computational Biology Meet-Up

Date: Saturday, July 13
Time: 18:30
Location: Meet at the Lipstick Forest (1st Floor) Palais des Congrés de Montréal

Scan for full Social Event details:

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SAVE THE DATE!

ISMB/ECCB
2025
JULY 20 -24
LIVERPOOL

JULY 20–24, 2025

LIVERPOOL, ENGLAND

UPCOMING TUTORIALS

IntelliGenes: AI/ML pipeline for biomarker discovery and predictive analysis

Date: September 5, 2024, 11:00 AM

In this tutorial, we present IntelliGenes, a novel Artificial Intelligence (AI) and machine learning (ML) pipeline to discover biomarkers significant in disease prediction with high accuracy. IntelliGenes is based on a novel approach, which consists of nexus of conventional statistical techniques and cutting-edge AI/ML algorithms using multi-genomic, clinical, and demographic data. By integrating these approaches, we outperformed single algorithms, resulting in enhanced accuracy, deeper insights, and more precise predictions, essential for personalized early disease-risk detection in individuals. IntelliGenes introduces a new metric i.e., Intelligent Gene (I-Gene) score to measure the importance of individual biomarkers for prediction of complex traits. I-Gene scores can be utilized to generate I-Gene profiles of individuals to comprehend the intricacies of ML used in disease prediction. IntelliGenes is user-friendly, portable, and a cross-platform application, compatible with Microsoft Windows, macOS, and UNIX operating systems. IntelliGenes not only holds the potential for personalized early detection of common and rare diseases in individuals, but also opens avenues for broader research using novel ML methodologies, ultimately leading to personalized interventions and novel treatment targets. We are proud to share that IntelliGenes is the first peer reviewed published AI/ML pipeline for biomarker discovery and predictive analysis using integrated clinical and multi-genomic profiles. It is recently published in the Bioinformatics journal by Oxford University Press and the International Society for Computational Biology (ISCB). [PMID: 38096588, and DOI: 10.1093/bioinformatics/btad755].

Understanding and curating Intrinsically Disordered Proteins: using DisProt, MobiDB, and PED in research and biocuration

Date: January 14, 2025, 9:00 AM

Intrinsically disordered proteins (IDPs) are involved in a plethora of biological processes, yet their study requires specialized resources. This tutorial aims to introduce participants to three key resources in the field: DisProt (http://www.disprot.org), MobiDB (https://mobidb.org/) and the Protein Ensemble Database (PED) (http://proteinensemble.org). This session will provide insights into how these databases complement each other and their effective utilization in research. The tutorial will begin with an overview of the importance of studying IDPs, followed by general training on accessing and extracting data from DisProt, MobiDB, and PED. Participants will learn to navigate MobiDB to extract data and predictions of intrinsically disordered regions, and utilize PED to gain insights into the structural ensembles of IDPs. An exploration of how PED serves as a key resource for understanding the conformational diversity of IDPs will be included. A dedicated section will provide specialized biocuration training for DisProt, focusing on the curation process, structuring IDP-related data with ontologies, retrieving and defining IDP-related experiments, annotating states, transitions, and functions of IDPs, adhering to MIADE standards, and exploring thematic datasets and use cases in DisProt curation. By the end of the session, attendees will be equipped with the necessary knowledge to utilize key IDP resources and with the skills to contribute to the expansion of DisProt, providing them with IDP-specific biocuration skills and giving them the opportunity to expand the resource for the scientific community

UPCOMING CONFERENCES

Did you know that ISCB Members Get Discounts on these Conferences?

11TH INTERNATIONAL WORK CONFERENCE ON BIOINFORMATICS AND BIOMEDICAL ENGINEERING

July 15 - 17
Gran Canaria, Spain
15% Discount

QUEST FOR ORTHOLOGS 8

July 17
Montréal, Canada
15% Discount

20TH SYMPOSIUM ON BIOINFORMATICS RESEARCH AND APPLICATIONS

July 19 - 21
Kunming, China
15% Discount

19TH CONFERENCE ON COMPUTATIONAL INTELLIGENCE METHODS FOR BIOINFORMATICS AND BIOSTATISTICS

September 4 - 6
Benevento, Italy
15% Discount

ECCB 2024

September 16 - 20
Turku, Finland
10% Discount

RSGDREAM 2024

October 1 - 3
Madison, Wisconsin
20% Discount

APJBC 2024

October 22-25
Okinawa, Japan
$100 USD Discount

ISCB-LATAM SOIBIO CCBCOL 2024

November 12-15
Medellin, Colombia
20% Discount

PSB 2025

Kohala Coast
Big Island, HI
$50 USD Discount

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