ISMB 2025 ECCB 2025 Liverpool July 20-24



and

ISCB July Newsletter



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A LETTER FROM THE ISCB PRESIDENT, PREDRAG RADIVOJAC

Dear ISCB Members,

I am delighted to connect with you through this July edition of our Newsletter and to share several important developments that highlight the strength, growth, and ongoing evolution of our Society.

ISCB continues to thrive, with our membership levels reaching a record high, now surpassing 4,200 members worldwide. This milestone is a testament to the vibrancy of our community and the critical role ISCB plays in advancing computational biology. Thank you for making ISCB your professional home!

In line with our mission to support the global community, ISCB has significantly expanded its affiliated conference program. In the fourth quarter of 2024, we welcomed the Asia & Pacific Joint Bioinformatics Conference and supported Australian **Bioinformatics** the and Computational Society Annual Meeting. So far in 2025, added two new topical conferences, 3DBioinfo and BiGEvo, as well as JBI -Symposium on Bioinformatics coming up later this year. After a short hiatus, ISCB-Africa ASBCB welcomed nearly 200 participants to Cape Town, South Africa. Mark your calendars for these additional conferences for 2025, INCOB, GIW ISCB-Asia and ABACBS. Upcoming in 2026, we will welcome the ISCB-UK and Bioinfomatics.ca conferences. This strategic

growth creates more opportunities to collaborate with regional and international partners, to foster scientific exchange, and to support our members and colleagues around the world. The program expansion has also allowed us to offer more conference discounts, broaden access to ISCB membership, and increase the ability for researchers to present their work, truly core to our mission of advancing scientific knowledge.

We also remain steadfast in our commitment not just to our field but also to every one of our current or potential members. This commitment continues to guide our culture and drive our pursuit of scientific excellence. We believe that one of the strengths of our community lies in its diversity, and we are dedicated to fostering an environment where all voices are valued and respected. Through fellowships. travel registration and membership waivers, and through various funding programs, we work actively to reduce barriers and expand opportunities in computational biology. ISCB is a Society for all. We deeply value the unique contributions each of you brings.

This year, ISCB leadership also undertook an important update to our Code of Ethics and Professional Conduct. We have identified areas where the Code could be clearer to

ensure it is fully understood across our global membership. Each researcher, practitioner, technician, student, and supplier in our field is a citizen of the community of science, and each shares responsibility for its welfare. Science is best advanced when built on mutual trust and honest behavior. As such, our Society expects all members to uphold the highest standards of honesty and integrity in all their actions, both within and beyond ISCB activities. I encourage you to read the detailed article in this newsletter that explains these updates and reinforces our shared commitment to these principles.

Finally, I want to celebrate the incredible support of our members, which has helped us achieve the highest ISMB participation for the conference in the past two decades. ISMB/ECCB 2025 welcomes 2,164 in-person participants and another 228 online from 70 countries, and the number will go up by the time you read the Newsletter. Whether you joined us in person or virtually for ISMB/ECCB 2025, thank you for taking the time to present your work, share your insights, and help drive our field forward.

I am inspired by your dedication to computational biology and grateful for the energy and talent you bring to ISCB. Together, we continue to strengthen our Society and advance our science.

Warm regards, Predrag Radivojac President, ISCB

HOW YOU CAN SUPPORT ISCB

Donate Now!

ANNA TRAMONTANO

The goal of the Anna Tramontano Fellowship Fund is to help reduce the financial burder 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 giver year.





STUDENT FELLOWSHIP CAMPAIGN

future of computational biology and bioinformatics by supporting tomorrows researchers. By donating to ISCB student travel fellowships, you are investing in the future of our science.

GENERAL RESOURCES

ISCB delivers valuable information about training, education, employment, and relevanews, 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



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

STRENGTHENING RESPECT: ISCB'S UPDATED CODE OF ETHICS AND PROFESSIONAL CONDUCT

ISCB is proud to share important updates to our Code of Ethics and Professional Conduct. These refinements represent our commitment to fostering a scientific community rooted in respect, integrity, and inclusion.

Why These Changes?

Over the past year, we recognized the need to expectations within clarify our code. Ambiguities can undermine trust and leave for conduct that damages collaborative spirit on which science thrives. In addition, we have observed instances within the broader community that run counter to our values, underscoring the urgency to reinforce our principles.

What's New?

Our updated code now explicitly outlines how we expect members to interact as colleagues, scientists, and global citizens. Among the notable clarifications:

- Respect and courtesy as the standard: ISCB members are called to treat contributors to our field with respect and dignity, embracing differences in worldviews, scientific approaches, and cultures.
- Integrity in sharing and critique: Members should share ideas honestly, give proper credit for others' contributions, and engage in scientific critique that focuses on the work, not the person. Peer review should be conducted constructively and never serve as a venue for personal attacks, belittlement, or defamation.

- Accuracy in science: Reporting should be thorough and free from distortion, ensuring scientific discourse is built on a foundation of truth.
- A clear stance against harassment and discrimination: The code now details examples of unacceptable behavior, from bullying and intimidation to discriminatory or harassing speech. It makes clear that ISCB spaces, whether virtual or in person, are welcoming and safe for all, regardless of race, gender identity, sexual orientation, disability, national origin, or other identities.
- Professionalism in every forum: Whether serving on a committee, participating in a COSI, or posting on social media, members are expected to uphold the highest standards of collegiality and respect.

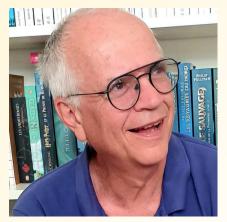
By refining these expectations, ISCB aims to cultivate an environment where science can flourish, where ideas are debated rigorously but respectfully, and where all participants feel valued and secure. We view this as a shared responsibility. Every researcher, practitioner, technician, student, and supplier within the field plays a role in upholding these standards, modeling the professionalism that strengthens our field and inspires the next generation.

We invite all members to read the updated Code of Ethics and Professional Conduct in full and reflect on how each of us can contribute to a community defined by excellence, fairness, and mutual respect.

ISCB AWARD WINNERS

As part of the ISMB/ECCB 2025 conference, ISCB will be presenting its four annual awards to this year's very deserving recipients! Each awardee has a full-length article that can be found in the ISMB/ECCB 2025 Proceedings Supplement in *Bioinformatics*, but you can read a short summary of each article below!

2025 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD: DR. AMOS BAIROCH



Dr. Amos Bairoch is the 2025 recipient of the Accomplishments by a Senior Scientist Award, recognized for his leadership and transformative contributions to bioinformatics. Inspired early by a love of science and space, he turned to biochemistry and computing, laying the groundwork for accessible computational biology. His development of Swiss-Prot revolutionized protein sequence analysis, making critical resources available to researchers worldwide and supporting the growth of bioinformatics infrastructure.

As a mentor and research leader, Bairoch focused on empowering young scientists and building strong institutional support, helping establish the Swiss Institute of Bioinformatics to ensure long-term stability for the field. He values the evolving nature of science and technology, with projects like Swiss-Prot and Cellosaurus growing far beyond their original scope. Honored to receive this award, Bairoch reflects on a career dedicated to advancing bioinformatics and fostering the next generation of researchers.

Read the full article here: https://doi.org/10.1093/bioinformatics/btaf262

2025 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD: DR. LUCIA PEIXOTO



Dr. Lucia Peixoto is the 2025 recipient of the Outstanding Contributions to ISCB Award, recognized for her leadership, service, and dedication to building an inclusive scientific community. From volunteering at the 2007 Student Council Symposium to helping launch the first ISCB Latin America conference in Uruguay, she has worked to expand access and opportunities for scientists everywhere.

As founding chair of ISCB's Equity, Diversity, and Inclusion committee, Peixoto applies data-driven approaches to advance

equity in science. Her research in neurodevelopmental disorders has been shaped by listening to patient communities, inspiring her focus on sleep and autism. Grateful for this recognition, she hopes it encourages scientists to see service as an essential part of scientific excellence.

Read the full article here: https://doi.org/10.1093/bioinformatics/btaf263

2025 ISCB INNOVATOR AWARD: DR. FABIAN THEIS

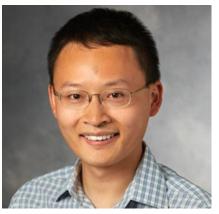


Dr. Fabian Theis is the 2025 recipient of the ISCB Innovator Award, recognized for his pioneering contributions and commitment to exploring new directions in computational biology. Drawn early to computers through programming his own games, Theis discovered during his PhD that computational methods could bring structure to biological complexity. This insight led him to apply machine learning to biological data, uncovering patterns that traditional methods might miss and driving impactful innovations like the widely used single-cell analysis tool, ScanPy.

As a mentor and research leader, Theis values collaboration, interdisciplinary training, and giving students the freedom to explore their interests, encouraging them to develop their own research identities. He credits mentors, colleagues, and especially his students for shaping his career and pushing his work in new directions. Honored and humbled by this award, Theis emphasizes that it recognizes not just his own efforts, but the creativity and dedication of his entire team.

Read the full article here: https://doi.org/10.1093/bioinformatics/btaf260

2025 OVERTON PRIZE AWARD: DR. JAMES ZOU



Dr. James Zou is the 2025 recipient of the ISCB Overton Prize, recognized for his significant contributions to computational biology and commitment to interdisciplinary research. Drawn early to mathematics for its logic and challenge, Zou's fascination deepened in college when he discovered computational biology, ultimately leading him to apply machine learning to biological questions during his PhD at Harvard. His curiosity about cellular reprogramming and epigenomics shaped a research path focused on using computation to uncover complex biological mechanisms.

As a mentor and PI, Zou emphasizes giving students the tools and freedom to explore ambitious questions, recruiting trainees from diverse backgrounds and encouraging interdisciplinary collaboration. His lab has delivered notable breakthroughs, such as using tissue imaging to predict gene expression and developing AI systems for biomedical discovery, including designing antibodies for COVID variants. Grateful and humbled by the Overton Prize, Zou views it as a recognition of the students, mentors, and collaborators who have inspired and shaped his research journey.

Read the full article here: https://doi.org/10.1093/bioinformatics/btaf261



Intelligent Systems for Molecular Biology

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Biology



Details and info: https://www.iscb.org/ismbeccb2025/register

THE 2025 CLASS OF FELLOWS

The ISCB Fellows program recognizes excellence in computational biology, honoring individuals who have made outstanding contributions through leadership, research, and service. ISCB Fellows have played a pivotal role in advancing bioinformatics and computational biology, shaping the field through innovation and collaboration. This prestigious distinction reflects a career of significant impact and a dedication to the scientific community.



Yana Bromberg, Emory University, Atlanta, GA, USA

Yana Bromberg is a pioneering researcher in variant effect prediction, microbiome annotation, and evolutionary biology. She was the first to apply machine learning to predict the impact of single amino acid variants on protein function, leading to the widely cited SNAP tool. Her groundbreaking work has expanded to include gnomAD-based predictions of non-synonymous variant effects and innovative microbiome annotation methods, such as LookingGlass, which sheds light on the "microbial dark matter."

An active ISCB leader, Bromberg co-founded the SNP-SIG (now VarI-COSI), served on the Board of Directors since 2016, and played a critical role as ISCB Vice President during the COVID years. With over 100 publications and 5,000+ citations, her research continues to shape computational biology.



Charlotte Deane, University of Oxford, UK

Charlotte Deane has made major contributions to computational biology, particularly in protein structure and function, immune molecule analysis, and drug design. Her widely used tools and databases, including SAbDab and PanDDA, have advanced immunoinformatics and small-molecule drug discovery. Deane's research, cited over 14,000 times, bridges AI, statistics, and structural biology to address key biomedical challenges. A dedicated leader in training and equity in bioinformatics, she has

mentored over 95 doctoral students and played a pivotal role in expanding access to graduate education. Beyond academia, she has served in national leadership roles, including as COVID-19 Response Director for UKRI, and now leads the UK's Engineering and Physical Sciences Research Council.



Toni Gabaldon, IRB Barcelona and Barcelona Supercomputing Center

Toni Gabaldón is a leader in comparative genomics and phylogenomics, developing widely used computational methods for high-throughput sequencing analysis. His tools, including trimAl, ETE, and PhylomeDB, have shaped phylogenetic research and garnered over 10,000 citations. Gabaldón's groundbreaking discoveries have reshaped our understanding of genome evolution, from redefining the origins of eukaryotic cells to



Rachel Karchin, Johns Hopkins University

Rachel Karchin is a pioneer in computational cancer genomics, developing innovative algorithms for variant interpretation and tumor evolution. She created CHASM, the first widely used statistical learning method to distinguish driver from passenger mutations, and led the development of OpenCRAVAT, a widely adopted open-source variant annotation toolkit. Her contributions extend to immuno-oncology, where her deep learning-based BigMHC model advances neoantigen prioritization for precision

medicine. A leader in the field, Karchin has played key roles in major cancer research initiatives, served on multiple advisory boards, and mentored the next generation of computational biologists.



David Landsman, National Library of Medicine, part of the National Institutes of Health

David Landsman is a leading figure in computational biology, known for his pioneering work in histone biology, chromatin structure, and gene regulation. His research has advanced the understanding of histone modifications, non-histone chromosomal proteins, and transcriptional regulation, shaping current knowledge of genome organization. As a key contributor to NCBI resources, he developed the Histone

Database and played a vital role in expanding bioinformatics infrastructure. A dedicated mentor, Landsman has guided numerous early-career researchers and actively contributed to international bioinformatics initiatives, editorial leadership, and scientific advisory boards.



Su-In Lee, University of Washington

Su-In Lee is a leader in explainable AI, pioneering methods that enhance the interpretability of machine learning in biomedicine. She developed the widely used SHAP framework and key algorithms like Tree SHAP and Deep SHAP, transforming how AI models uncover insights in biology and healthcare. Her research has driven discoveries in cancer, Alzheimer's disease, and precision oncology while shaping the future of AI auditing and cost-aware AI frameworks. As director

of UW's Computational Molecular Biology program and co-founder of the MLCB conference, she actively advances interdisciplinary education and collaboration.



Jian Ma, Carnegie Mellon University

Jian Ma is a leading figure in computational genomics, developing AI-driven methods to unravel genome organization, single-cell epigenomics, and spatial transcriptomics. His work has transformed how researchers analyze 3D genome structure and gene regulation, with applications in evolution, health, and disease. A highly cited researcher with over 130 publications, Ma has also played a pivotal role in major NIH initiatives and interdisciplinary collaborations. As founding director of CMU's

Center for Al-Driven Biomedical Research, he continues to push the boundaries of computational biology.



Nicola Mulder, University of Cape Town

Nicola Mulder has been a driving force in building bioinformatics capacity across Africa, leading the H3ABioNet network for over a decade and training thousands in genomics and computational biology. Her work developing resources like the African Genome Variation Database and African Genomic Medicine Portal has strengthened the continent's role in global genomics research. A leader in education and infrastructure, she has played key roles in ISCB, GA4GH, and ASBCB, and recently secured funding to

establish an African Bioinformatics Institute, marking a major milestone for computational biology in Africa.



Robert F. Murphy, Carnegie Mellon University

Robert F. Murphy is a pioneer in applying machine learning to biomedical image analysis, transforming how subcellular structures are studied. His groundbreaking work demonstrated that computational models could outperform human experts in classifying fluorescence microscopy images, laying the foundation for modern bioimage informatics. His contributions extend to generative models of cell structures, advancing cellular modeling and immune signaling research. Murphy has

also played a key role in shaping computational biology education, founding multiple academic programs and leading initiatives to integrate bioinformatics and imaging analysis into the field.



Itsik Pe'er, Columbia University

Itsik Pe'er is a leading computational geneticist whose work has reshaped our understanding of human genetics and microbial dynamics. He pioneered identity-by-descent (IBD) analysis, enabling researchers to trace population history, detect genetic associations, and refine disease risk predictions. His contributions extend to microbiome research, where his FEAST tool and modeling approaches have advanced studies of microbial evolution and health. A dedicated mentor and

educator, Pe'er has trained the next generation of leaders in genomics and computational biology while fostering interdisciplinary collaboration across genetics, machine learning, and mathematical modeling.



Lucia Peixoto, Washington State University

Lucia Peixoto, this year's Outstanding Contributions to ISCB award winner, has been a dedicated leader in ISCB for over 15 years, playing a key role in and being a consistent champion of strengthening the society's global reach, fostering an inclusive scientific community, and supporting career development for early-stage researchers She was instrumental in launching the ISCB-Latin America conference series, forging international collaborations that continue to expand ISCB's impact. As co-chair

of the ISCB Equity, Diversity, and Inclusion committee, Peixoto has helped shape ISCB's code of conduct and leadership in promoting diversity and accessibility in computational research. Beyond her leadership, she is an accomplished researcher investigating the molecular links between sleep disorders and autism, pioneering single-nucleus RNA-seq analysis strategies to uncover critical transcriptional changes in neurons. Her contributions exemplify the intersection of rigorous computational biology and dedicated community leadership.



Predrag Radivojac, Northeastern University, USA

Predrag Radivojac is a pioneer in applying machine learning to protein function prediction and genome interpretation. His groundbreaking work includes the development of computational methods for variant impact assessment, including the widely used MutPred suite, and leading large-scale community challenges such as CAFA and CAGI. His contributions extend to computational mass spectrometry, machine learning for biased data, and fundamental advances

in positive-unlabeled learning. A dedicated leader in computational biology, he has served on the ISCB Board of Directors for nine years and played a key role in establishing Bioinformatics Advances, ISCB's official journal. Now serving as ISCB President, he continues to shape the future of the field.



Ana Tereza Ribeiro de Vasconcelos, National Laboratory for Scientific Computing

Ana Tereza Ribeiro de Vasconcelos is a leader in bioinformatics and computational biology in Brazil, playing a key role in expanding genomics research and infrastructure across Latin America. Her lab has pioneered high-throughput sequencing applications, developed computational tools for genome analysis, and contributed to research on human genetic diseases, microbial genomics, and infectious diseases like Zika

and COVID-19. A founder of the Brazilian Association for Bioinformatics and Computational Biology (AB3C), she has trained over 70 PhD and master's students, strengthening the region's scientific capacity. Her contributions have positioned Brazil as a major player in global bioinformatics research.



Remo Rohs, University of Southern California

Remo Rohs is a world leader in computational biology, pioneering research on DNA shape readout and protein-DNA interactions. His widely used computational methods have transformed the understanding of gene regulation by integrating genomics, structural biology, and Al-driven modeling. He has advanced predictive models for protein-DNA binding, RNA structure, and drug design, publishing extensively in top journals. As the founding chair of USC's Department of

Quantitative and Computational Biology, Rohs has shaped interdisciplinary education and recruited a new generation of computational biologists. His leadership and scientific contributions have had a profound impact on the field.



Julio Saez-Rodriguez, EMBL-EBI

Julio Saez-Rodriguez is a leader in computational systems biology, pioneering methods that integrate prior knowledge with multi-omics data to uncover disease mechanisms. His work spans machine learning, mechanistic modeling, and multi-omics analysis, with applications in signal transduction, gene regulation, and microbiome-host interactions. A co-leader of the DREAM Challenges, he has championed rigorous benchmarking of computational tools. Beyond his research, he has shaped the

field through mentorship, open science initiatives, and leadership in European computational biology. His impact continues to drive innovation in systems medicine and disease biology.



Cenk Sahinalp, NCI/NIH

Cenk Sahinalp is a leader in algorithmic methods for cancer genomics, structural variation, and tumor evolution. His contributions have shaped computational approaches for detecting genomic rearrangements, reconstructing tumor progression, and ensuring privacy in genomic data analysis. His tools, widely used in projects like the 1000 Genomes Project and NIH's All of Us, have advanced our understanding of genomic diversity and cancer progression. A dedicated mentor

and community leader, he has trained the next generation of computational biologists and played a key role in RECOMB conferences, reinforcing his impact on the field.



Donna Slonim, Tufts University

Donna Slonim has pioneered the application of machine learning to transcriptomics and disease research, particularly in maternal and fetal health. From her early work distinguishing leukemia subtypes using gene expression to developing innovative anomaly detection methods like CSAX and TEMPO, her research has had direct clinical impact. She has contributed significantly to understanding fetal development through maternal blood and the effects of maternal opioid use.

A dedicated community leader, she has served on ISCB's Board of Directors, ISMB Proceedings Committee, and multiple advisory boards, shaping the future of computational biology.



Zemin Zhang, Peking University

Zemin Zhang is a leader in computational cancer biology, pioneering single-cell sequencing methods to decode tumor microenvironment heterogeneity. His groundbreaking work has revealed key immune cell dynamics across cancers, informing immunotherapy strategies. He developed widely used bioinformatics tools like GEPIA and STARTRAC, advancing cancer genomics research. With nearly 50,000 citations and major contributions in Nature, Cell, and Science, his impact

spans computational methods, tumor biology, and clinical applications, shaping the future of precision oncology.



Hongyu Zhao, Yale University

Hongyu Zhao is a pioneering statistician whose computational methods have advanced genetics, genomics, and biomedical data science. His contributions include novel statistical frameworks for cross-population trait prediction, genetic correlation analysis, and transcriptome-wide association studies, shaping our understanding of complex diseases. With over 600 publications and leadership in major precision medicine initiatives like the Million Veteran Program, his impact

spans research, mentorship, and community-building in computational biology.

Congratulations to the ISCB 2025 Class of Fellows!

WELGOWE, ISMB 2025 ECCB 2025

Liverpool July 20-24



WELCOME TO ISMB/ECCB 2025!

On behalf of the ISMB/ECCB 2025 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 exciting city of Liverpool, and if you're joining us virtually, we welcome you to the hybrid conference experience.

We are sure you will have an excellent time while in Liverpool and attending ISMB/ECCB. 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, thematic COSI sessions showcasing cutting-edge research, plus tutorials, special sessions, the hybrid Student Council Symposium, the Youth Bioinformatics Symposium, and poster sessions.

Be sure to visit the Exhibit Hall in Hall 2 of the Lower Galleria, where you can engage with our 28 conference exhibitors while enjoying complimentary coffee during breaks. This year's exhibition features leading bioinformatics tools and technologies, academic and research institutions, publishing partners, and organisations driving innovation in data science and healthcare.

For those joining us virtually through ISCB's

Nucleus platform, you can interact with all ISMB/ECCB 2025 participants, including exhibitors, via the Collaboration Hub. 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 from no-reply@iscb.org.

While viewing a live-stream 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/ECCB.

Highlights of the ISMB/ECCB 2025 Programme include:

- An opening keynote address from John Jumper, and a Fireside Chat with David Baker, co-recipients of the 2024 Nobel Prize in Chemistry
- Additional keynote talks featuring three of ISCB's 2025 Award winners
- 22 community-led COSI Tracks
- Special sessions including:
 - Bioinformatics in the UK
 - o DREAM Challenges
 - ELIXIR/NIH-ODSS
 - Innovation at the Intersection:
 Industry's Role in Bioinformatics

- NIH Track on Gen Al Cyberinfrastructure, Digital Twins, and Quantum Computing
- Stewardship of Critical Infrastructure
- 18 Technology Track presentations
- 17 pre-conference Tutorials (8 in-person, 9 virtual)
- the Career Fair
- the Success Circles networking event
- 1000+ posters

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 <u>Nucleus</u> 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, Conference 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 wish to thank the Steering Committee for their efforts in planning and organising the conference. We also want to thank our conference <u>sponsors</u> and <u>exhibitors</u> for their ongoing support.

Finally, as many of you know, without the highly skilled ISCB staff, there would be no ISMB/ECCB meeting. We are immensely grateful to the entire ISCB team for their dedication and effort in organizing the logistics of this complex meeting while enabling a hybrid experience for those unable to attend in person. Our sincere thanks to Bel Hanson (Senior Director, Operations and Seth Munholland Programs), (Lead Technologist), Diane Kovats (CEO), Mallory Wiper (Communications Specialist), Justine Morris (Coordinator. Operations Programs), and Nína-Mari Grobler (Executive Assistant).

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/ECCB 2025!

Welcome to Liverpool!

Yours sincerely,

Carole Goble, João Carlos Setubal,
Conference Co-Chair Conference Co-Chair

Dame Janet M. Thornton, Honorary Chair

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Professor of Bioinformatics and Department Head Department of Biochemistry, Institute of Chemistry University of São Paulo



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BIOINFORMATICS OF MICROBES AND MICROBIOMES

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BIOMEDICAL INFORMATICS

Niko Beerenwinkel, ETH Zurich, Switzerland

Jenna Wiens, University of Michigan, USA

Giulio Caravagna, University of Trieste, Italy

EQUITY AND DIVERSITY IN COMPUTATIONAL BIOLOGY RESEARCH

Larry Hunter, University of Chicago, USA

Alejandra Medina Rivera, Universidad Nacional Autónoma de México, Mexico

EVOLUTIONARY, COMPARATIVE AND POPULATION GENOMICS

Flora Jay, Université Paris-Saclay, France

Erin Molloy, University of Maryland, USA

GENERAL COMPUTATIONAL BIOLOGY

Ben Raphael, Princeton, USA

Simone Zaccaria, UCL Cancer Institute, UK

GENOME SEQUENCE ANALYSIS

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Tobias Marschall, Heinrich Heine University Düsseldorf, Germany

AREA CHAIRS, CONTINUED

MACROMOLECULAR SEQUENCE, STRUCTURE, AND FUNCTION

Jianlin Cheng, University of Missouri, USA

Mark Wass, University of Kent, UK

PRIVACY AND SECURITY FOR COMPUTATIONAL BIOLOGY

Michael Baudis, University of Zurich,

Kana Shimizu, Waseda University, Japan

Switzerland

REGULATORY AND FUNCTIONAL GENOMICS

Kimberly Glass, Harvard Medical School, USA

Saurabh Sinha, Georgia Institute of Technology, USA

SYSTEMS BIOLOGY AND NETWORKS

Anaïs Baudot, Aix Marseille Université, CNRS, INSERM, France

Nataša Pržulj, MBZUAI, UAE & University College London, UK

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R. Gonzalo Parra

Kana Shimizu

Luis Pedro Coelho

Farzana Rahman

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Chair: Jennifer Kelly, IBM Research, UK

Salvador Capella-Gutierrez, Spanish

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Bioinformatics

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Stephen Piccolo, Brigham Young University USA **Farzana Rahman**, Kingston University London, UK

ABSTRACT AREA CHAIRS

3DSIG: STRUCTURAL BIOINFORMATICS AND COMPUTATIONAL BIOPHYSICS

Douglas Pires, University fo Melbourne,

R. Gonzalo Parra, Barceolna Supercomputing Center, Spain

Australia

BOKR: BIO-ONTOLOGIES AND KNOWLEDGE REPRESENTATIONS

Tiffany Callahan, IBM Research, USA

Augustin Luna, NLM, USA

BIOINFO-CORE

Madelaine Gogol, Stowers Institute, USA Lorena Pantano Rubino, Harvard School of Public Health, USA

Alberto Riva, Human Technopole, Italy Yuvanesh Vedaraju, Houston Methodist, USA

BIOINFORMATICS IN THE UK

Carole Goble, The University of Manchester,

Janet Thornton, EBI/EMBL, UK

UK

BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Zeynep Gümüş, Icahn School of Medicine at Mount Sinai, USA **Robert Krueger**, NYU Tandon, USA

Jen Rogers, Glasgow School of Art, UK

Qianwen Wang, University of Minnesota, 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
Tazro Ohta, Chiba University
Jessica Maia, BD

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

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

ABSTRACT AREA CHAIRS, CONTINUED

COMPUTATIONAL AND SYSTEMS IMMUNOLOGY

Ferhat Ay, La Jolla Institute for

Immunology, USA

Jishnu Das, University of Pittsburgh

School of Medicine, USA

COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Wout Bittremieux, University of

Antwerp, Belgium

Timo Sachsenberg, University of

Tübingen, Germany

Isabell Bludau, Heidelberg University

Hospital, Germany

Lindsay Pino, Talus Bio, USA

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

Alejandra Medina Rivera, Universidad

Nacional Autonoma de Mexico, Mexico

Farzana Rahman, Kingston University London,

UK

EVOLCOMPGEN: EVOLUTION & COMPARATIVE GENOMICS

Nadia El-Mabrouk, University of

Montreal, Canada

Janani Ravi, University of Colorad<mark>o Anschut</mark>z

Medical Campus, USA

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

ABSTRACT AREA CHAIRS, CONTINUED

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

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

ABSTRACT AREA CHAIRS, CONTINUED

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Shaimaa Bakr, Stanford University, USA Matteo Barberis, University of Surrey, UK 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, UK

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

Ben Raphael, Princeton, USA

Simone Zaccaria, UCL Cancer Institute, UK

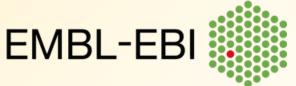


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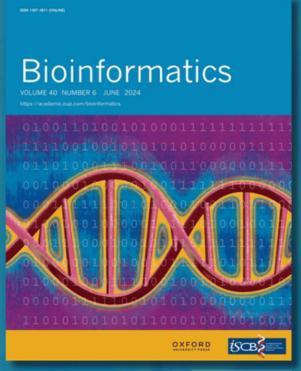
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Room 1A										
Day	Time	Title and Speaker								
Sunday, July 20	18:30	Extending AlphaFold to make predictions across the universe of biomolecular interactions John Jumper								
Monday, July 21	9:00	Plus ça change, plus c'est la même chose": from Swiss-Prot to Cellosaurus, 40 years of biocuration Amos Bairoch								
Tuesday, July 22	9:00	Computational biology in the age of AI agents James Zou								
Wednesday, July 23	9:00	Building the future of Al-driven structure-based drug discovery Charlotte Deane								
Thursday, July 24	16:20	A Conversation with Nobel Laureate David Baker: Inspiration from a Life in Science David Baker								
	16:45	Decoding cellular systems: From observational atlases to generative interventions Fabian Theis								

^{*}Click here to visit the Distinguished Keynotes page.

Read on for a preview of the abstracts for each keynote happening taking place at ISMB/ECCB 2025!

JOHN JUMPER

Time: Sunday, July 20, 2025 at 6:30PM

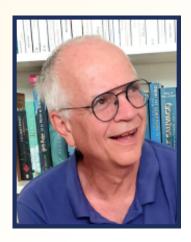


Extending AlphaFold to make predictions across the universe of biomolecular interactions

The high accuracy of AlphaFold 2 in predicting protein structures and protein-protein interactions raises the question of how to extend the success of AlphaFold to general biomolecular modeling, including protein-nucleic and protein-small molecule structure predictions as well as the effects of post-translational modification. In this talk, I will discuss our latest work on AlphaFold 3 to develop a single deep learning system that makes accurate predictions across these interaction types, as well as examine some of the remaining challenges in predicting the universe of biologically-relevant protein interactions.

AMOS BAIROCH

Time: Monday, July 21, 2025 at 9:00AM



Plus ça change, plus c'est la même chose": from Swiss-Prot to Cellosaurus, 40 years of biocuration

Amos Bairoch will reflect on 40 years of biocuration, from Swiss-Prot to Cellosaurus, highlighting how core challenges and values have endured despite the many developments in computational biology over that time.

JAMES ZOU

Time: Tuesday, July 22, 2025 at 9:00AM

Computational biology in the age of AI agents

Al agents—large language models equipped with tools and reasoning capabilities—are emerging as powerful research enablers. This talk will explore how computational biology is particularly well-positioned to benefit from rapid advances in agentic AI. I'll first introduce the Virtual Lab—a collaborative team of AI scientist agents conducting in silico research meetings to tackle open-ended research projects. As an example application, the Virtual Lab designed new nanobody binders to recent Covid variants that we experimentally validated. Then I will present CellVoyager, a data science agent that analyzes complex genomics data to derive new insights. Finally I will discuss using AI agents to discover and explain new biological concepts encoded by large protein foundation models (interPLM). I will conclude by discussing limits of agents and a roadmap for human researcher-AI collaboration.

CHARLOTTE DEANE

Time: Wednesday, July 23, 2025 at 9:00AM



Building the future of Al-driven structure-based drug discovery

The development of new therapeutics typically takes many years and requires over \$1bn in investment. Computational methods and in particular, machine learning, have shown great promise for increasing the speed and reducing the cost of therapeutic development. In this talk I will describe some of the novel computational tools and databases we are pioneering from accurate rapid structure prediction to the prediction of their affinity and binding, looking at both their promise and limitations.

DAVID BAKER

Time: Thursday, July 24, 2025 at 4:20PM



A Conversation with Nobel Laureate David Baker: Inspiration from a Life in Science

This special fireside chat features Nobel Laureate David Baker in a candid and inspiring conversation with Christine Orengo. Rather than exploring the technical details of his groundbreaking research, this 20-minute session will highlight the moments, mindsets, and motivations that shaped his journey—from early curiosity to Nobel recognition. Together, they'll reflect on the role of creativity, perseverance, and vision in scientific discovery, offering insight and encouragement for the next generation of researchers.

FABIAN THEIS

Time: Thursday, July 24, 2025 at 4:45PM



Decoding cellular systems: From observational atlases to generative interventions

Over the past decade, the field of computational cell biology has undergone a transformation — from cataloging cell types to modeling how cells behave, interact, and respond to perturbations. In this talk, I will review and explore how machine learning is enabling this shift, focusing on two converging frontiers: integrated cellular mapping and actionable generative models.

I'll begin with a brief overview of recent advances in representation

learning for atlas-scale integration, highlighting work across the Human Cell Atlas and beyond. These efforts aim to unify diverse single-cell and spatial modalities into shared manifolds of cellular identity and state. As one example, I will present our recent multimodal atlas of human brain organoids, which integrates transcriptomic variation across development and lab protocols.

From there, I'll review the emerging landscape of foundation models in single-cell genomics, including our work on Nicheformer, a transformer trained on millions of spatial and dissociated cells. These models offer generalizable embeddings for a range of tasks—but more importantly, they set the stage for predictive modeling of biological responses.

I'll close by introducing perturbation models leveraging generative AI to model interventions on these systems. As example I will show Cellflow, a generative framework that learns how perturbations such as drugs, cytokines or gene edits — shift cellular phenotypes. It enables virtual experimental design, including in silico protocol screening for brain organoid differentiation. This exemplifies a move toward models that not only interpret biological systems, but help shape them.

EXHIBITORS

We have so many exhibitors to connect with at ISMB/ECCB 2025! Make sure to stop by the Exhibit Area in Hall 2 of the Lower Galleria. To see the map of the exhibition area, visit the Exhibitors page or view the Resources page on the virtual platform.











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2025 Green Challenges



Let's go green, together! Each day of the conference is a chance to take small but meaningful steps toward a more sustainable future. Join the daily challenges, share your actions, and inspire your fellow attendees to make a difference one eco-friendly choice at a time.



Sunday, July 20: "Come Together" and Take the Green Pledge!

Kick off the week by signing the ISCB Green Pledge and commit to sustainable practices! Your pledge is a powerful step toward a greener scientific community. Let's come together and make it count!



Monday, July 21: "Strawberry Fields Forever"

Go meatless for the day and enjoy plant-based meals! Share your favorite veggie dish or recipe on Nucleus using #greeniscb.



Tuesday, July 22: "Carry That Weight" (Lightly)

Wear your oldest ISMB shirt and pack light! Post a photo of your retro look or minimalist luggage on the Nucleus Newsfeed using #greeniscb.



Wednesday, July 23: "All You Need is Less"

Ditch single-use items! Share a photo of your reusable tote bag, water bottle, or coffee mug on the Nucleus Newsfeed using #greeniscb. Or, show it off at the ISCB booth to grab a sticker!



Thursday, July 24: "Get Back" to Low Carbon Living

Take action by donating to the ISCB Groves to plant trees and offset CO2 emissions. Together, we can "get back" to a healthier planet and embrace sustainable living. Share your pledge or donation on the Nucleus Newsfeed using #greeniscb and inspire others to join the movement!

Interested in joining the Green Committee? Email green@iscb.org

ABRIDGED AGENDA

Sunday, July 20								
9:00 - 16:30	ISCB Board of Directors Meeting							
9:00 - 18:00	Tutorials							
9:00 - 18:00	Student Council Symposium and Poster Session							
9:00 - 18:00	Youth Bioinformatics Symposium and Scientific Challenge							
15:30 - 18:00	Fellows Workshop (by invitation only)							
16:00 - 18:00	Career Fair							
18:30 - 19:30	Keynote Speaker - John Jumper							
19:30 - 21:00	Welcome Networking Reception							

Visit the Abridged Agenda page.

	Monday, July 21												
8:40 - 9:00	Morning Welcome and Keynote Introduction, including the presentation of the 2025 Class of Fellows												
9:00 - 10:00	Keynote Speaker — Amos Bairoch (2025 Accomplishments by a Senior Scientist award winner)												
10:00 - 11:20	Caffeinate and Connect with Posters and Exhibitors - Coffee Break												
10:00 - 18:00	Wikipedia Hackathon - complimentary registration required												
11:20 - 13:00	MLCSB	UK	Gen Comp	BOSC	3D	Varl	NIH	Tech Track	Public- ations: Navigating Journal Submissions	Evol Comp Gen			
13:00 - 14:00	Lunch and Bioinformatics4Women Meet-Up												
14:00 - 16:00	MLCSB	UK	Gen Comp	BOSC	3D	Varl	NIH	Tech Track	DREAM	Evol Comp Gen			
16:00 - 16:40	Caffeinate and Connect with Posters and Exhibitors - Coffee Break												
16:40 - 18:00	MLCSB	UK	Gen Comp	BOSC	3D	Varl	NIH	Tech Track	DREAM	Evol Comp Gen			
18:00 - 19:30	Bioinformatics in the UK Reception - ticketed event										- ,		

					Tuesday,	, July 22					
8:40 - 9:00	Morning Welco	me and Keynote	Introduction								
9:00 - 10:00	Keynote Speak	er — James Zou (2025 Overton	Prize Award winn	ier)						
10:00 - 11:20	Caffeinate and	Connect with Po	osters and Exh	ibitors - Coffee Bı	reak						
11:20 - 13:00	MLCSB	NetBio	CSI	BOSC & BOKR	3D	SysMod	CompMS	Tech Tracks		Function &EvolCom pGen	TransMed
13:00 - 14:00	Lunch and LBG	iTQ+ Meet Up									
14:00 - 16:00	MLCSB	NetBio	CSI	BOSC & BOKR	3D	SysMod	CompMS	Tech Tracks	Function	EvolComp Gen	TransMed
16:00 - 16:40	Caffeinate and	Connect with Po	osters and Exh	ibitors - Coffee Bı	reak						
16:40 - 18:00	MLCSB	NetBio	CSI	BOSC & BOKR	3D	SysMod	CompMS	Tech Tracks	Function	EvolComp Gen	TransMed
18:00 - 19:30	Success Circles	s - Reinvented Ne	etworking whe	ere participants ar	e grouped in	to small circles, e	each led by a kno	wledgeable fa	acilitator		

Visit the <u>Abridged Agenda</u> page.

					Wednesday, Jul	y 23					
8:40 - 9:00	Morning We	lcome and Keyr	note Introducti	on, including th	e presentation of the 202	5 Outstanding	Contributions t	to ISCB Awar	d to Lucia Peixoto		
9:00 - 10:00	Keynote Spe	eaker — Charlot	te Deane								
10:00 - 11:20	Caffeinate a	nd Connect wit	th Posters and I	Exhibitors - Coff	fee Break						
11:20 - 13:00	HitSeq	NetBio	CAMDA	BOKR	Innovation at the Intersection: Industry's Role in Bioinformatics	Educa- tion	BioInfo Core	Code Fest	NIH-ODSS/ Elixir	RegSys	iRNA
13:00 - 14:00	Lunch and IS	SCB Town Hall									
14:00 - 16:00	HitSeq	NetBio & Micro- biome	CAMDA	BOKR		Educa- tion	BioInfo Core	Code Fest	NIH-ODSS/ Elixir	RegSys	iRNA
16:00 - 16:40	Caffeinate a	nd Connect wit	th Posters and I	Exhibitors - Coff	fee Break						
16:40 - 18:00	HitSeq	Micro- biome	CAMDA	BOKR		Educa- tion	BioInfo Core	Code Fest	NIH-ODSS/ Elixir	RegSys	iRNA
18:00 - 18:45	JPI Meet-Up)									
19:00 - 21:00	All Conferer	nce Networking	Event at Punch	n Tarmeys and A	ArCains - Ticketed Event						

Visit the <u>Abridged Agenda</u> page.

					Thursday, Jul	y 24						
8:40 - 10:00	HitSeq	Micro- biome	Gen Comp	CAMDA	Stewardship Critical Infrastructure	BioVis	WEB	Code Fest	Text mining	RegSys	iRNA	
10:00 - 11:20	10:00 - 11:20 Caffeinate and Connect with Posters and Exhibitors - Coffee Break											
11:20 - 13:00	HitSeq	Micro- biome	Gen Comp	CAMDA	Stewardship Critical Infrastructure	BioVis	WEB	Code Fest	Text mining	RegSys	iRNA	
13:00 - 14:00	Lunch with	Posters										
14:00 - 16:00	HitSeq	Micro- biome	Gen Comp	CAMDA	Stewardship Critical Infrastructure	BioVis	WEB	Code Fest	Text mining	RegSys	iRNA	
16:00 - 16:20	Grab and G	o Coffee Break										
16:20 - 18:00	Keynote Sp	eakers (David Ba	aker & Fabian T	heis, the 2025 I	nnovator Award winr	ner) and Closin	ng Ceremoni	es				

Visit the <u>Abridged Agenda</u> page.

VETUAL (ALD) REESON TUNCION DHAILS

VIRTUAL TUTORIALS

TUTORIAL VT1: VISUALISING AND INTERPRETING YOUR - OMICS RESULTS USING GGPLOT2 AND R

Date: July 14, 2025; 9:00 — 14:00

Organizer: Emily Johnson

Speakers:

Emily Johnson, University of Liverpool Lauren Mee, University of Liverpool

Euan McDonnell, University of Liverpool

This full-day tutorial introduces participants to the principles of impactful data visualisation and equips them with the skills to create publication-ready visualisations for -omics data. Designed for beginners with basic knowledge of the R programming language, the tutorial will guide attendees through creating and interpreting key visualisations such as volcano plots, box plots, heatmaps, dot plots, and network diagrams.

Participants will work with real biological datasets in Quarto notebooks and learn how to use tools like ggplot2, ComplexHeatmap, igraph, ggraph, and ClusterProfiler. Through hands-on coding exercises and interactive lectures, attendees will develop an intuition for ggplot2's grammar of graphics, best practices in data visualisation, and the application of functional enrichment methods to contextualise results.

Whether you are a student or researcher wanting to improve your visualisation skills, or a computational biologist looking to enhance the presentation of your results, this tutorial will provide the tools and knowledge to produce professional-quality figures.

See the full schedule here.

TUTORIAL VT2: OMICSVIZ: INTERACTIVE VISUALIZATION AND ML FOR OMICS DATA

Date: July 15, 2025; 9:00 — 18:00 **Organizer:** Ragothaman M. Yennamalli

Speakers:

Ragothaman M. Yennamalli, SASTRA Deemed to be University

Shashank Ravichandran, Incedo Inc

Megha Hegde, Kingston University London

Jean-Christophe Nebel, Kingston University London

Farzana Rahman, Kingston University London

Data Science and Machine Learning are intricately connected, particularly in computational biology. In a time when biological data is being produced on an unprecedented scale — encompassing genomic sequences, protein interactions, and metabolic pathways- meeting the demand has never been more crucial.

Data visualization plays a crucial role in biological data sciences since it allows the transformation of complex, often incomprehensible raw data into visual formats that are easier to understand and interpret. This allows biologists to recognize patterns, anomalies, and correlations that would otherwise be lost in the sheer volume of data. In addition, machine learning (ML) has brought about a revolution in the analysis of biological data. Exploiting extensive datasets, ML provides tools to model complex systems and generate predictions. Indeed, ML algorithms excel at uncovering subtle patterns in data, contributing to tasks like predicting protein structures, comprehending genetic variations and their implications for diseases, and even facilitating drug discovery by predicting molecular interactions.

The integration of data visualization and machine learning is particularly powerful. In particular, visualization may aid in interpreting machine learning models, allowing biologists to understand and trust their predictions. It could also help fine-tune these models by identifying outliers or anomalies in the data.

Due to its remarkable capability, there has been a surge in the development and application of tools that combine data visualization and machine learning in biology. Platforms that integrate these technologies enable biologists to conduct comprehensive analyses without needing deep expertise in computer science. Assuredly, this democratization of data science and ML has empowered more and more biologists to engage in sophisticated, data-driven research.

See the full schedule here.

TUTORIAL VT3: COMPUTATIONAL APPROACHES FOR DECIPHERING CELL-CELL COMMUNICATION FROM SINGLE-CELL TRANSCRIPTOMICS AND SPATIAL TRANSCRIPTOMICS DATA

Date: July 15, 2025; 9:00 — 13:00

Organizer: Giulia Cesaro

Speakers:

Giulia Cesaro, University of Padova James Shiniti Nagai, RWTH Aachen University Mayra Ruiz, RWTH University Hospital Barbara di Camillo, University of Padova Ivan G. Costa, RWTH University Hospital Giacomo Baruzzo, University of Padova

Tissues and organs are complex and highly-organized systems composed of diverse cells that work together to maintain homeostasis, drive development and mediate complex disease

progression as Myocardial Infarction (Kuppe et al. 2022). A key focus of modern biology is understanding how heterogeneous populations of cells coexist and communicate with each other (intercellular signaling), how they properly respond (intracellular signaling) within a tissue and organ system and how these processes vary across different experimental conditions (comparative analysis). Recently, a rapid expansion of computational tools exploring the expression of ligand and receptor has enabled the systematic inference of cell-cell communication from single-cell transcriptomics and spatial transcriptomics data (Armingol et al. 2021; Armingol, Baghdassarian, and Lewis 2024). These are crucial in unravelling the complex landscape of biological systems.

This tutorial aims to provide a comprehensive introduction to computational approaches for cell-cell communication inference using high throughput transcriptomics data. It covers the fundamental concepts of cellular communication and assumptions underlying analysis focusing on the main computational methods used in the field. This includes computational approaches for inter-cellular communication inference (CellphoneDB (Efremova et al. 2020); LIANA (Dimitrov et al. 2022, 2024)) and for intra-cellular signals communication (scSeqComm (Baruzzo, Cesaro, and Di Camillo 2022); NicheNet (Browaeys, Saelens, and Saeys 2019)). Next, we will describe approaches for comparative analysis of cell-cell networks in distinct biological conditions (CrossTalkeR (Nagai et al. 2021)) and methods for spatially resolved cell-cell communications (Ischia (Regan-KomitoDaniel 2024); DeepCOLOR (Kojima et al. 2024)).

In the first part of the tutorial, participants will be introduced to the theoretical basis of state-of-the-art computational approaches and will learn how to use representative tools for inferring intercellular signaling and intracellular signaling pathways. In the second part, we will focus on the comparative analyses, i.e. changes of cell-cell communication in two conditions, and subsequently highlighting the unique insights spatial transcriptomics data can provide for understanding tissue architecture and cellular communication. Both sections will be followed by a hands-on component based on the analysis of single cell and spatial transcriptomics data from the myocardial infarction atlas (Kuppe et al. 2022). To promote transparency, all the codes, software tools and the datasets used throughout the tutorial will be available and accessible through open-access repositories (e.g. GitHub repositories or Zenodo platforms).

See the full schedule <u>here</u>.

TUTORIAL VT4: AN APPLIED GENOMICS APPROACH TO CROP BREEDING: A SUITE OF TOOLS FOR EXPLORING NATURAL AND ARTIFICIAL DIVERSITY

Date: July 15, 2025; 14:00 — 18:00

Organizer: Maria Skrabisova

Speakers:

Trupti Joshi, University of Missouri-Columbia
Yen On Chan, University of Missouri-Columbia

Maria Skrabisova, Palacky University in Olomouc

Jana Biova, Palacky University in Olomou

The urgent need for crop improvement is hindered by the lack of precision in crop breeding. Although significant progress has been made in genomics, many causal genes of important agronomic and nutritional traits remain unknown. This is due to the inefficient identification of causal genetic features in candidate genes. With the growing body of sequencing data and phenotype information, current advances in genomics and the development of bioinformatics tools offer improvements in candidate gene selection. In this workshop, SoyHUB, the suite of tools, strategies, and solutions for soybean applied genomics, will be presented along with its extension to other crops at KBCommons. Our methodology for data integration, curation, reuse, and leveraging will be highlighted. Practical utilization of integrated data with the tools will be demonstrated. We will focus on the selection of best-performing markers, identification of causal genes, and exploration of alleles and genomic variation. We will cover simple Mendelian traits, showing how to analyze variation in protein-coding regions and promoters and touch on copy number variation. Solutions for complex cases, such as multiple independent alleles in a single gene or quantitative traits, will also be introduced. This workshop will highlight recent achievements in leveraging big data to improve precision in GWAS-driven discoveries and, therefore, accelerate the breeding of soybean and other crops.

See the full schedule here.

TUTORIAL VT5: COMPREHENSIVE BIOINFORMATICS AND STATISTICAL APPROACHES FOR HIGH-THROUGHPUT SEQUENCING DATA ANALYSIS, INCLUDING SCRNA-SEQ, IN BIOMARKER DISCOVERY

Date: July 14, 2025; 14:00 - 18:00

Organizer: Xiaoli Zhang

Speakers:

Xiaoli Zhang and Lianbo Yu

With the significant advancements in genomic profiling technologies and the emergence of selective molecular targeted therapies, biomarkers have played an increasingly pivotal role in

both the prognosis and treatment of various diseases, most notably cancer. This workshop is designed to begin with an introductory overview of basic concepts of biomarkers, the diverse categories of biomarkers, commonly employed biotechnologies for biomarker detection, with a special focus on gene mutation and gene expression using DNA-seq, RNA-seq, and scRNA-seq data. Furthermore, we will discuss processes of biomarker discovery and development, and outlining the key steps involved and the current analytical methodologies utilized. Following this, we will discuss the identification of driver gene mutations and altered gene expression, using The Cancer Genome Atlas (TCGA) lung cancer data and PBMC scRNA-seq data as illustrative examples with using R code as practical demonstrations to enhance understanding. In the latter part of this workshop, we will discuss commonly utilized biostatistics and bioinformatics tools, including data visualization, survival analysis and machine learning methods, which are employed to predict disease progression and patient survival outcomes based on these critical biomarkers. By the conclusion of this course, participants will have acquired a broad and fundamental understanding of biomarker discovery, particularly in cancer. This encompasses key concepts, data sources, data analysis techniques, and interpretation strategies. Such expertise will equip participants with the knowledge necessary in contributing to the development of precision medicine in cancer patient treatment.

See the full schedule <u>here</u>.

TUTORIAL VT6: BEYOND BIOINFORMATICS: SNAKEMAKE FOR VERSATILE COMPUTATIONAL WORKFLOWS

Date: July 14, 2025; 9:00 – 13:00 **Organizer:** Carlos H. M. Rodrigues

Speakers: Carlos H. M. Rodrigues, Australian Centre for Disease Preparedness

Snakemake is a powerful, Python-based workflow management system that revolutionises how computational tasks are designed, executed and reproduced. By allowing researchers to define workflows as a series of interconnected rules, Snakemake simplifies complex computational pipelines and ensures reproducibility across diverse scientific domains. This intensive workshop introduces participants to the full potential of Snakemake, moving beyond traditional bioinformatics applications to demonstrate its versatility in machine learning and data analysis.

Designed for researchers dealing with complex computational challenges, this tutorial will explore Snakemake's capabilities through practical, hands-on examples that span multiple disciplines. Participants will learn how to create robust, scalable, and efficient workflows that can adapt to various research challenges. By the end of the workshop, attendees will have a comprehensive understanding of workflow management principles and the skills to implement sophisticated pipelines using Snakemake.

See the full schedule <u>here</u>.

TUTORIAL VT7: ASSESSING AND ENHANCING DIGITAL ACCESSIBILITY OF BIOLOGICAL DATA AND VISUALIZATIONS

Date: July 15, 2025; 14:00 — 18:00

Organizers and Speakers:

Sehi L'Yi Thomas C. Smits Lawrence Weru Nils Gehlenborg

As computational biologists, we produce biological datasets, visualizations, and computational tools. Our shared goal is to make our data and tools widely usable and accessible. However, we often fail to meet the needs of certain groups of people. Our recent comprehensive evaluation [1] (https://inscidar.org) shows that biological data resources are largely inaccessible to people with disabilities, with severe accessibility issues in almost 75% of all 3,112 data portals included in the study. To address the critical accessibility barriers, it is important to increase awareness of accessibility in the community and teach the workforce practical ways to enhance the accessibility of biological data resources. While there are existing resources and training opportunities that focus on content that includes no or little data, there is a lack of solutions and resources that provide insights into how to make data-intensive content accessible.

Our tutorial is designed to help participants understand the importance of digital accessibility in computational biology and practice various approaches to test and implement digital accessibility of biological data and visualizations. We will demonstrate our evaluation results [1] to help participants understand the critical barriers in biological research and education for people with disabilities, such as those involving vision, cognitive, and physical function. We will use hands-on examples that are familiar to and widely used by computational biologists, such as computational notebooks, genome browsers, and other visualizations. Our tutorial will conclude by introducing open problems and recent innovations, such as the accessibility of interactive genomics data visualizations [2]. We will ensure that our tutorial and all the materials are accessible.

Liya Zaygerman

TUTORIAL VT8: GENERATIVE AI FOR SINGLE-CELL PERTURBATION MODELING: THEORETICAL AND PRACTICAL CONSIDERATIONS

Date: July 14, 2025; 14:00 — 18:00

Organizers: Speakers:

Marina Esteban-Medina George Gavriilidis, Centre for Research and Technology Hellas

Konstantinos I. Giatras, National and Kapodistrian University of

Rosario Astaburuaga-García Athens

Aspasia Orfanou Gobikrishnan Subramaniam, Queen's University Belfast

Vasileios Vasileiou Sabrina Jagot, Institut NeuroMyoGen

Alejandro Madrid, Barcelona Supercomputing Center

Single-cell perturbation modelling is revolutionising our ability to predict how genes, drugs and external stimuli reshape cellular physiology. In this half-day virtual tutorial you will get hands-on with two highly performant Generative AI models—scGen and scPRAM—and learn how to benchmark them rigorously with the latest Perturb-Bench workflows. You will preprocess real single-cell datasets, train each model, evaluate them with metrics such as R² and Energy-distance, and discuss best practices for extrapolating to unseen patients and even across datasets. Practical notebooks, datasets and slides are distributed under a permissive CC-BY licence via GitHub and Jupyter Book (https://jupyterbook.org/en/stable/intro.html). Recorded versions of taught material will be available via YouTube after the conference.

See the full schedule here.

TUTORIAL VT9: BIOMEDICAL TEXT MINING FOR KNOWLEDGE EXTRACTION

Date: July 15, 2025; 9:00 — 13:00

Organizer: Jake Lever

Speakers:

Jake Lever, University of Glasgow Zaiqiao Meng, University of Glasgow

Javier Sanz-Cruzado Puig, University of Glasgow

Modern bioinformatics analyses rely heavily on the existing knowledge of the role of genes and mutations in different diseases, as well as the complex interactions between genes, proteins and drugs. However, access to this information is often limited for many biomedical problems, especially niche areas, due to lack of knowledge bases and large curation costs. The information is often locked in the text of the original research papers. Machine learning methods, particular

natural language processing techniques, offer an automated approach to extracting knowledge from the research literature to build bespoke knowledge bases for scientists' needs. This tutorial will provide a hands-on introduction to the core tasks in biomedical natural language processing (BioNLP). These include identifying mentions of important concepts (e.g. phenotypes, cell-lines, etc) and extracting nuanced relationships between them. Finally, it will show how large language models have changed how information can be quickly extracted, but also highlight their challenges.

See the full schedule here.

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IN-PERSON TUTORIALS

TUTORIAL IP1: MACHINE LEARNING FOR OMICS: BEST PRACTICES AND REAL-LIFE INSIGHTS WITH TIDYMODELS

Room: 11A

Date: July 20, 2025; 9:00 – 18:00

Organizer: Jamie Soul

Speakers:

Jamie Soul, University of Liverpool

Eva Caamano Gutierrez, University of Liverpool

Anthony Evans, University of Liverpool

Omics data analysis presents unique challenges due to its high dimensionality and complexity. Supervised machine learning (ML) offers powerful tools for gaining insights from these data but currently faces a crisis of reproducibility due to poor adherence to best practices when undertaking feature selection, model evaluation, and needs for further interpretability.

This full-day tutorial introduces participants to the common pitfalls and best practices of applying ML to omics research. It exemplifies good practice through example using the Tidymodels framework for ML workflows in R, tailored to omics applications. The course will feature a mixture of lectures, quizzes, real-life coding tutorials and hands-on practicals with 1-1 support. Example applications will illustrate regression analysis with methylation clocks, gene prioritisation and classification with cancer biomarker discovery.

Special attention will be paid to challenges in working with highly multivariate data and integrating various data types as well as providing tips to extract meaningful insights from complex data. Beginner-level R skills are required, and attendees will leave with practical skills to apply Tidymodels to their own datasets.

TUTORIAL IP2: MASSIVELY PARALLEL REPORTER ASSAYS IN FUNCTIONAL REGULATORY GENOMICS AND AS PART OF THE IGVF DATA RESOURCE

Room: 03A

Date: July 20, 2025; 9:00 — 18:00

Organizer: Martin Kircher

Speakers:

Martin Kircher, University of Lübeck and Kiel University
Max Schubach, Berlin Institute of Health at Charité
Arjun Devadas, University of Lübeck and University Hospital Schleswig-Holstein
Kilian Salomon, Berlin Institute of Health at Charité

This tutorial is designed to empower bioinformatics researchers with the knowledge and skills to effectively utilize Massively Parallel Reporter Assays (MPRAs) data in their work. MPRAs are gaining wider applications across the functional genomics community and are used as part of the Impact of Genomic Variation on Function (IGVF) Consortium. IGVF is a collaborative research initiative funded by the NHGRI that aims to systematically study how genomic variations affect genome function and, consequently, phenotypes. By integrating experimental and computational approaches, IGVF seeks to map and predict the functional impacts of genetic variants, providing a comprehensive catalog of these effects.

This tutorial provides a thorough introduction in MPRAs and IGVF data resources, practical training on MPRA data, and insights into advanced analysis methods for such data. Participants will gain an understanding of MPRA experiments, including their various experimental designs and the rationale for using them in functional genomics. This will involve learning the process of associating tags/barcodes with sequences incorporated in the reporter constructs from raw sequencing reads and counting barcodes from DNA sequencing and RNA expression. The tutorial will guide participants through data processing using MPRAsnakeflow, a streamlined snakemake workflow developed with IGVF for efficient MPRA data handling and QC reporting. Statistical analysis for sequence-level and variant-level effect testing of MPRA count data will be introduced using BCalm, a barcode-level MPRA analysis package developed as part of our IGVF efforts.

Further, the tutorial will provide a starting point for training (deep learning) sequence models on MPRA data and related functional genomics datasets. Participants will learn how to extract meaningful insights from their datasets by investigating the sequence activity relationship and extracting important sequence motifs. By integrating these topics and methods, participants will leave the tutorial equipped with both theoretical knowledge and practical skills necessary for analyzing and using MPRA data effectively.

TUTORIAL IP3: GENOMIC VARIANT INTERPRETATION & PRIORITISATION FOR CLINICAL RESEARCH

Room: 4AB

Date: July 20, 2025; 9:00 — 18:00

Organizer: Aleena Mushtaq

Speakers:

Mallory Freeberg, EMBL's European Bioinformatics Institute (EMBL-EBI)
Aleena Mushtaq, EMBL's European Bioinformatics Institute (EMBL-EBI)
Diana Lemos, EMBL's European Bioinformatics Institute (EMBL-EBI)
James Stephenson, EMBL's European Bioinformatics Institute (EMBL-EBI)
Sarah Hunt, EMBL's European Bioinformatics Institute (EMBL-EBI)
Irene Lopez Santiago, Open Targets Bioinformatician (EMBL - EBI)
Genevieve Evans, EMBL's European Bioinformatics Institute (EMBL-EBI)

The interpretation of genetic variation is important for understanding human health and disease. Increased knowledge leads to societal benefits including faster disease diagnosis, a better understanding of disease progression, more efficient identification and prioritisation of drug targets for testing, resulting in overall better health outcomes for a population. Whilst the speed and cost of sequencing has reduced, the complexity of variant interpretation remains a bottleneck for understanding. This tutorial will explore the variety of annotations and techniques available to assess human variation and the implications of variant effects on human health and disease.

See the full schedule here.

TUTORIAL IP4: QUANTUM MACHINE LEARNING FOR MULTI-OMICS ANALYSIS

Room: 3B

Date: July 20, 2025; 9:00 – 18:00

Organizer: Aritra Bose

Speakers:

Aritra Bose, IBM Research Laxmi Parida, ISCB Fellow

Hakan Doga, IBM Research Bryan Raubenolt, Cleveland Clinic

Akhil Mohan, Cleveland Clinic Filippo Utro, IBM Research

Single-cell and population-level multi-omics analyses have greatly enhanced our understanding of biological complexity. By integrating various types of biological data—such as genomics, proteomics, and transcriptomics, collectively known as multi-omics—these approaches have

provided deep insights into the molecular mechanisms underlying complex diseases, both at the cellular level and across patient populations. As the size and complexity of multi-omics data continues to grow, the need to leverage emerging technologies such as artificial intelligence (AI) and quantum computing (QC) also grows. Recently, advances in QC have shown promise in solving real-world problems in machine learning and optimization in biomedicine, drug discovery, biomarker discovery, clinical trials, among other healthcare and life sciences objectives [1,2,3,4,5].

In this tutorial, participants will learn the fundamental concepts of QC, engage in hands-on experiments that apply classical machine learning (ML) techniques. They will also learn best practices for pre-processing multi-omics data in preparation for quantum machine learning (QML) tasks. Through a systematic evaluation of various data complexity measures and their impact on the performance of different ML and QML models, participants will gain insights into when to effectively utilize QML models. Additionally, they will explore quantum-classical hybrid workflows for ML, with a focus in biomedical data analysis.

See the full schedule here.

TUTORIAL IP5: INTRODUCTION TO CAUSAL ANALYSIS USING MENDELIAN RANDOMISATION

Room: 12

Date: July 20, 2025; 9:00 — 13:00 Organizer: Handan Melike Dönertaş

Speakers:

Handan Melike Dönertaş, Fritz Lipmann Institute on Aging

Mark Olenik, Fritz Lipmann Institute on Aging Tayyaba Alvi, Fritz Lipmann Institute on Aging

Mendelian randomisation (MR) is a method that uses genetic variation associated with an exposure (e.g., behaviours, biomarkers) to infer its causal effect on an outcome (e.g. health status). In statistical terms, it functions as an "instrumental variable" approach.

By mimicking the design of a randomised controlled trial through genetic inheritance, MR provides a framework for addressing confounding and reverse causation, making it a valuable tool in epidemiological and biomedical research.

This workshop offers a beginner-friendly introduction to the key concepts and assumptions underlying MR, such as the use of genome-wide association study (GWAS) data and the three key assumptions for valid instrumental variables: relevance, independence, and exclusion restriction. Participants will explore common challenges in MR analysis, including pleiotropy,

population stratification, and measurement error while learning strategies to overcome these using advanced methods. The workshop also includes a two-hour hands-on session in which attendees will work with real-world data to conduct MR analyses using R. By the end of the session, participants will have a clear understanding of MR principles, the ability to critically evaluate MR studies, and practical skills to apply MR methods in their own research.

See the full schedule here.

TUTORIAL IP6: HELLO NEXTFLOW: GETTING STARTED WITH WORKFLOWS FOR BIOINFORMATICS

Room: 11BC

Date: July 20, 2025; 9:00 — 13:00

Organizer and Speaker: Geraldine Van der Auwera

Nextflow is a powerful and flexible open-source workflow management system that simplifies the development, execution, and scalability of data-driven computational pipelines. It is widely used in bioinformatics and other scientific fields to automate complex analyses, making it easier to manage and reproduce large-scale data analysis workflows.

This training workshop is intended as a "getting started" course for students and early-career researchers who are completely new to Nextflow. It aims to equip participants with foundational knowledge and skills in three key areas: (1) understanding the logic of how data analysis workflows are constructed, (2) Nextflow language proficiency and (3) command-line interface (CLI) execution.

Participants will be guided through hands-on, goal-oriented exercises that will allow them to practice the following skills:

- Use core components of the Nextflow language to construct simple multi-step workflows effectively.
- Launch Nextflow workflows locally, navigate output directories to access results, interpret
 log outputs for insights into workflow execution, and troubleshoot basic issues that may
 arise during workflow execution.

By the end of the workshop, participants will be well-prepared for tackling the next steps in their journey to develop and apply reproducible workflows for their scientific computing needs. Additional study-at-home materials will be provided for them to continue learning and developing their skills further.

TUTORIAL IP7: AI LARGE CELLULAR MODELS AND IN-SILICO PERTURBATION

Room: 11BC

Date: July 20, 2025; 14:00 — 18:00

Organizer: Xuegong Zhang

Speakers:

Xuegong Zhang, Tsinghua University

Chen Li, Tsinghua University

Erpai Luo, Tsinghua University
Mo Chen, Tsinghua University

Transformer-based large language models (LLMs) are changing the world. The capabilities they illustrated in sophisticated natural language, vision and multi-modal tasks have inspired the development of large cellular models (LCMs) for single-cell transcriptomic data, such as scBERT, Geneformer, scGPT, scFoundation, GeneCompass, scMulan, etc. After pretraining on massive amount of single-cell RNA-seq data agnostic to any downstream task, these transformer-based models have demonstrated exceptional performance in various tasks such as cell type annotation, data integration, gene network inference, and the prediction of drug sensitivity or perturbation responses. Such advancements, albeit still in their early stage, suggested promising revolutionary approaches for leveraging AI to understand the complex system of cells from extensive datasets beyond human analytical capacity. Especially, such models have made it possible to conduct in-silico perturbation on cells of various types to predict their responses to gene perturbations without doing experiments on the cells. These models provided prototypes of digital virtual cells that can be used to reconstruct and simulate live cells, which will revolutionize many aspects of future biomedical studies.

Although the community is high enthusiastic to these exciting progresses, the structures and algorithms of LCMs and other similar-scale AI models are mysterious to many people who were not equipped with relevant backgrounds. This tutorial will try to fill this gap. In the tutorial, we will begin from an introduction of basic principles of deep neural networks, and explain the basic structure and algorithm of the original Transformer for natural language tasks. We'll show to the attendees how to build such models based on current machine learning platforms. Then we'll introduce several successful ways to build large cellular models based on the basic Transformer model, and overview how such models are pretrained on single-cell RNA-seq data. We'll show and let the attendees to practice how to use LCMs for basic tasks such as cell type annotation, and look into the specific application of LCMs on in-silico perturbation tasks. Attendees will engage in hands-on activities such as building basic transformer models and executing downstream single-cell tasks, including cell type annotation and in-silico perturbation. These activities will remove the mystery of LCMs for the attendees and help them better understand and feel how LCMs can be built and applied.

TUTORIAL IP8: REPRESENTATION LEARNING AND FEATURE ENGINEERING FOR GENOMIC SEQUENCES ANALYSIS

Room: 12

Date: July 20, 2025; 14:00 — 18:00

Organizer: Fabiana Goes

Speakers:

Fabiana Goes, The Rosalind Franklin Institute

Aparajita Karmakar, The University of Edinburgh and The Rosalind Franklin Institute, UK

Machine learning (ML) has been successfully applied in different omics problems, such as sequence classification in the field of genomics. The effectiveness of ML methods relies greatly on the selection of the data representation, or features, that extract meaningful information from sequences. Genomic sequences can be viewed as one-dimensional strings of successive letters representing nucleotides. However, to make these sequences compatible with ML methods, they must first be transformed into structured numerical representations, such as vectors or matrices. Traditional methods for sequence classification often rely on manually crafted or pre-defined features, which require domain expertise and may not fully capture the complexity of the underlying biological information. Recently, representation learning has emerged as a powerful alternative, enabling the automatic extraction of latent patterns directly from raw data and reducing the dependence on manually crafted features. In genomics, representation learning methods have been introduced to characterize DNA and RNA sequences. In genomics, techniques like Word2Vec, Convolutional Neural Networks (CNNs) and Large Language Models (LLMs) have demonstrated the ability to learn optimal sequence representations that effectively capture both local and global patterns in DNA and RNA sequences.

This tutorial provides a comprehensive introduction to feature engineering and representation learning for genomic sequences (DNA/RNA). Participants will explore traditional techniques for extracting features from genomic sequences, building a foundation in classical approaches. Furthermore, the tutorial will cover representation learning, introducing concepts such as embeddings and their applications. Topics include methods such as Word2vec and LLMs to obtain meaningful representations from genomic sequences. Through hands-on exercises and comparative analyses, attendees will learn to combine traditional feature engineering with representation learning approaches, developing practical skills and insights that are adaptable to diverse genomic research challenges. The goal is to offer participants the knowledge and tools to enhance genomic sequence analysis using different techniques for sequence representation.

POSTER SESSIONS

<u>Posters</u> will take place on the Poster Pitch (Arena) in the Lower Galleria of the ACC Liverpool.

There will be four poster presentation sessions at ISMB/ECCB 2025:

- Session A: Monday, July 21, 2025, 10-11:20 AM and 16:00-16:40 PM
- Session B: Tuesday, July 22, 2025, 10-11:20 AM and 16:00-16:40 PM
- Session C: Wednesday, July 23, 2025, 10–11:20 AM and 16:00–16:40 PM
- Session D: Thursday, July 24, 2025, 10-11:20 AM and 13:00-14:00 PM

Please review the schedule below for poster set up and dismantle times.

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

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

DISPLAY SCHEDULE

Session A (July 21) and Session B (July 22) Posters:

Poster set up: Monday, July 21 between 8:00 - 8:40

Poster dismantle: Tuesday, July 22 at 18:00

Session C (July 23) and Session D (July 24) Posters:

Poster set up: Wednesday, July 23 between 8:00 - 8:40

Poster dismantle: Thursday, July 24 at 16:00



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



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COSITRACIA SCHEDULES





Online schedule found here.

Monday, July 21; Room 3B Time **Title and Speaker** Decoding Immunity: Structural and Dynamical Insights Driving Antibody Innovation 11:20 Franca Fraternali Rapid and accurate prediction of protein homo-oligomer symmetry using Seq2Symm 12:00 Meghana Kshirsagar Probing Homo-Oligomeric Interaction Signals in Protein Language Models 12:20 **Zhidian Zhang** OrgNet: Orientation-gnostic protein stability assessment using convolutional neural networks. 12:40 **Petr Popov** Simulations in the age of AlphaFold: dynamics, drug resistance and enzyme design 14:00 Adrian Mulholland FlowProt: Classifier-Guided Flow Matching for Targeted Protein Backbone Generation in the de 14:40 novo DNA Methyltransfarase Family Ali Baran Taşdemir Molecular design and structure-based modeling with generative deep learning 15:00 Remo Rohs BC-Design: A Biochemistry-Aware Framework for Highly Accurate Inverse Protein Folding 15:20 Xiangru Tang DivPro: Diverse Protein Sequence Design with Direct Structure Recovery Guidance 15:40 Xinyi Zhou AlphaPulldown2—a general pipeline for high-throughput structural modeling 16:40 **Dmitry Molodenskiy** Extending 3Di: Increasing Protein Structure Search Sensitivity with a Complementary Alphabet 16:50 Michel van Kempen

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3DSIG

	Monday, July 21; Room 3B
Time	Title and Speaker
17:00	PPI3D clusters: non-redundant datasets of protein-protein, protein-peptide and protein-nucleic acid complexes, interaction interfaces and binding sites Justas Dapkunas
17:10	From GWAS to Protein Structures: Illuminating Stress Resistance in Plants Su Datt Lam
17:30	Chromatin as a Coevolutionary Graph: Modeling the Interplay of Replication with Chromatin Dynamics Sevastianos Korsak
17:40	RNA-TorsionBERT: leveraging language models for RNA 3D torsion angles prediction Clément Bernard



- **Registration is free!**
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https://www.iscb.org/iscbacademy-webinars



Tuesday, July 22; Room 3B

Time	Title and Speaker
11:20	A (bio)computational perspective on protein folding, function and evolution Diego Ulises Ferreiro
12:00	Structural Phylogenetics: toward an evolutionary model capturing both sequence and structure David Moi
12:20	The structural and functional plasticity of the GNAT fold: A case of convergent evolution Joel Roca Martinez
12:40	Virus targeting as a dominant driver of interfacial evolution in the structurally resolved human-virus protein-protein interaction network Wan-Chun Su
14:00	Novel structural arrangements from a billion-scale protein universe Nicola Bordin
14:20	Towards a comprehensive view of the pocketome universe – biological implications and algorithmic challenges Hanne Zillmer
14:40	Towards a Biophysical Description of the Protein Universe Miguel Fernandez-Martin
14:50	Computational methods for the characterisation and evaluation of protein-ligand binding sites Javier Sánchez Utgés
15:00	FlowDock: Geometric Flow Matching for Generative Protein-Ligand Docking and Affinity Prediction Alex Morehead
15:20	Mapping and characterization of the human missense variation universe using AlphaFold 3D models Alessia David



Tuesday, July 22; Room 3B

Time	Title and Speaker
15:40	CATH-ddG: towards robust mutation effect prediction on protein–protein interactions out of CATH homologous superfamily Guanglei Yu
16:40	Investigating Enzyme Function by Geometric Matching of Catalytic Motifs Raymund Hackett
17:00	Cellular location shapes quaternary structure of enzymes. Gyorgy Abrusan
17:20	In silico design of stable single-domain antibodies with high affinity Gabriel Cia
17:40	An improved deep learning model for immunogenic B epitope prediction Rakshanda Sajeed



BIOINFO-CORE

Online schedule found here.

	Wednesday, July 23; Room 4AB
Time	Title and Speaker
11:20	Bioimage analysis in the age of AI: lessons and a path forward from a core facility perspective. Damian Dalle Nogare
12:00	The rise of computational imaging
14:00	The practical use of AI in cores
15:00	Benchmarking Variant-Calling Workflows: The nf-core/variant benchmarking Pipeline within the GHGA Framework Kübra Narcı
15:00	Assembly Curator: rapid and interactive consensus assembly generation for bacterial genomes Thomas Roder
15:20	Long Read Sequencing at Genomics England Adam Giess
15:20	Autonomous Single Cell Transcriptomics Analysis in Persist-seq Anil S. Thanki
15:40	Advancing The Expression Atlas Resources: A Scalable Single-Cell Transcriptomics Pipeline to Facilitate Scientific Discoveries Iris Diana Yu
15:40	Mixed effects models applied to single nucleus RNA-seq data identify cell types associated with animal level pathological trait of Alzheimer's disease Ayushi Agrawal
15:40	Optimizing Clustering Resolution for Multi-subject Single Cell Studies Natalie Gill



BIOINFO-CORE

	Wednesday, July 23; Room 4AB
Time	Title and Speaker
16:40	GEO Uploader: Simplifying the data deposition in the GEO repository Hubert Rehrauer
16:40	Enhancing Bioinformatics Workflows with Analytical Visualization Tools Carlos Prieto
16:40	Competency framework profiles to reflect career progression within bioinformatics core facility scientists Patricia Carvajal-López
17:00	Breakout Groups



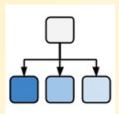


Online schedule found here.

	Thursday, July 24; Room 4AB
Time	Title and Speaker
8:40	Opening
8:45	The Visual Genome: An attempt to classify multi-omics visualization Kay Nieselt
9:40	GENET: AI-Powered Interactive Visualization Workflows to Explore Biomedical Entity Networks Bum Chul Kwon
11:20	Prostruc: an open-source tool for 3D structure prediction using homology modeling Olaitan I. Awe
11:40	ClusterChirp: A GPU-Accelerated Web Platform for AI-Supported Interactive Exploration of High- Dimensional Omics Data Zeynep H. Gümüş
12:00	Can LLMs Bridge Domain and Visualization? A Case Study onHigh-Dimension Data Visualization in Single-Cell Transcriptomics Qianwen Wang
12:20	Automatic Generation of Natural Language Descriptions of Genomics Data Visualizations for Accessibility and Machine Learning Thomas C. Smits
12:40	Sketch, capture and layout Phylogenies Daniel Huson
12:40	PhageExpressionAtlas - a comprehensive transcriptional atlas of phage infections of bacteria Maik Wolfram-Schauerte



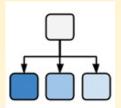
	Thursday, July 24; Room 4AB
Time	Title and Speaker
14:00	SEAL: Spatially-resolved Embedding Analysis with Linked Imaging Data Simon Warchol
14:00	Nightingale - A collection of web components for visualizing protein related data Swaathi Kandasaamy
14:00	A Multimodal Search and Authoring System for Genomics Data Visualizations Huyen N. Nguyen
14:00	Tersect Browser: characterising introgressions through interactive visualisation of large numbers of resequenced genomes Tomasz Kurowski
14:40	Visual Data Analysis Research in Biomedical Applications: Navigating the Line Between Scientific Novelty and Practical Impact Ingrid Hotz



Online schedule found here.

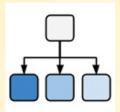
Tuesday, July 22; Room 3A

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Time	Title and Speaker
11:20	Open Knowledge Bases in the Age of Generative AI Chris Mungall
12:20	textToKnowledgeGraph: Generation of Molecular Interaction Knowledge Graphs Using Large Language Models for Exploration in Cytoscape Favour James
12:40	BMFM-RNA: An Open Framework for Building and Evaluating Transcriptomic Foundation Models built on Biomed-Multi-Omic Bharath Dandala
12:40	DOME Registry - Supporting ML transparency and reproducibility in the life sciences Gavin Farrell
12:40	AutoPeptideML 2: An open source library for democratizing machine learning for peptide bioactivity prediction Raúl Fernández-Díaz
14:00	BioPortal: a rejuvenated resource for biomedical ontologies J. Harry Caufield
14:20	Formal Validation of Variant Classification Rules Using Domain-Specific Language and Meta-Predicates Michael Bouzinier
14:40	BioChatter: An open-source framework integrating knowledge graphs and large language models for Accessible Biomedical AI Sebastian Lobentanzer
15:00	Applications of Bioschemas in FAIR, AI and knowledge representation Nick Juty
15:20	RO-Crate: Capturing FAIR research outputs in bioinformatics and beyond Phil Reed





	Tuesday, July 22; Room 3A
Time	Title and Speaker
15:20	PheBee: A Graph-Based System for Scalable, Traceable, and Semantically Aware Phenotyping David Gordon
15:20	The role of the Ontology Development Kit in supporting ontology compliance in adverse legal landscapes Damien Goutte-Gattat
15:40	10 years of the AberOWL ontology repository: moving towards federated reasoning and natural language access Robert Hoehndorf
16:40	The global biodata infrastructure: how, where, who, and what? Guy Cochrane
16:50	Panel: Data Sustainability
17:50	Closing Remarks

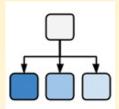




Wednesday, July 23; Room 3A

Time	Title and Speaker
11:20	Knowledge-Graph-driven and LLM-enhanced Microbial Growth Predictions Marcin Joachimiak
11:40	ProDiGenIDB – a unified resource of disease-associated genes, their protein products, and intrinsic disorder annotations Jovana Kovacevic
12:00	Causal knowledge graph analysis identifies adverse drug effects Sumyyah Toonsi
12:20	CROssBARv2: A Unified Biomedical Knowledge Graph for Heterogeneous Data Representation and LLM-Driven Exploration Bünyamin Şen
12:40	Benchmarking Data Leakage on Link Prediction in Biomedical Knowledge Graph Embeddings Galadriel Brière
12:45	A machine learning framework for extracting and structuring biological pathway knowledge from scientific literature Mun Su Kwon
12:50	Poster Madness
14:00	ScGOclust: leveraging gene ontology to find functionally analogous cell types between distant species Yuyao Song
14:20	Integrating autoantibody-related knowledge in an ontology populated using a curated dataset from literature Fabien Maury
14:40	Ontology pre-training improves machine learning predictions of aqueous solubility and other metabolite properties Charlotte Tumescheit

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Wednesday, July 23; Room 3A		
Time	Title and Speaker	
15:00	Building the Aging Biomarkers Ontology and Its Applications in Aging Research Hande McGinty	
15:20	Discovering cellular contributions to disease pathogenesis in the NLM Cell Knowledge Network Richard Scheuermann	
15:40	Cat-VRS for Genomic Knowledge Curation: A Hyperintensional Representation Framework for FAIR Categorical Variation Daniel Puthawala	
16:40	Knowledge Graphs: Theory, Applications and Challenges Ian Horrocks	
17:40	Bridging Language Barriers in Bio-Curation: An LLM-Enhanced Workflow for Ontology Translation into Japanese Mark Streer	
17:45	Enabling FAIR Single-Cell RNAseq Data Management with COPO Felix Shaw	
17:50	Cancer Complexity Knowledge Portal: A centralized web portal for finding cancer related data, software tools, and other resources Susheel Varma	
17:55	COSI Closing Remarks	



Online schedule found here.

Monday, July 21; Room 3A

Time Title and Speaker 11:20 Welcome to BOSC; Open Bioinformatics Foundation update; CoFest announcement; sponsor video 11:40 Working together to develop, promote and protect our data resources: Lessons learnt developing CATH and TED Christine Orengo 12:40 Analytical code sharing practices in biomedical research Serghei Mangul 12:40 Connecting Data, People, and Purpose: How Open Science is Advancing Bioinformatics in a Low-Resource region (Nigeria) Seun Olufemi 12:40 Introducing the Actionable Guidelines for FAIR Research Software Task Force Bhavesh Patel 14:00 NAPy: Efficient Statistics in Python for Large-Scale Heterogeneous Data with Enhanced Support for Missing Data Fabian Wolter 14:00 pyANI-plus — whole-genome classification of microbes using Average Nucleotide Identity and similar methods Peter Cock 14:00 AMRColab: An Open-Access, Modular Bioinformatics Suite for Accessible Antimicrobial Resistance Genome Analysis Su Datt Lam 14:20 InterProScan 6: a modern large-scale protein function annotation pipeline Matthias Blum Real-time base modification analysis for nanopore sequencing Suneth Samarasinghe	Monday, July 21, Room 3A		
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Matthias Blum Real-time base modification analysis for nanopore sequencing	14:00	Resistance Genome Analysis	
ΙΔ'ΔΙΙ	14:20		
	14:40		

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Monday, July 21; Room 3A		
Time	Title and Speaker	
14:40	Open-Source GPU Acceleration for State-of-the-Art Nanopore Basecalling with Slorado Bonson Wong	
14:40	Voyager-SDK: integrating and automating pipeline runs using Voyager-SDK and Voyager platform Sinisa Ivkovic	
15:00	Empowering Bioinformatics Communities with nf-core: The success of an open-source bioinformatics ecosystem Jose Espinosa-Carrasco	
15:20	JASPAR-Suite: An open toolkit for accessing TF binding motifs Aziz Khan	
15:20	VueGen: automating the generation of scientific reports Sebastian Ayala-Ruano	
15:20	The world's biomedical knowledge in less than a gram: introducing the PGP incubator	
15:40	Slivka: a new ecosystem for wrapping local code as web services Jim Procter	
16:40	FAIRDOM-SEEK: Platform for FAIR data and research asset management Munazah Andrabi	
17:00	BFVD – A release of 351k viral protein structure predictions Rachel Seongeun Kim	
17:00	Walkthrough of GA4GH standards and interoperability it provides for genomic data implementations Jimmy Payyappilly	
17:00	LiMeTrack: A lightweight biosample management platform for the multicenter SATURN3 consortium	

Laura Godfrey



Monday, July 21; Room 3A	
Time	Title and Speaker
17:20	AI-readiness for biomedical data: Bridge2AI recommendations Monica Munoz-Torres
17:40	Bridging the gap: advancing aging & dementia research through the open-access AD Knowledge Portal Susheel Varma
17:50	The ELITE Portal: A FAIR Data Resource For Healthy Aging Over The Life Span Susheel Varma

Tuesday, July 22; Room 3A	
Time	Title and Speaker
11:20	Open Knowledge Bases in the Age of Generative AI Chris Mungall
12:20	textToKnowledgeGraph: Generation of Molecular Interaction Knowledge Graphs Using Large Language Models for Exploration in Cytoscape Favour James
12:40	AutoPeptideML 2: An open source library for democratizing machine learning for peptide bioactivity prediction Raúl Fernández-Díaz
12:40	DOME Registry - Supporting ML transparency and reproducibility in the life sciences Gavin Farrell
12:40	BMFM-RNA: An Open Framework for Building and Evaluating Transcriptomic Foundation Models built on Biomed-Multi-Omic Bharath Dandala



DOOO		
Tuesday, July 22; Room 3A		
Time	Title and Speaker	
14:00	BioPortal: a rejuvenated resource for biomedical ontologies J. Harry Caufield	
14:20	Formal Validation of Variant Classification Rules Using Domain-Specific Language and Meta- Predicates Michael Bouzinier	
14:40	BioChatter: An open-source framework integrating knowledge graphs and large language models for Accessible Biomedical AI Sebastian Lobentanzer	
15:00	Applications of Bioschemas in FAIR, AI and knowledge representation Nick Juty	
15:20	RO-Crate: Capturing FAIR research outputs in bioinformatics and beyond Phil Reed	
15:20	PheBee: A Graph-Based System for Scalable, Traceable, and Semantically Aware Phenotyping David Gordon	
15:20	The role of the Ontology Development Kit in supporting ontology compliance in adverse legal landscapes Damien Goutte-Gattat	
15:40	10 years of the AberOWL ontology repository: moving towards federated reasoning and natural language access Robert Hoehndorf	
16:40	The global biodata infrastructure: how, where, who, and what? Guy Cochrane	
16:50	Panel: Data Sustainability	
17:50	Closing Remarks	





Wednesday, July 23; Room 1C	
Time	Title and Speaker
11:20	Genome-based prediction of microbial traits Thomas Rattei
12:20	The Anti-Microbial Resistance Prediction Challenge - Introduction Leonid Chidelevitch
12:40	A Hybrid Pipeline for Feature Reduction, and Ordinal Classification to Predict Antimicrobial Resistance from Genetic Profiles Anton Pashkov
14:00	Predicting Antimicrobial Resistance Using Microbiome-Pretrained DNABERT2 and DBGWAS-Derived Genomic Features Jack Vaska
14:40	The Antimicrobial Resistance Prediction Challenge Alper Yurtseven
15:00	Antimicrobial Resistance Prediction via Binary Ensemble Classifier and Assessment of Variable Importance Owen Visser
15:00	A Highly Accurate Workflow for Inference of Antimicrobial Resistance from Genetic Data Based on Machine Learning and Global Data Curation David Danko
15:20	The Gut Microbiome Health Index Challenge - Introduction Kinga Zielińska
15:40	Integrating Taxonomic and Functional Features for Gut Microbiome Health Indexing Rafael Pérez Estrada



CAMDA

Wednesday, July 23; Room 1C	
Time	Title and Speaker
16:40	Building a Rare-Disease Microbiome Health Index: Integrating Gut Metagenomes, Synthetic PKU EHRs and Rare-Variant Profiles to Forecast Phenylalanine Crises
17:20	Toward the Development of a Novel and Comprehensive Gut Health Index: An Ensemble Model Integrating Taxonomic and Functional Profiles Vincent Mei
17:40	Topology-Enabled Integration of Taxonomic and Functional Microbiome Profiles Reveals Distinct Subgroups in Healthy Individuals Doroteya Staykova
17:40	Ensemble-Based Topic Selection for Text Classification via a Grouping, Scoring, and Modeling Approach

Thursday, July 24; Room 1C	
Time	Title and Speaker
8:40	Data, Diagnoses, and Discovery: Improving Healthcare through Electronic Health Records Spiros Denaxas
9:40	Stage-Disease Grouping, Scoring, and Modeling for Predicting Diabetes Complications from Electronic Health Records Daniel Voskergian
11:20	Benchmarking for Better Private Algorithms Antti Honkela
12:00	The Health Privacy Challenge - Introduction Hakime Öztürk





Thursday, July 24; Room 1C	
Time	Title and Speaker
12:20	The Health Privacy - panel discussion
14:00	Synthetic genomic data generation through Differential Privacy-enhanced Non-Negative Matrix Factorization (DP-NMF) Andrew Wicks
14:20	Synthetic Data Generation for bulk RNA-seq Data: A CAMDA Health Challenge Analysis Steven Golob
14:40	Comparison of Single Cell RNA Synthetic Data Generators: A CAMDA Health Challenge Analysis Patrick McKeever
14:40	NoisyDiffusion: Privacy Preserving Synthetic Gene Expression Data Generation Jules Kreuer
15:00	Reusability of Public Omics Data Across 6 Million Publications Serghei Mangul
15:00	Pre-publication sharing of omics data improves paper citations Serghei Mangul
15:20	HI-MGSyn: A Hypergraph and Interaction-aware Multi-Granularity Network for Predicting Synergistic Drug Combinations Yuexi Gu
15:40	CAMDA Trophy
15:40	Closing remarks



	Tuesday, July 22; Room 2F
Time	Title and Speaker
11:20	The elephant in the (metabolomics) room: computational approaches for small molecule structural annotation from single biological study to data repositories Warwick Dunn
12:00	MetaboT: AI-based agent for natural language-based interaction with metabolomics knowledge graphs Madina Bekbergenova
12:20	Reference data-driven analysis for joint metabolome–microbiome readout from untargeted mass spectrometry data Alejandro Mendoza Cantu
12:40	Combined MS and MS/MS deconvolution of SWATH DIA data with the DIA-NMF software for comprehensive annotation in metabolomics Diana Karaki
12:40	Towards mzTab-M 2.1 - Evolving the HUPO-PSI standard format for reporting of small molecule mass spectrometry results Nils Hoffmann
14:00	Enhanced spectrum clustering for interpretable molecular networking Janne Heirman
14:20	Deep Learning for Small Molecule Analog Discovery From Untargeted Mass Spectrometry Juan Sebastian Piedrahita Giraldo
14:40	Mass Spectrometry and Machine Learning Reveal Stool-Based Multi-Signatures for Diagnosis and Longitudinal Monitoring of Inflammatory Bowel Disease Elmira Shajari
14:40	Rapid Deployment of Interactive and Visual Web Applications for Computational Mass Spectrometry Tom David Müller

	Tuesday, July 22; Room 2F
Time	Title and Speaker
15:00	PepSi-Print: Unraveling Protein Fingerprints through Pairwise Intensity Ratios with a Peptide Siamese Network Zixuan Xiao
15:20	Identification of novel proteins by integrating ribosome profiling data into a transcriptomic language model for deeper mass spectrometry analyses Nicolas Provencher
15:20	Zero-shot retention time prediction for unseen post-translational modifications with molecular structure encodings Ceder Dens
15:40	Open modification proteogenomics fosters reproducible detection of non-canonical proteins Valeriia Vasylieva
15:40	PCI-DB: A novel primary tissue immunopeptidome database to guide next-generation peptide-based immunotherapy development Steffen Lemke
16:40	CellPick: a cell selection toolkit for spatial proteomics Lucas Miranda
17:00	A living proteomics benchmark for comprehensive evaluation of deep learning-based de novo peptide sequencing tools Marina Pominova
17:00	Mavis: An Ensemble of Methods for Mean-Variance Trend Modeling and Bayesian Decision in Comparative Proteomics
17:20	Making Proteomics Al-Ready: From Metadata Extraction to Biomarker Discovery



Tuesday, July 22; Room 4AB	
Time	Title and Speaker
11:20	Knowledge-based machine learning to study cellular regulation from spatial multi-omics data Julio Saez-Rodriguez
12:00	Flexible and robust cell type annotation for highly multiplexed tissue images Robert F. Murphy
12:20	Dual-Graph Attention Network for Protein Imputation from Spatial Transcriptomics Haoyu Wang
12:40	Single-cell and spatial atlas of the Human Ageing Thymus Veronika Kedlian
14:00	TBD
14:40	Network-based integration of epigenetic and transcriptomic landscapes unveils molecular programs underlying T follicular helper cell differentiation Alisa Omelchenko
15:00	Tissue first single cell RNA seq strategy reveals renal tumour specific expansion of regulatory DN1 B cells Isabella Withnell
15:20	ImmunoMatch learns and predicts cognate pairing of heavy and light immunoglobulin chains Dongjun Guo
15:40	Taxon-specific linear B-cell epitope prediction with phylogeny-aware transfer learning Felipe Campelo





Tuesday, July 22; Room 4AB	
Time	Title and Speaker
16:40	Iterative Attack-and-Defend Framework for Improving TCR-Epitope Binding Prediction Models Pengfei Zhang
17:00	NeoPrecis: A Computational Framework for Assessing Neoantigen Immunogenicity to Advance Cancer Immunotherapy Ko-Han Lee
17:20	SHISMA: Shape-driven inference of significant celltype-specific subnetworks from time series single-cell transcriptomics Antonio Collesei
17:40	Unraveling Immune Signatures of Whole-Cell vs. Acellular Pertussis Vaccine Priming through Multi- Omics Feature Fusion Divya Sitani
17:45	BepiCon: A Geometric Deep Learning Framework for Conformational B Cell Epitope Prediction Bünyamin Şen
17:50	NanoAIRR: full-length adaptive immune receptor profiling from Nanopore long-read sequencing Jonas Schuck



EDUCATION

Online schedule found here.

Wednesday, July 23; Room 11A

Time	Title and Speaker
11:20	Cross-Sector Collaboration in Bioinformatics and Data Science: Tackling Skill Development Challenges in Academia and Industry Gabriela Rustici
12:00	Building Omics Skills through the CFDE Training Center Allissa Dillman
12:20	From live webinar series to self-paced learning resource: Creating structured bioinformatics learning pathways Ajay Mishra
12:40	Breaking Down Barriers to Learning: Bioinformatics for Biologists Massive Open Online Courses Dusanka Nikolic
14:00	An educator framework for organizing Wikipedia editathons for computational biology Farzana Rahman
14:20	Automated Assignment Grading with Large Language Models: Insights From a Bioinformatics Course Pavlin G. Poličar
14:40	Teaching LLM literacy improves AI-aided data analysis in a bioinformatics course Aparna Nathan
15:00	Integrating Bioinformatics into Undergraduate Biology Education: Innovation, Experiential Learning, and Sustainable Program Design Inimary Toby-Ogundeji



EDUCATION

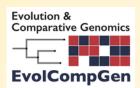
Wednesday, July 23; Room 11A	
Time	Title and Speaker
15:20	GeneLab for Colleges and Universities (GL4U): On-Demand Bioinformatics Training Using Space Biology Omics Data Amanda Saravia-Butler
15:40	A Scalable Curriculum Model to Empower Rural Youth in Open Science Through Secondary Research and Peer-to-Peer Collaboration Nadiia Kasianchuk
16:40	Capacity Building for Pathogen Surveillance through Pathogen Genomics and Bioinformatics Training in Africa Nicola Mulder
17:00	The emerging ecosystem of competitive educational programs in bioinformatics in Ukraine Alina Frolova
17:20	Fostering communities of practice in bioinformatics education and training Patricia Carvajal-López

POSTING TO SOCIAL MEDIA AT ISMB/ECCB 2025

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- 2. Images should be of title slides only.
- 3. Be positive about others' research.
- 4. Never use bad language or disparaging comments.
- 5. Never take/share video or voice recordings (GDPR thanks you!).
- 6. If conference organizers or speakers ask you to remove a post, do it.



Monday, July 21; Room 11A	
Time	Title and Speaker
11:20	Fair molecular feature selection unveils universally tumor lineage-informative methylation sites in colorectal cancer Cenk Sahinalp
11:40	Fast tumor phylogeny regression via tree-structured dual dynamic programming Henri Schmidt
12:00	Bayesian inference of fitness landscapes via tree-structured branching processes Xiang Ge Luo
12:20	MiClone: A Probabilistic Method for Inferring Cell Phylogenies from Mitochondrial Variants Emilia Hurtado
12:40	scVarID: Mapping Genetic Variants at Single-Cell Resolution to Uncover Precursor Cells in Cancer Jonghyun Lee
12:50	High-Resolution Discovery of Lineage-Specific SVs in Pan Genus Through Assembly Comparisons Aisha
14:00	Tracing the functional divergence of duplicated genes Irene Julca
14:20	Duplication Episode Clustering in Phylogenetic Networks Agnieszka Mykowiecka
14:40	PhytClust: Accurate and Fast Clustering in Phylogenetic Trees Katyayni Ganesan
15:00	Learning the Language of Phylogeny with MSA Transformer Ruyi Chen

Monday, July 21; Room 11A	
Time	Title and Speaker
15:20	Accurate multiple sequence alignment at protein-universe scale with FAMSA 2 Adam Gudys
15:40	Community detection at unprecedented scales with ExoLabel Erik Wright
16:40	EdgeHOG: Scalable and Fine-Grained Ancestral Gene Order Inference Across the Tree of Life Charles Bernard
17:00	JIGSAW: Accurate inference of exact copy numbers from targeted single-cell DNA sequencing Sophia Chirrane
17:20	EASYstrata: a fully integrated workflow to infer evolutionary strata along sex chromosomes and other supergenes Ricardo C. Rodriguez de la Vega
17:40	The Phylogenetic Dynamic Regulatory Module Networks (P-DRMN) study infers Cis-regulatory features responsible for evolution of mammalian gene regulatory programs in aortic endothelium Suvojit Hazra

Tuesday, July 22; Room 11A	
Time	Title and Speaker
11:20	Introduction
11:30	Evolution of function in light of gene expression Marc Robinson-Rechavi
12:10	Convergent evolution to similar proteins confounds structure search Erik Wright
12:20	Evolution of the Metazoan Protein Domain Toolkit Revealed by a Birth-Death-Gain Model Maureen Stolzer
12:30	Deep Phylogenetic Reconstruction Reveals Key Functional Drivers in the Evolution of B1/B2 Metallo- β -Lactamases Samuel Davis
12:40	A compendium of human gene functions derived from evolutionary modeling Paul D. Thomas
12:50	pLM in functional annotation: relationship between sequence conservation and embedding similarity Ana Rojas
14:00	Disentangling SARS-CoV-2 Lineage Importations and the Role of NPIs Using Bayesian Phylogeography of 1.8 Million Genomes Sama Goliaei
14:20	SARS-CoV-2 Intra-Host Evolution in Immuno-Compromised Individuals: A Fractal Perspective on Genome Geometry Nicole A. Rogowski
14:40	Antarctica as a Viral Reservoir: Insights from Comparative Genomics and Metagenomics Caroline Martiniuc

Tuesday, July 22; Room 11A	
Time	Title and Speaker
15:00	Computational Genomics and Biosynthetic Potential Analysis of a Dead Sea Penicillium sp. Milana Frenkel-Morgenstern
15:10	Unravelling the pangenome of autotrophic bacteria: Metabolic commonalities, evolutionary relationships, and industrially relevant traits Dr. Karan Kumar
15:20	Spatiotemporal patterns in the human gut dysbiosis contrasted to healthy families Falk Hildebrand
15:30	Marker discovery in the large Beatriz Vieira Mourato
15:40	Whole-genome detection and origin identification of orphan genes in plant-parasitic nematodes Ercan Seçkin
15:50	Construction and Analysis of the <i>Moniliophthora roreri</i> pangenome Isabella Gallego
16:40	Recomb-Mix: fast and accurate local ancestry inference Yuan Wei
17:00	WINDEX: A hierarchical integration of site- and window-based statistics for modeling the footprint of positive selection Hannah Snell
17:20	Position-specific evolution in transcription factor binding sites, and a fast likelihood calculation for the F81 model Pavitra Selvakumar
17:30	Concluding remarks



FUNCTION

Tuesday, July 22; Room 11A	
Time	Title and Speaker
11:20	Introduction
11:30	Evolution of function in light of gene expression Marc Robinson-Rechavi
12:10	Convergent evolution to similar proteins confounds structure search Erik Wright
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	Room 12
12:40	A compendium of human gene functions derived from evolutionary modeling Paul D. Thomas
12:50	pLM in functional annotation: relationship between sequence conservation and embedding similarity Ana Rojas
14:00	GOAnnotator: Accurate protein function annotation using automatically retrieved literature Huiying Yan
14:20	Semi-Supervised Data-Integrated Feature Importance Enhances Performance and Interpretability of Biological Classification Tasks Jun Kim



17:20

17:40

M. Clara De Paolis Kaluza

Erva Ulusoy

Biological Knowledge Graphs and Language Models

FUNCTION

Tuesday, July 22; Room 12 **Time** Title and Speaker On the completeness, coherence, and consistency of protein function prediction: lifting function 14:40 prediction from isolated proteins to biological systems **Rund Tawfig** Contextual Gene Set Analysis with Large Language Models 15:00 Chih-Hsuan Wei Fine-tuning protein language models with a disorder-aware vocabulary improves intrinsic disorder 15:20 classification and function prediction Harsh Srivastava A Novel Computational Pipeline for the Functional Characterization and Deorphanization of G-Protein 15:40 **Coupled Receptors Catherine Zhou** VaLPAS: Leveraging variation in experimental multi-omics data to elucidate protein function 15:50 Jason McDermott Accelerating protein family classification in InterPro with AI innovations 16:40 **Matthias Blum** Thousands of confident genetic interactions in an Escherichia coli mutant collection elucidate 17:00 numerous gene functions Simon Jeanneau Present and future of the critical assessment of protein function annotation algorithms (CAFA)

ProtHGT: Heterogeneous Graph Transformers for Automated Protein Function Prediction Using





Wednesday, July 23; Room 1A **Title and Speaker Time** Learning variant effects on chromatin accessibility and 3D structure without matched Hi-C data 11:20 Valentina Boeva Spatial transcriptomics deconvolution methods generalize well to spatial chromatin accessibility 12:20 data Laura D. Martens Towards Personalized Epigenomics: Learning Shared Chromatin Landscapes and Joint De-Noising of 12:40 **Histone Modification Assays** Tanmayee Narendra Alevin-fry-atac enables rapid and memory frugal mapping of single-cell ATAC-Seq data using virtual 14:00 colors for accurate genomic pseudoalignment **Noor Pratap Singh** Oarfish: Enhanced probabilistic modeling leads to improved accuracy in long read transcriptome 14:20 quantification Zahra Zare Jousheghani Identification of interactions defining 3D chromatin folding from micro to meso-scale 14:40 Leonardo Morelli SpliSync: Genomic language model-driven splice site correction of long RNA reads 15:00 Liliana Florea adverSCarial: a toolkit for exposing classifier vulnerabilities in single-cell transcriptomics 15:20 **Ghislain Fievet** Transcriptome Assembly at Single-Cell Resolution with Beaver 15:40 Qian Shi





Wednesday, July 23; Room 1A	
Time	Title and Speaker
16:40	Bioinformatics analysis for long-read RNA sequencing: challenges and promises Elizabeth Tseng
17:00	Quality assessment of long read data in multisample lrRNA-seq experiments using SQANTI-reads Netanya Keil
17:20	Quantifying RNA Expression and Modifications using Long Read RNA-Seq Jonathan Göke

Thursday, July 24; Room 1A	
Time	Title and Speaker
8:40	Pangenome based analysis of structural variation Tobias Marschall
9:40	Resolving Paralogues and Multi-Copy Genes with Nanopore Long-Read Sequencing Sergey Nurk
11:20	GreedyMini: Generating low-density DNA minimizers Arseny Shur
11:40	Exploiting uniqueness: seed-chain-extend alignment on elastic founder graphs Nicola Rizzo
12:00	FroM Superstring to Indexing: a space-efficient index for unconstrained k-mer sets using the Masked Burrows-Wheeler Transform (MBWT) Ondřej Sladký





Thursday, July 24; Room 1A	
Time	Title and Speaker
12:20	The Alice assembler: dramatically accelerating genome assembly with MSR sketching Roland Faure
12:40	BINSEQ: A Family of High-Performance Binary Formats for Nucleotide Sequences Noam Teyssier
14:00	Ultrafast and Ultralarge Multiple Sequence Alignments using TWILIGHT Yu-Hsiang Tseng
14:20	CREMSA: Compressed Indexing of (Ultra) Large Multiple Sequence Alignments Mikaël Salson
14:40	LYCEUM: Learning to call copy number variants on low coverage ancient genomes Mehmet Alper Yilmaz
15:00	POPSICLE: a probabilistic method to capture uncertainty in single-cell copy-number calling Lucrezia Patruno
15:20	MutSuite: A Toolkit for Simulating and Evaluating Mutations in Aligned Sequencing Reads Kendell Clement
15:40	Landscape of The Dark Genome's variants and their influence on cancer Joao P. C. R. Mendonca





Wednesday, July 23; Room 2N **Time Title and Speaker** 11:20 Introduction to iRNA Sequential verification of transcription by Integrator and Restrictor 11:30 **Steven West** CIRI-Deep Enables Single-Cell and Spatial Transcriptomic Analysis of Circular RNAs with Deep 12:10 Learning Yuan Gao Enhancing circRNA-miRNA Interaction Prediction with Structure-aware Sequence Modeling 12:20 **Juseong Kim** 12:40 Flash talks Predicting relevant snoRNA genes across any eukaryote genome using SnoBIRD 14:00 Étienne Fafard-Couture Charting the dynamics of the tRNAome in health and disease with AMaNITA 14:20 Xanthi Lida Katopodi Identification and characterization of chromatin-associated long non-coding RNAs in human 14:40 Lina Ma Toward a Computational Pipeline for Prokaryotic miRNAs: The Case of Pseudomonas aeruginosa in 15:00 Lung Disease Laura Veschetti Characterisation of the role of SNORD116 in RNA processing during cardiomyocyte differentiation 15:10 Sofia Kudasheva EpiCRISPR: Improving CRISPR/Cas9 on-target efficiency prediction by multiple epigenetic marks, high-throughput datasets, and flanking sequences 15:20 Yaron Orenstein

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IRNA

Wednesday, July 23; Room 2N

Time	Title and Speaker
15:30	Enhancing CRISPR/Cas9 Guide RNA Design Using Active Learning Techniques Stefano Roncelli
15:40	Single-base tiled screen reveals design principles of PspCas13b-RNA targeting and informs automated screening of potent targets Syed Faraz Ahmed
16:40	Gene regulation of human cell systems Roser Vento-Tormo
17:20	EdiSetFlow: A robust pipeline for RNA editing detection and differential analysis in bulk RNA-seq Jacob Munro
17:40	EnsembleDesign: Messenger RNA Design Minimizing Ensemble Free Energy via Probabilistic Lattice Parsing Liang Huang







Thursday, July 24; Room 2N	
Time	Title and Speaker
8:40	Prediction and validation of Split Open Reading Frames across cell types Christina Kalk
9:00	Bridging the Gap: Recalibrating In-vitro Models for Accurate In-vivo RBP Binding Predictions Ilyes Baali
9:20	Multi-Tool Intron Retention Analysis in Autism Adi Gershon
9:40	Detection of statistically robust interactions from diverse RNA-DNA ligation data Timothy Warwick
11:20	Building the future of RNA tools Blake Sweeney
11:50	Sci-ModoM: a quantitative database of transcriptome-wide high-throughput RNA modification sites promoting cross-disciplinary collaborative research Etienne Boileau
12:00	RNAtranslator: A Generative Language Model for Protein-Conditional RNA Design A. Ercument Cicek
12:10	miRXplain: transformer-driven explainable microRNA target prediction leveraging isomiR interactions Giulia Cantini
12:20	Designing functional RNA sequences using conditional diffusion models Cho Joohyun
12:30	The future of RNA tools





Thursday, July 24; Room 2N	
Time	Title and Speaker
14:00	Decoding RNA language in plants
14:40	The tangled dynamics of H/ACA snoRNAs to channel Pseudouridine Levels in the Human Ribosome Baudouin Seguineau de Préval
15:00	Machine learning-guided isoform quantification in bulk and single-cell RNA-seq using joint short- and long-read modeling Hamed Najafabadi
15:20	Long-read RNA sequencing unveils a novel cryptic exon in MNAT1 along with its full-length transcript structure in TDP-43 proteinopathy Yoshihisa Tanaka
15:40	Transcriptome Universal Single-isoform COntrol (TUSCO): A Framework for Evaluating Transcriptome Quality Tianyuan Liu
15:50	Concluding remarks and poster prizes



Wednesday, July 23; Room 1B	
Time	Title and Speaker
14:40	Microbiome multitudes and metadata madness Fiona Brinkman
15:20	Species-level taxonomic profiling of Earth's microbiomes with mOTUs4 Marija Dmitrijeva
15:30	Accurate profiling of microbial communities for shotgun metagenomic sequencing with Meteor2 Amine Ghozlane
15:40	Benchmarking metagenomic binning tools on real datasets across sequencing platforms and binning modes Shanfeng Zhu
15:50	Metagenomics-Toolkit: The Flexible and Efficient Cloud-Based Metagenomics Workflow Nils Kleinbölting
16:40	TBA
17:20	DNABERT-S: Pioneering Species Differentiation with Species-Aware DNA Embeddings Weimin Wu
17:40	MGnify Genomes: generating richly annotated, searchable biome-specific genome catalogues Tatiana Gurbich
17:50	Rapid and Consistent Genome Clustering for Navigating Bacterial Diversity with Millions of Genomes Johanna von Wachsmann



Thursday, July 24; Room 1B	
Time	Title and Speaker
8:40	GiantHunter: Accurate detection of giant virus in metagenomic data using reinforcement-learning and Monte Carlo tree search Jiayu Shang
9:00	CAMI Benchmarking Portal: online evaluation and ranking of metagenomic software Fernando Meyer
9:10	CAMI community exchange Alice McHardy
9:20	NanoGraph: Mapping Nanopore Squiggles to Graphs Enables Accurate Taxonomic Assignment Wenhuan Zeng
9:30	MEGAN7: Enhanced Optimization and Advanced Functionality for Metagenomic Analysis Anupam Gautam
9:40	TaxSEA: Rapid Interpretation of Microbiome Alterations Using Taxon Set Enrichment Analysis and Public Databases Feargal Ryan
9:50	SinProVirP: a Signature Protein-based Approach for Accurate and Efficient Profiling of the Human Gut Virome Junhua Li
11:20	Leveraging Large Language Models to Predict Antibiotic Resistance in Mycobacterium tuberculosis Conrad Testagrose
11:40	De novo discovery of conserved gene clusters in microbial genomes with Spacedust Johannes Soeding
11:50	Nerpa 2: linking biosynthetic gene clusters to nonribosomal peptide structures Ilia Olkhovskii

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Thursday, July 24; Room 1B	
Time	Title and Speaker
12:00	Phylo-Spec: a phylogeny-fusion deep learning model advances microbiome status identification Xiaoquan Su
12:10	Beyond Taxonomy and Function: Protein Language Models for Scalable Microbial Representations Petra Matyskova
12:20	Guided tokenizer enhances metagenomic language models performance Ali Rahnavard
12:30	REMAG: recovery of eukaryotic genomes from metagenomes using reference-free contrastive learning Daniel Gómez-Pérez
12:40	Flexible Log-odds Homology Features for Plasmid Identification Tomas Vinar
12:50	Accurate plasmid reconstruction from metagenomics data using assembly-alignment graphs and contrastive learning Pau Piera Lindez
14:00	Predicting coarse-grained representations of biogeochemical cycles from metabarcoding data Arnaud Belcour
14:20	CroCoDeEL: accurate control-free detection of cross-sample contamination in metagenomic data Florian Plaza Oñate
14:30	Longflow: A comprehensive end-to-end solution for long-read metagenomics. Sebastien Raguideau



Thursday, July 24; Room 1B	
Time	Title and Speaker
14:40	Long-reads metagenome-assembled genomes can be higher quality than reference genomes: the case of the Shanghai pet dog microbiome catalog Luis Pedro Coelho
14:50	Use of Long-Read SMRT PacBio Sequencing for Detailed Genomic and Epigenetic Studies of Complex Microbial Communities in the Wheat Rhizosphere to Abiotic Stress Oleg Reva
15:00	proMGEflow: recombinase-based detection of mobile genetic elements in bacterial meta(genomes) Anastasiia Grekova
15:10	Extracting host-specific developmental signatures from longitudinal microbiome data Balazs Erdos
15:20	Complex SynCom inoculations to study root community assembly Gijs Selten
15:30	Spatial and temporal variation of marine microbial interactions around the west Antarctic Peninsula Julia C Engelmann
15:40	Associations between Microbiome-Associated Variants and Diseases Tess Cherlin
15:50	Detecting Synergistic Associations in Microbial Communities via Multi-Dimensional Feature Selection Witold Rudnicki





Monday, July 21; Room 1A	
Time	Title and Speaker
11:20	Where does it hurt (in your genome)?
12:20	Locality-aware pooling enhances protein language model performance across varied applications Minh Hoang
12:40	NEAR: Neural Embeddings for Amino acid Relationships Daniel Olson
14:00	LoRA-DR-suite: adapted embeddings predict intrinsic and soft disorder from protein sequences Gianluca Lombardi
14:20	TCR-epiDiff: Solving Dual Challenges of TCR Generation and Binding Prediction Se Yeon Seo
14:40	Incorporating Hierarchical Information into Multiple Instance Learning for Patient Phenotype Prediction with scRNA-seq Data Chau Do
15:00	PANDORA: Peptide-based ANtimicrobial Design Optimized by Reinforcement Automation Julián García-Vinuesa
15:10	NetStart 2.0: Prediction of Eukaryotic Translation Initiation Sites Using a Protein Language Model Line Sandvad Nielsen
15:20	Towards a more inductive world for drug repurposing approaches Uxía Veleiro
15:30	Hierarchical Multi-Agent Reinforcement Learning For Optimizing CRISPR-Based Polygenic Therapeutic Design Nhung Duong



MLCSB

Monday, July 21; Room 1A	
Time	Title and Speaker
15:40	Developing a Deep Learning Model for Single-Cell RNA Splicing Analysis Luyang Li
15:50	Evolutionary constraints guide AlphaFold2 in predicting alternative conformations and inform rational mutation design Francesca Cuturello
16:40	Integrating Machine Learning and Systems Biology to rationally design operational conditions for in vitro / in vivo translation of microphysiological systems Nikolaos Meimetis
16:50	Data Splitting Against Information Leakage with DataSAIL Roman Joeres
17:00	Generative AI for Unlocking the Complexity of Cells



Tuesday, July 22; Room 1A	
Time	Title and Speaker
11:20	Toward Mechanistic Genomics: Advances in Sequence-to-Function Modeling
12:20	Deep learning models for unbiased sequence-based PPI prediction plateau at an accuracy of 0.65 Judith Bernett
12:40	Accurate PROTAC targeted degradation prediction with DegradeMaster Jie Liu
14:00	GPO-VAE: Modeling Explainable Gene Perturbation Responses utilizing GRN-Aligned Parameter Optimization Seungheun Baek
14:20	Fast and scalable Wasserstein-1 neural optimal transport solver for single-cell perturbation prediction Yanshuo Chen
14:40	Recovering Time-Varying Networks From Single-Cell Data Euxhen Hasanaj
15:00	Sliding Window INteraction Grammar (SWING): a generalized interaction language model for peptide and protein interactions Jishnu Das
15:10	Benchmarking foundation cell models for post-perturbation RNA-seq prediction Gerold Csendes
15:20	scPRINT: pre-training on 50 million cells allows robust gene network predictions Jeremie Kalfon
15:30	MGCL-ST: Multi-view Graph Self-supervised Contrastive Learning for Spatial Transcriptomics Enhancement Hongmin Cai



Tuesday, July 22; Room 1A	
Time	Title and Speaker
15:40	Characterizing cell-type spatial relationships across length scales in spatially resolved omics data Rafael dos Santos Peixoto
15:50	Segger: Fast and accurate cell segmentation of imaging-based spatial transcriptomics data Elyas Heidari
16:40	Dissecting cellular and molecular mechanisms of pancreatic cancer with deep learning Aarthi Venkat
16:50	SpliceSelectNet: A Hierarchical Transformer-Based Deep Learning Model for Splice Site Prediction Yuna Miyachi
17:00	Is distribution shift still an AI problem Sanmi Koyejo





Tuesday, July 22; Room 1B	
Time	Title and Speaker
11:20	Multi-modal learning for single-cell data integration Laura Cantini
12:00	Nichesphere: A method to identify disease specific physical cell-cell interactions and underlying cellular communication networks Mayra Luisa Ruiz Tejada Segura
12:20	NetREm: Network Regression Embeddings reveal cell-type transcription factor coordination for gene regulation Saniya Khullar
12:40	Cell-specific Graph Operation Strategy on Signaling Intracellular Pathways Giulia Cesaro
14:00	Prediction of Gene Regulatory Connections with Joint Single-Cell Foundation Models and Graph-Based Learning Sindhura Kommu
14:20	Enhanced Gaussian noise augmentation-based contrastive learning for predicting the longevity effects of genes using protein-protein interaction networks Ibrahim Alsaggaf
14:40	Uncovering the systems-level mutational landscape of intrinsically disordered regions in cancer Kivilcim Ozturk
15:00	Advancing Network Biology with FunCoup 6 Erik Sonnhammer
15:20	SPACE: STRING proteins as complementary embeddings Dewei Hu
15:40	Disentangling the genetic and non-genetic origin of disease co-occurrences Beatriz Urda-García



NetBio NETBIO

Tuesday, July 22; Room 1B	
Time	Title and Speaker
16:40	GRACKLE: An interpretable matrix factorization approach for biomedical representation learning Lucas Gillenwater
17:00	Quantum Random Walks for Biomarker Discovery in Biomolecular Networks Aritra Bose
17:20	Quantum computing for network medicine-based epistatic disease mechanism mining - Fake it till you make it? Jan Baumbach

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Fiona Brinkman

NETBIO

Wednesday, July 23; Room 1B **Time Title and Speaker** MixingDTA: Improved Drug-Target Affinity Prediction by Extending Mixup with Guilt-By-11:20 Association **Dongmin Bang** Interactome-based computational solutions to support personalized drug therapy decisions in 11:40 glioblastoma Nicoleta Siminea Improving Target-Adverse Event Association Prediction by Mitigating Topological Imbalance in 12:00 Knowledge Graphs Terence Egbelo A Nextflow Pipeline for Network-Based Disease Module Identification and Drug 12:20 Repurposing **Johannes Kersting** Graph Antiviral Target Explorer (GATE): predicting disease genes in viral infections with Message Passing Neural Networks 12:40 Samuele Firmani Multilayer Networks Identify Clinically Relevant Patient Endotypes in COVID-19 and Sepsis 14:00 Piotr Sliwa Cytoscape Visualization Competition Results 14:20 **Chad Myers** Microbiome multitudes and metadata madness 14:40



Wednesday, July 23; Room 11BC Time **Title and Speaker** Exploring cellular plasticity: 4D epigenomes in the context of the tumour microenvironment 11:20 Vera Pancaldi Leveraging Transcription Factor Physical Proximity for Enhancing Gene Regulation Inference 12:00 Yijie Wang miRBench: novel benchmark datasets for microRNA binding site prediction that mitigate against 12:20 prevalent microRNA Frequency Class Bias Panagiotis Alexiou Flash Talk Session 1 12:40 Unicorn: Enhancing Single-Cell Hi-C Data with Blind Super-Resolution for 3D Genome Structure 14:00 Reconstruction Oluwatosin Oluwadare Predicting gene-specific regulation with transcriptomic and epigenetic single-cell data 14:20 Laura Rumpf Biophysical deep learning resolves how TF and DNA sequence specify the genome state of every cell 14:40 population in human embryogenesis Vitalii Kleshchevnikov Nona: A unifying multimodal masked modeling framework for functional genomics 15:00 **Surag Nair** SCRIMPy: Single Cell Replication Inference from Multiome data using Python 15:20 Tatevik Jalatyan Uncovering Novel Cellular Programs and Regulatory Circuits Underlying Bifurcating Human B Cell 15:40 States Jishnu Das



REGSYS

Wednesday, July 23; Room 11BC	
Time	Title and Speaker
16:40	Ledidi: Programmatic design and editing of cis-regulatory elements Jacob Schreiber
17:00	Lilliput: Compact native regulatory element design with machine learning-guided miniaturization Laura Gunsalus
17:20	What can the diversity of life of Earth teach us about disease? Mafalda Dias

Thursday, July 24; Room 11BC	
Time	Title and Speaker
8:40	"Gene regulation of human cell systems" Roser Vento-Tormo
9:20	Anomaly Detection in Spatial Transcriptomics via Spatially Localized Density Comparison Gary Hu
9:40	Flash Talk Session 2
11:20	GASTON-Mix: a unified model of spatial gradients and domains using spatial mixture-of-experts Uthsav Chitra
11:40	Refinement Strategies for Tangram for Reliable Single-Cell to Spatial Mapping Merle Stahl



REGSYS

Thursday, July 24; Room 11BC	
Time	Title and Speaker
12:00	Encoding single-cell chromatin landscapes as probability distributions with optimal transport Cassandra Burdziak
12:20	scooby: Modeling multi-modal genomic profiles from DNA sequence at single-cell resolution Laura D. Martens
12:40	Soffritto: a deep-learning model for predicting high-resolution replication timing Dante Bolzan
14:00	Detection of Cell-type-specific Differentially Methylated Regions in Epigenome-Wide Association Studies Yingying Wei
14:20	MutBERT: Probabilistic Genome Representation Improves Genomics Foundation Models Weicai Long
14:40	Detecting and avoiding homology-based data leakage in genome-trained sequence models Abdul Muntakim Rafi
15:00	Predicting gene expression using millions of yeast promoters reveals cis-regulatory logic Susanne Bornelöv
15:20	Learning the Regulatory Genome by Destruction and Creation Luca Pinello



SYSMOD

Online schedule found here.

Tuesday, July 22; Room 1C **Time Title and Speaker** 11:20 Opening Talk 11:30 Variational kinetics: a variational formulation of reaction kinetics A dynamic multi-tissue metabolic reconstruction reveals interindividual variation in postprandial 12:10 metabolic fluxes Shauna O'Donovan Decoding organ-specific breast cancer metastasis through single-cell metabolic modeling 12:30 **Garhima Arora** Enzyme activation network facilitates regulatory crosstalk between metabolic pathways 12:50 Cell-cycle dependent DNA repair and replication unifies patterns of chromosome instability 12:55 Bingxin Lu Virtual Tumours for Predictive Precision Oncology 14:00 Jasmin Fisher A community benchmark of off-lattice multiscale modelling tools reveals differences in methods 14:40 and across-scales integrations **Arnau Montagud** Multi-objective Reinforcement Learning for Optimizing JAK/STAT Pathway Interventions: A Quantitative System Pharmacology Study 15:00 Tien Nguyen Decoding CXCL9 regulatory mechanisms by integrating perturbation screenings with active learning 15:20 of mechanistic logic-ODE models **Bi-Rong Wang**



SYSMOD

Tuesday, July 22; Room 1C	
Time	Title and Speaker
15:40	ARTEMIS integrates autoencoders and Schrödinger Bridges to predict continuous dynamics of gene expression, cell population and perturbation from time-series single-cell data
16:40	Calibrating agent-based models of colicin-mediated inhibition in microfluidic traps using single-cell time-lapse microscopy Ati Ahmadi
17:00	Inferring metabolic activities from single-cell and spatial transcriptomic atlases Erick Armingol
17:20	Spatiotemporal Variational Autoencoders for Continuous Single-Cell Tissue Dynamics Koichiro Majima
17:40	Computational Modeling of Shortening and Reconstruction of Telomeres Marek Kimmel
17:45	TFvelo: gene regulation inspired RNA velocity estimation Jiachen Li
17:50	Closing remarks



TEXT MINING

Thursday, July 24; Room 12	
Time	Title and Speaker
8:40	Opening remarks
9:00	Keynote - TBA
9:40	Poster lightning talks
11:20	Representations of Cells in the Biomedical Literature: First Look at the NLM CellLink Corpus Noam H. Rotenberg
11:40	Contextualizing phenotypes in medical notes with small language models Connor Grannis
12:00	CSpace: A concept embedding space for bio-medical applications Danilo Tomasoni
12:20	VectorSage: Enhancing PubMed Article Retrieval with Advanced Semantic Search Rahul Brahma
12:40	Large Language Model Applications on the Uniprot Protein Sequence and Annotation Database Melike Akkaya
14:00	Human-AI Collaboration for Cancer Knowledge Verification: Insights from the CIViC-Fact Dataset Caralyn Reisle
14:20	Named entity recognition and relationship extraction to mine minimum inhibitory concentration of antibiotics from biomedical text Tiffany Ta



TEXT MINING

Thursday, July 24; Room 12	
Time	Title and Speaker
14:40	Enhancing Biomedical Relation Extraction with Directionality Chih-Hsuan Wei
15:00	Metadata extraction: Large Language Models (LLMs) to the rescue Daniela Gaio
15:20	Large-scale semantic indexing of Spanish biomedical literature using contrastive transfer learning Shanfeng Zhu
15:40	Reading papers: Extraction of molecular interaction networks with large language models Enio Gjerga



TRANSMED

Online schedule found here.

Tuesday, July 22; Room 2N	
Time	Title and Speaker
11:20	TBD
12:00	How (poly)phenols can shape a healthier life? A nutri-omics investigation on their cardiometabolic health effects Mirko Treccani
12:20	Genomic Scars of Survival: Translating Therapy-Induced Mutagenesis into Clinical Insights in Childhood Cancer Mehdi Layeghifard
12:30	MOSAIC-AD: Multilayered Patient Similarity Analysis Integrating Omics and Clinical Data for Patient Stratification in Atopic Dermatitis Lena Möbus
12:40	Gene mutant dosage determine prognosis and metastatic tropism in 60,000 clinical cancer samples Nicola Calonaci
14:00	Top-DTI: Integrating Topological Deep Learning and Large Language Models for Drug Target Interaction Prediction Serdar Bozdag
14:20	Unraveling Early Changes in Alzheimer's Disease: Causal Relationships Among Sleep Behavior, Immune Dynamics, and Cognitive Performance Through Multimodal Data Fusion Sophia Krix
14:30	Combining Clinical Embeddings with Multi-Omic Features for Improved Interpretability in Parkinson's Disease Patient Classification Barry Ryan
14:40	Generating Synthetic Genotypes using Diffusion Models Philip Kenneweg

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TRANSMED

Tuesday, July 22; Room 2N	
Time	Title and Speaker
15:00	Predicting fine-grained cell types from histology images through cross-modal learning in spatial transcriptomics Jian Liu
15:20	Spatial Regulatory Landscape of the Glioblastoma Tumor Immune Microenvironment Hatice Osmanbeyoglu
15:40	SpatialPathomicsToolkit: A Comprehensive Framework for Pathomics Feature Analysis and Integration Shilin Zhao
15:50	CellTFusion: A novel approach to unravel cell states via cell type deconvolution and TF activity estimated from bulk RNAseq data identifies clinically relevant cell niches Marcelo Hurtado
16:40	TRESOR: a disease signature integrating GWAS and TWAS for therapeutic target discovery in rare diseases Satoko Namba
16:50	GENIUS: Genomic Evaluation using Next-generation Intelligence for Understanding & Swift Diagnosis Peter White
17:00	SIDISH Identifies High-Risk Disease-Associated Cells and Biomarkers by Integrating Single-Cell Depth and Bulk Breadth Yasmin Jolasun
17:10	TBD





Online schedule found here.

Monday, July 21; Room 4AB Time **Title and Speaker** Enhancing Multi-Task CNNs for Regulatory Genomics Through Allelic and High-Resolution 11:20 **Training Alexander Sasse** Combining massively parallel reporter assays and graph genomics to assay the regulatory effects of 12:00 indels and structural variants **Lindsey Plenderleith** Multilingual model improves zero-shot prediction of disease effects on proteins 12:20 Ruyi Chen X-MAP: Explainable AI Platform for Genetic Variant Interpretation 12:30 **Marco Anteghini** StructGuy: Data leakage free prediction of functional effects of genetic variants. 12:40 **Alexander Gress** Functional characterization of standing variation around disease-associated genes using Massively 12:50 Parallel Reporter Assays Kilian Salomon Variant Interpretation at Scale, for safer and more effective disease treatment 14:00 Ellen McDonagh scFunBurd: Quantifying the cellular liability for complex disorders of all rare gene-disrupting 14:40 variants. **Thomas Renne** Biostatistical approaches to single-cell perturbation screens to create a prospective map of 15:00 mutational impact Magdalena Strauss SpliceTransformer predicts tissue-specific splicing linked to human diseases 15:20 **Ning Shen**

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Monday, July 21; Room 4AB	
Time	Title and Speaker
15:30	Cell type-specific epigenetic regulatory circuitry of coronary artery disease loci Dennis Hecker
15:40	MultiPopPred: A Trans-Ethnic Disease Risk Prediction Method, and its Evaluation on Low Resource Populations Ritwiz Kamal
15:50	Rethink gender as confounder in non linear PRS for human height prediction Huijiao Yang
16:40	Somatic mutations in normal tissues Andrew Lawson
17:20	Revisiting Cancer Predisposition: Identifying Altered Genes with Protective and Recessive Effects Michal Linial
17:40	COBT: A gene-based rare variant burden test for case-only study designs using aggregated genotypes from public reference cohorts Antoine Favier
17:50	Concluding remarks and prizes

Monday, July 21; Room 2N	
Time	Title and Speaker
11:20	Harnessing Deep Learning for Proteome-Scale Detection of Amyloid Signaling Motifs Witold Dyrka
11:40	From High-Throughput Evaluation to Wet-Lab Studies: Advancing Mutation Effect Prediction with a Retrieval-Enhanced Model Bingxin Zhou
12:00	BE3D: A Computational Workflow for Integrative Structure-Function Analysis of Base-Editor Tiling Mutagenesis Data Yoochan Myung
12:20	Enhanced protein evolution with inverse folding models using structural and evolutionary constraints Yunjia Li
12:40	Precise Prediction of Hotspot Residues in Protein-RNA Complexes Using Graph Attention Networks and Pre-trained Protein Language Models Siyuan Shen
14:00	Trustworthy Causal Biomarker Discovery: A Multiomics Brain Imaging Genetics based Approach Jin Zhang
14:20	SVQ-MIL: Small-Cohort Whole Slide Image Classification via Split Vector Quantization Yao-Zhong Zhang
14:40	Genetic Confounding and Comorbidity: Re-evaluating Causal Inference in Disease Associations Hadasa Kaufman
15:00	Sparse modeling of interactions enables fast detection of genome-wide epistasis in biobank-scale studies Julian Stamp

Monday, July 21; Room 2N	
Time	Title and Speaker
15:20	Pan-cancer analysis in the real-world setting uncovers immunogenomic drivers of acquired resistance post-immunotherapy Mohamed Reda Keddar
15:40	Beyond Mutation Frequency: A Bayesian Framework for Identifying Functional Cancer Drivers from Single-Cell Data Komlan Atitey
16:40	AdaGenes: A streaming processor for high-throughput annotation and filtering of sequence variant data Nadine S. Kurz
17:00	Comprehensive framework for assessing discrepancies in genomic content and species-level annotations across microbial reference genomes Serghei Mangul
17:20	Building Ultralarge Pangenomes Using Scalable and Compressive Techniques Sumit Walia
17:40	Information Content as a metric to evaluate and compare DNA Language Models Melissa Sanabria

Thursday, July 24; Room 3A	
Time	Title and Speaker
8:40	ADME-Drug-Likeness: Enriching Molecular Foundation Models via Pharmacokinetics-Guided Multi- Task Learning for Drug-likeness Prediction Dongmin Bang
9:00	Understanding the Sources of Performance in Deep Drug Response Models Reveals Insights and Improvements Nikhil Branson
9:20	FACT: Feature Aggregation and Convolution with Transformers for predicting drug classification code Gwang-Hyeon Yun
9:40	Efficient 3D kernels for molecular property prediction Ankit
11:20	Haplotype-specific copy number profiling of cancer genomes from long reads sequencing data Tanveer Ahmad
11:40	Multi-omics and liquid biopsy profiling of rapid autopsies reveals evolutionary dynamics and heterogeneity in metastatic bladder cancer Pushpa Itagi
12:00	Using spatial transcriptomics to elucidate the primary site of Cancers of Unknown Primary (CUPs) Oscar González Velasco
12:20	Inherited genetic risk factors associated with young adult versus late-onset lung cancers Zeynep H. Gümüş
12:40	pC-SAC: Method for High-Resolution 3D Genome Reconstruction from Low-Resolution Hi-C Data Carlos Angel

Thursday, July 24; Room 3A	
Time	Title and Speaker
14:00	HIDE: Hierarchical cell-type Deconvolution Franziska Görtler
14:20	RVINN: A Flexible Modeling for Inferring Dynamic Transcriptional and Post-Transcriptional Regulation Using Physics-Informed Neural Networks Osamu Muto
14:40	A deep learning framework for predicting single gene expression from cell-free DNA Robert Patton
15:00	MAGPIE: Multi-modal alignment of genes and peaks for integrated exploration of spatial transcriptomics and spatial metabolomics data
15:20	Randomized Spatial PCA (RASP): a computationally efficient method for dimensionality reduction of high-resolution spatial transcriptomics data lan Gingerich
15:40	CAdir: Fast Clustering and Visualization of Single-Cell Transcriptomics Data by Direction in CA Space Clemens Kohl

SPECIAL SESSION SCHEDULES

BIOINFORMATICS IN THE UK

Online schedule found here.

	Monday, July 21; Room 1B
Time	Title and Speaker
11:20	Molecular Digitisation and Biodiversity Bioinformatics Paul Kersey
12:00	KnetMiner for Smarter Science: Leveraging Knowledge Graphs & LLMs for Productive Gene Research Arne De Klerk
12:20	Lichen Cell Atlas: Tools for exploring photosymbiotic associations Ellen Cameron
12:40	How can emerging AI technologies benefit multi-omic analysis for crop and soil sustainability Laura-Jayne Gardiner
14:00	Civic Data-Driven Innovation for Global Health and AI for All lain Buchan
14:20	Health data organisation and landscape across the UK Emily Jefferson
14:30	The COALESCE study Angela Wood
15:00	TRE-FX platform for federated analytics of sensitive data in Trusted Research Environments Tim Beck
15:20	SurvivEHR: A Primary Care Foundation Prediction Model for Multiple Long-Term Conditions

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Charles Gadd

BIOINFORMATICS IN THE UK

	Monday, July 21; Room 1B
Time	Title and Speaker
15:40	Pathogen Analysis System (PAS): A Scalable Genomic Data Processing Framework Integrated with the European Nucleotide Archive David Yuan
15:50	AI in Histopathology Explorer for comprehensive analysis of the evolving AI landscape in histopathology Heba Sailem
16:40	Generative machine learning to model cellular perturbations Mo Lotfollahi
17:00	Building the world's largest, ethically-sourced database of biological information to pioneer a new class of foundational AI models Carla Greco
17:10	Multimodal generative machine learning for non-clinical safety evaluations in drug discovery and development Arijit Patra
17:20	CUPiD: a machine learning approach for determining tissue-of-origin in cancers of unknown primary from cell-free DNA methylation profiles Steven M. Hill
17:30	Introduction to AIBIO UK
17:35	Al: Careers and trajectories

DREAM CHALLENGES

Online schedule found here.

	Monday, July 21; Room 12
Time	Title and Speaker
14:00	Benchmarking foundation models in biology: where we are, and we where we want to go with the community Julio Saez-Rodriguez
14:15	Building Foundation Models for Single-cell Omics and Imaging
14:45	Predicting Perturbation Effects: Are We Really There? Maria Brbic
15:00	AI Alliance: Benchmarking foundation models for drug discovery Pablo Meyer-Rojas
15:15	Benchmarking in Service of Virtual Cell Models: Challenges, Opportunities, and a Path Forward Elizabeth Fahsbender
15:30	Deep learning models of regulatory DNA: A critical analysis of model design choices Anshul Kundaje
16:40	Benchmarking Multi-Modal Large Language Models for Metastatic Breast Cancer Prognosis Justin Guinney
16:55	Crowdsourcing Experiment
17:30	Evaluating and Benchmarking Foundation Models



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ELIXIR/NIH-ODSS

Wednesday, July 23; Room 12	
Time	Title and Speaker
11:20	Disease Ontology Knowledgebase: A Global BioData hub for FAIR disease data discovery Lynn Schriml
11:40	Integrating Data Treasures: Knowledge graphs of the DSMZ Digital Diversity Julia Koblitz
12:00	Metabolomics Workbench: Data Sharing, Analysis and Integration at the National Metabolomics Data Repository Mano Maurya
12:20	Building sustainable solutions for federally-funded open-source biomedical tools and technologies Karamarie Fecho
12:40	SEA CDM: An Ontology-Based Common Data Model for Standardizing and Integrating Biomedical Experimental Data in Vaccine Research Yongqun He
14:00	The Evolution of Ensembl: Scaling for Accessibility, Performance, and Interoperability Mallory Freeberg
14:20	Insights from GlyGen in Developing Sustainable Knowledgebases with Well-Defined Infrastructure Stacks Kate Warner
14:40	TBD
15:00	Production workflows and orchestration at MGnify, ELIXIR's Core Data Resource for metagenomics Martin Beracochea

ELIXIR/NIH-ODSS

Wednesday, July 23; Room 12	
Time	Title and Speaker
15:20	A SCALE-Able Approach to Building "Hybrid" Repositories to Drive Sustainable, Data Ecosystems Robert Schuler
15:40	From Platforms to Practice: How the ELIXIR Model Enables Impactful, Sustainable Biodata Resources Fabio Liberante
15:50	NIH-ODSS
16:40	Meeting user expectations in a resource constrained environment: Europe PMC's approach Melissa Harrison
17:00	Coopetition as a Catalyst for Researcher Engagement with Open Data Mark Hahnel
17:20	Evaluating the Impact of Biodata Resources: Insights from EMBL-EBI's Impact Assessments Eleni Tzampatzopoulou
17:40	TBD

INDUSTRY'S ROLE IN BIOINFORMATICS SESSION

Wednesday, July 23; Room 3B	
Time	Title
11:20	Opening Remarks & Framing the Ecosystem
11:40	Startup Ecosystems & Translational Science
12:00	Public-Private Partnerships and Career Navigation
12:20	Funding & Government Innovation Strategies
12:40	How Industry & Academia Can Work Together in Computational Biology:Panel Discussion

ISCB-CHINA WORKSHOP

Monday, July 21; Room 1C	
Time	Title
14:00	Welcome Address
14:05	Single Cell Spatial Transcriptomics: Decoding Cellular Heterogeneity in Spatial Dimensions
14:30	Seq2Image: Computational Paradigm and Genomic Applications
14:50	Language AI for Viruses, Vaccines, and Drugs
15:10	Single Cell Spatial Transcriptomics: Decoding Cellular Heterogeneity in Spatial Dimensions
15:30	Bioinformatics @ China
16:40	Learning Multiscale Cellular Organization and Interaction
17:10	Language-guided biology
17:30	Al and Bioinformatics: The Next Era



NIH TRACK ON GENAI, CYBERINFRASTRUCTURE, DIGITAL TWINS, AND QUANTUM COMPUTING

	Monday, July 21; Room 2F
Time	Title and Speaker
11:20	Opening Remarks for NIH Track
11:40	Graph Kolmogorov-Arnold Networks for Interpretable Alzheimer's Disease Diagnosis from Structural MRI Liang Dong
12:00	Network Science for Cyber-physical Twinning of Human Heart
12:20	A Digital Twins Prototype for Monitoring and Predicting Dynamic Diet-related Health Conditions Honggang Wang
12:40	Multiscale Digital-Twin Modeling and Estimation with Indirect, Neurological Data Matthew F. Singh
14:00	Advancing Discovery through GenAI and Scalable Infrastructure
14:20	A Global Model for FAIR and Open Research: Scalable, Collaborative Infrastructure in Action Kristi Holmes
14:40	Beyond Data Sharing: AI-Powered Solutions for Effective Biomedical Data Reuse Luca Foschini
15:00	Reusable Cyberinfrastructure and Use Cases for the Cancer Research Data Commons (CRDC) Tanja Davidsen

NIH TRACK ON GENAI, CYBERINFRASTRUCTURE, DIGITAL TWINS, AND QUANTUM COMPUTING

Monday, July 21; Room 2F	
Time	Title and Speaker
15:20	Power Your Kids First or INCLUDE Data Analysis on The Interoperable CAVATICA Cloud Analytics Workspace Jared Rozowsky
15:40	The Gene Set Browser: An interoperable and AI/ML-ready tool for gene set analysis in the Common Fund Data Ecosystem (CFDE) Julie Jurgens
16:40	NIH Quantum Computing Initiatives Fenglou Mao
17:00	Advancing quantum algorithms for elementary mode and metabolic flux analysis Chi Zhang
17:20	Efficient quantum algorithm to simulate open systems through a single environmental qubit Vischi Michele
17:40	Quantum Approximate Optimization for K-Area Clustering of Biological Data Yong Chen
18:00	Closing Remarks

PUBLICATIONS — NAVIGATING JOURNAL SUBMISSIONS

Monday, July 21; Room 12	
Time	Title and Speaker
11:20	Welcome and Introductions
11:22	Effective cover letter writing and manuscript preparation for submitting manuscripts in crowded research areas Thomas Lengauer
11:40	Choosing journals for submission in popular topics Laura Mesquita
11:50	How editors make decisions on submissions? Feilim Mac Gabhann
12:00	How do editors decide on accepting papers on highly similar topics? Michael J E Sternberg
12:10	How and why eLife selects papers for peer review Michael Markie
12:20	Panel Discussion

STEWARDSHIP OF CRITICAL INFRASTRUCTURE

Thursday, July 24; Room 3B	
Time	Title and Speaker
8:40	Introduction
9:00	Beyond Citations: Measuring the Economic and Scientific Impact of UniProt in the Biodata Ecosystem Alex Bateman
9:20:00	Challenges in biological data/infrastructure stewardship from an Asia-Pacific perspective Shoba Ranganathan
9:40	Indian Biological Data Centre: past, present and future
11:20	A Proposal on top of FAIR: Quality of Knowledge Representation (QKR) Julio Collado Vides
11:40	Perspectives on biological knowledgebase management and the advent of AI
12:00	Developing stewardship networks to sustain data, software and systems Peter Maccallum
12:20	Technical Discussion
14:00	The missing link in FAIR data policy: data resources Christophe Dessimoz

STEWARDSHIP OF CRITICAL INFRASTRUCTURE

Thursday, July 24; Room 3B		
Time	Title and Speaker	
14:20	Sustaining global biodata: from resources to sustained infrastructure Guy Cochrane	
14:40	NIH's Strategic Vision for Data Science	
15:00	Your Science Needs You	
15:20	Open Discussion	

STUDENT COUNCIL SYMPOSIUM

	Sunday, July 20; Room 2N
Time	Title and Speaker
9:00	TBD
9:00	Student Council Symposium
9:30	Nutri-omics: how omics investigation can help designing personalized nutrition research Mirko Treccani
9:45	Nocardia Genomes are a Large Reservoir of Diverse Gene Content, Biosynthetic Gene Clusters, and Species-specific Genes Kiran Kumar Eripogu
10:00	Lifting the veil on Challenging Medically Relevant Genes Victor Grentzinger
10:05:00	AccuRate: A Tool Supporting Genotype–Phenotype Analysis and Causal Mutation Discovery in Soybean Alžbeta Rástocká
10:10	Early colorectal cancer detection with deep learning on ultra-shallow whole genome sequencing of cell-free DNA Ritchie Yu
10:15	DNA-DistilBERT: A small language model for non-coding variant effect prediction from human DNA sequences Megha Hegde
10:30	Generative AI for Childhood and Adult Cancer Research Guillermo Prol Castelo
11:00	AutoPeptideML 2: An open source library for democratizing machine learning for peptide bioactivity prediction Raúl Fernández-Díaz

STUDENT COUNCIL SYMPOSIUM

Sunday, July 20; Room 2N		
Time	Title and Speaker	
11:05	ENQUIRE automatically reconstructs, expands, and drives enrichment analysis of gene and MeSH co- occurrence networks from context-specific biomedical literature Luca Musella	
11:15	TCRBench: A Unified Benchmark for TCR-Antigen Binding Prediction and Clustering Muhammed Hunaid Topiwala	
11:20	Fold first, ask later: structure-informed function prediction in Pseudomonas phages Hannelore Longin	
11:35	Exploring capabilities of protein language models for cryptic binding site prediction Vít Škrhák	
11:50	Coarse-grained and Multi-Scale Modeling of Lytic Polysaccharide Monooxygenases: Insights into Family-Specific Dynamics and Protein Frustration Nisha Nandhini Shankar	
11:55	Identification and structural modeling of the novel TTC33-associated core (TANC) complex involved in DNA damage response Małgorzata Drabko	
12:00	Functional Interfaces at Ordered–Disordered Transitions: Conserved Linear Motifs and Flanking Regions in Modular Proteins Carla Luciana Padilla Franzotti	
12:05	Automating Linear Motif Predictions to Map Human Signaling Networks Yitao Eric Sun	
12:10	Deep Phylogenetic Reconstruction Reveals Key Functional Drivers in the Evolution of B1/B2 Metallo-β- Lactamases Samuel Davis	

STUDENT COUNCIL SYMPOSIUM

Sunday, July 20; Room 2N		
Time	Title and Speaker	
12:25	Multilingual model improves zero-shot prediction of disease effects on proteins Ruyi Chen	
12:30	Integrated analysis of bulk and single-nuclei RNA sequencing data of primary and metastatic pediatric Medulloblastoma. Ana Isabel Castillo Orozco	
12:45	Investigating novel transcriptional regulators in symbiotic nodule development of Medicago truncatul Sara Eslami	
12:50	Meta-Analysis of Bovine Transcriptome Reveals Key Immune Gene Profiles and Signaling Pathways Vennila Kanchana Devi Marimuthu	
12:55	Post-translational regulation of stemness under DNA damage response contributes to the gingivobuccal oral squamous cell carcinoma relapse and progression Sachendra Kumar	
14:00	TBD	
15:00	TBD	
15:45	Closing remarks	

TECH TRACK

Monday, July 21; Room 11BC	
Time	Title and Speaker
11:20	UniProt: Evolving Tools and Data for Protein Science Daniel Rice
11:40	Genomics 2 Proteins portal: A resource and discovery platform for linking genetic screening outputs to protein sequences and structures
12:20	ModCRE: modelling protein–DNA interactions and transcription-factor co-operativity in cisregulatory elements Patrick Gohl
14:00	Orchestrating Microbiome Analysis with Bioconductor Tuomas Borman
14:20	Smart Turkana Beads: A Culturally Embedded IoT Innovation for Health Monitoring and Drug Adherence
14:40	Integrating Long-Read Sequencing and Multiomics for Precision Cell Line Engineering
15:00	Lonza Sponsor Talk
15:20	10x Genomics Sponsor Talk
15:40	10x Genomics Sponsor Talk

TECH TRACK

Tuesday, July 22; Room 11BC		
Time	Title and Speaker	
11:20	Scale with Seqera: Accelerate, Expand, and Collaborate Adam Talbot	
11:40	SimpleVM - Effortless Cloud Computing for Research Viktor Rudko	
12:00	Overture Prelude: A toolkit for small teams with big data problems Mitchell Shiell	
12:20	Al and Quantum in Healthcare and Life Sciences	
14:00	GPCRVS - AI-driven decision support system for GPCR virtual screening Dorota Latek	
14:20	Self-supervised generative AI enables conversion of two non-overlapping cohorts Supratim Das	
14:40	The Bioverse - Biomolecule data processing for AI made easy Tim Kucera	
15:00	Data, We Need to Chat Alberto Pepe	
15:20	BioInfore: A No-Code Genome Data Management System Based On AI Agents Zheng Chen	
15:40	Omi: Bridging the Informatics to Bio Gap with a Natural Language Co-pilot	

SOCIAL EVENTS AND OTHER ACTIVITIES



SUNDAY, JULY 20, 2025

Welcome Networking Reception with Exhibitors

Time: 19:30 - 21:00

Location: Room 1A, ACC Liverpool

MONDAY, JULY 21, 2025

Edit-A-Thon

Time: 10:00 - 18:00

Location: Room 13, ACC Liverpool **Note:** All in-person spaces are filled

ISCB-China Workshop

Time: 14:00 – 18:00

Location: Room 1C, ACC Liverpool

Bioinfo4Women Meet-Up:

Supporting Women in Bioinformatics

Time: 13:00 – 14:00

Location: 2F

Bioinformatics in the UK Reception

Time: 18:00

Location: Exhibition Centre Terrace Cost: £10 Students, £10 Post-Docs,

£20 Professionals

TUESDAY, JULY 22, 2025

LGBTQI+ Meet-Up

Time: 13:00 – 14:00

Location: Riverside Balcony,

ACC Liverpool

Success Circles

Time: 18:00 – 19:30

Location: Hall 2, ACC Liverpool

Cost: £10



SOCIAL EVENTS AND OTHER ACTIVITIES

WEDNESDAY, JULY 23, 2025

Come Together: A Night of

Networking & Fun

Time: 19:00 – 21:00

Location: Punch Tarmey's

Cost: £25 Students, £25 Post-Docs,

£50 Professionals

JPI Meet-Up

Time: 18:00

Location: Riverside Balcony

WEDNESDAY, JULY 23 AND THURSDAY, JULY 24, 2025

CollaborationFest

Time: Wed: 11:20 – 18:00

Thurs: 8:40 – 16:00

Location: Room 2F, ACC Liverpool



MONDAY, JULY 21 TO THURSDAY, JULY 24, 2025

Serene Stretch Symposium

Time: 7:30 – 8:00

Location: Upper Galleria, ACC Liverpool



Join us for Yoga 21–24 July 2025 7:30–8:00am Serene Stretch Symposium





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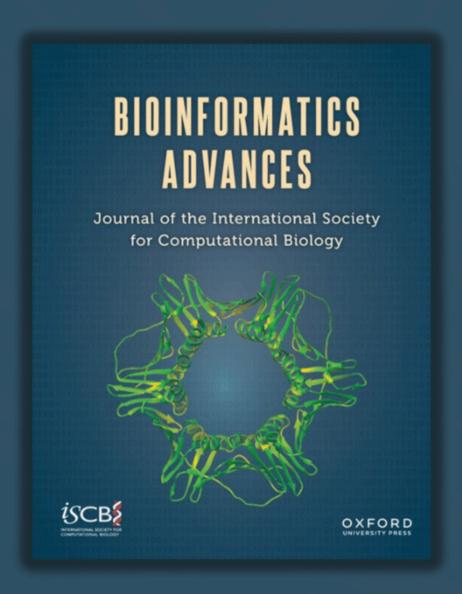
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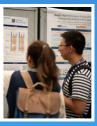


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