ISMB 2026

WASHINGTON, DC
JULY
12–16

CONFERENCE

PROGRAMME

and **ISCB July Newsletter**

ISMB
2026
WASHINGTON, DC
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NEWSLETTER

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CONFERENCE PROGRAMME

A LETTER FROM THE ISCB PRESIDENT, PREDRAG RADIVOJAC

Dear ISCB Members,
As my term as President of the International Society for Computational Biology nears a close, I have had the privilege of witnessing both the remarkable growth of our field and the continued strength of our Society. Over the past several years, ISCB, led by the Board of Directors and supported faithfully by its members who serve in many volunteer roles, has worked to transform strategic aspirations into meaningful action, expanding opportunities for our members while strengthening the Society's foundation.

One of our most significant achievements has been the introduction of the ISCB Conference Collaboration Program. Through this initiative, ISCB has expanded its support for regional and topical scientific meetings, creating new opportunities for researchers to present their work, build collaborations, and engage with the computational biology community closer to home. These partnerships have enabled seven new conferences to join the ISCB family, broadening our scientific reach and increasing opportunities for participation around the world.

Our commitment to scientific publishing also remains strong. During this term, ISCB successfully renewed the Editors-in-Chief agreements for *Bioinformatics Advances*, ensuring continued outstanding stewardship of the Society's journal. The journal continues to mature as an important venue for computational biology research and reflects our commitment to scientific excellence and innovation.

Supporting the next generation of scientists remains central to our mission. ISCB has increased funding for conference fellowships, allowing more students and early-career researchers to participate in our meetings and engage with the global community. We have also expanded support through our Innovation Fund, which provided support for five new educational and community initiatives that advance bioinformatics training and capacity building around the world.

These programs include educational activities in Africa, Latin America, Mexico, and Eastern Europe; sustainable computational research initiatives; and training programs that emphasize reproducibility, open science, and easy access to bioinformatics education.

The Society has also experienced encouraging growth in membership outside North America and Europe. Computational biology is a truly global discipline, and ISCB's expanding international membership reflects both the growth of our field and the Society's increasing relevance to scientists worldwide. Strong partnerships with regional organizations continue to strengthen our collective scientific community.

While we celebrate these accomplishments, the Board of Directors has also been diligently working to develop ISCB's next strategic plan. This work is guided by five interconnected pillars that will help shape the Society's future:

Scientific Excellence and Impact recognizes ISCB's responsibility to serve as the trusted global voice for computational biology. We must continue to define standards of scientific rigor, promote excellence in research and methodology, advocate for computational biology as a scholarly discipline, and demonstrate the impact of our science across the life sciences. ISCB must also serve as a bridge between innovation, entrepreneurship, and scientific discovery, helping connect transformative ideas with opportunities for societal impact.

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Ethical Leadership and Professional Integrity reflects our commitment to fostering a culture of integrity, respect, transparency, and responsible scientific conduct. Ethical practices must remain embedded throughout our conferences, publications, educational programs, and governance.

Global Community and Representation recognizes that our leadership, programs, and partnerships must reflect the computational biology community worldwide. Strong regional partnerships and meaningful participation from historically underrepresented regions will remain essential to our growth and future success.

Education, Training, and Career Pathways emphasizes ISCB's role in supporting scientists throughout their professional journeys. Accessible education, career development programs, and lifelong learning will strengthen both our members and the broader computational biology workforce.

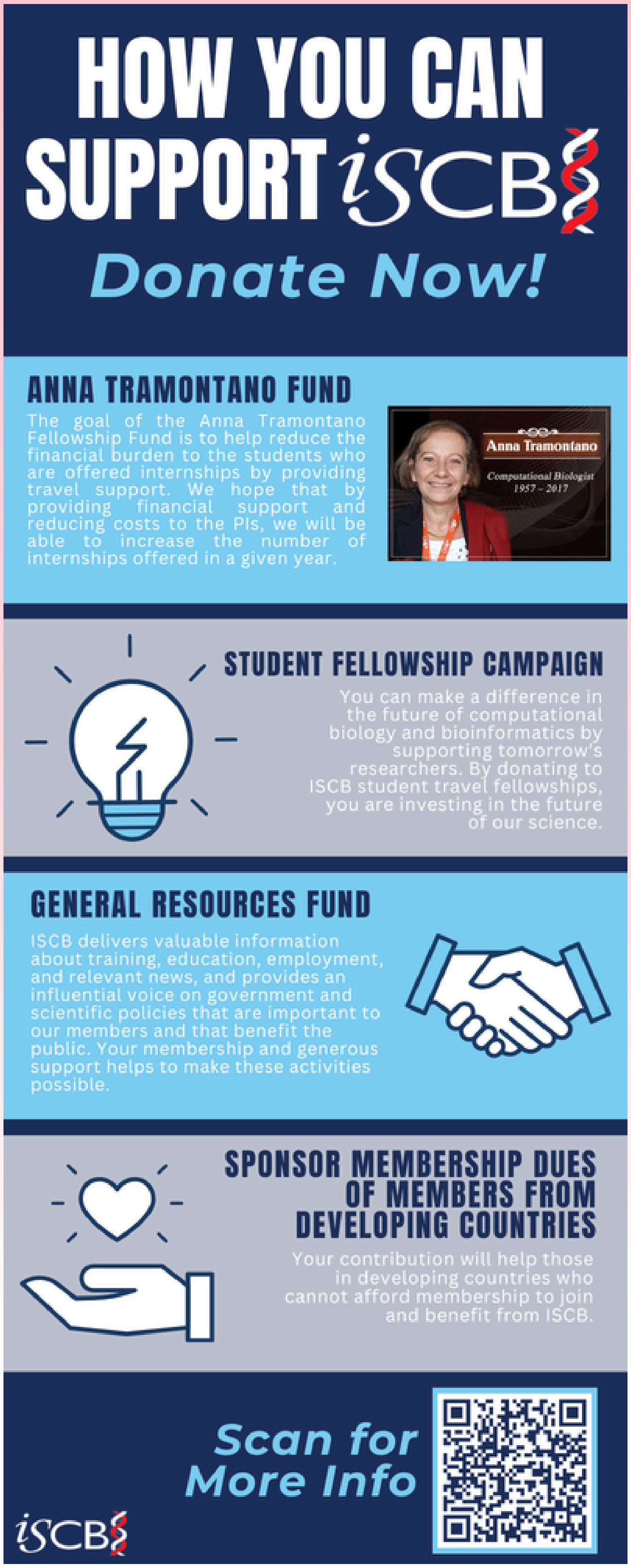
Organizational Sustainability and Stewardship ensures that ISCB remains financially responsible, operationally sustainable, and strategically positioned to serve future generations of scientists.

Computational biology has never been more important. Our discipline sits at the intersection of biology, medicine, artificial intelligence, computer science, data science, and technology. The discoveries and tools developed by our community increasingly influence every area of life sciences and ultimately benefit society as a whole.

I am deeply grateful to the Board of Directors, our volunteers, committee members, conference organizers, journal editors, staff, and, most importantly, our members for their dedication and service. Together, we have strengthened the Society, expanded our global reach, and positioned ISCB for continued success.

The future of computational biology is exceptionally bright, and I am confident that ISCB will continue to lead, support, and advance our field for many years to come.

Predrag Radivojac
President, International Society for Computational Biology



HOW YOU CAN SUPPORT ISCB

Donate Now!

ANNA TRAMONTANO FUND

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

STUDENT FELLOWSHIP CAMPAIGN

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

GENERAL RESOURCES FUND

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

SPONSOR MEMBERSHIP DUES OF MEMBERS FROM DEVELOPING COUNTRIES

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

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ISCB'S CODE OF ETHICS AND PROFESSIONAL CONDUCT

Ahead of us gathering together in Washington, DC for the 34th annual ISMB conference, we wanted to take this opportunity to remind you about the ISCB Code of Ethics and Professional Conduct, which explicitly outlines how we expect members and participants to interact as colleagues, scientists, and global citizens.

The principles within the code include, but are not limited to:

- **Respect and courtesy as the standard:** The ISCB community is expected to foster an environment of respect and dignity for all contributors to our field, recognizing and valuing differences in perspectives, scientific approaches, and cultures.

- **Integrity in sharing and critique:** 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.

- **A clear stance against harassment and discrimination:** The code 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 during the conference and beyond, members are expected to uphold the highest standards of collegiality and respect.

With these guidelines, 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.

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

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2026 ISCB AWARD WINNERS

As part of the ISMB 2026 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 2026 Proceedings Supplement in *Bioinformatics*, but you can read a short summary of each article below.

2026 ISCB OUTSTANDING SERVICE AWARD: DR. PHILIP E. BOURNE

Dr. Philip E. Bourne is the 2026 recipient of the ISCB Outstanding Service Award, recognized for his decades of leadership and service in advancing open, collaborative science within the computational biology community. An early presence at ISMB conferences, Bourne became ISCB President in 2002, working to professionalize the Society's operations and expand its global reach—including bringing ISMB 2006 to Brazil. During his tenure on the Publications Committee, he co-founded *PLOS Computational Biology* in 2005, giving the field broader visibility beyond its traditional audience.

Among his most enduring contributions is the "Ten Simple Rules" article series, born from an energetic Student Council Symposium in 2005 and now a widely used resource for professional development in science. His later roles as the first Chief Data Officer at the NIH and founder of the University of Virginia's School of Data Science reflected his commitment to bridging computational biology with the broader scientific ecosystem. ISCB is honored to celebrate Phil's lasting impact on the field and the community he so generously served.

Read the full article here: https://doi.org/10.1093/bioinformatics/btag280

2026 ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD: DR. RICHARD DURBIN

Dr. Richard Durbin is the 2026 recipient of the Accomplishments by a Senior Scientist Award, recognized for his foundational contributions to genome sequencing, genetic variation analysis, and evolutionary genomics. His path to computational biology wound through mathematics, a year learning to program, and a Fulbright Award that brought him to Harvard and into formal biology study. A PhD at Cambridge's MRC Laboratory of Molecular Biology and a post-doc at Stanford followed, before John Sulston invited him into the early sequencing effort at the Sanger Institute—placing him at the heart of the Human Genome Project.

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As a mentor, Durbin champions "constructive neglect," giving students freedom to develop independence and pursue their own interests. His work on population sequencing and imputation helped advance the Thousand Genomes Project, and he continues to advocate for a complete reference genome for all species. Honored to be recognized alongside so many respected peers, Durbin remains actively engaged, still writing code and developing new computational methods.

Read the full article here: https://doi.org/10.1093/bioinformatics/btag283

2026 ISCB INNOVATOR AWARD: DR. OLGA TROYANSKAYA

Dr. Olga Troyanskaya is the 2026 recipient of the ISCB Innovator Award, recognized for her work developing computational and machine learning approaches to interpret complex biological data and advance precision health. Her path to computational biology began with a childhood fascination with genetics and a determined undergraduate search for someone working at the intersection of computer science and biology—a search that led her to Steven Salzberg's lab at Johns Hopkins and introduced her to the field at a formative moment in genomic sequencing.

Graduate study at Stanford, under David Botstein and Russ Altman, sharpened her ability to ask the right scientific questions—a skill she considers central to good research and models in her own mentoring. Her lab's work spans neurodegeneration, kidney disease, and autism, and she currently leads Princeton Precision Health. Deeply honored by the award, Troyanskaya dedicates it to Botstein, whose mentorship she credits as foundational to her career.

Read the full article here: https://doi.org/10.1093/bioinformatics/btag281

2026 ISCB OVERTON PRIZE AWARD: DR. MARINKA ZITNIK

Dr. Marinka Zitnik is the 2026 recipient of the ISCB Overton Prize, recognized for her foundational AI methods to accelerate biomedical discovery. Though she initially planned to pursue medicine, learning about computational biology redirected her path—offering a way to combine her strengths in math and computer science to build tools with real impact for wet lab researchers. An undergraduate research opportunity with Blaz Zupan, collaborating with scientists at Baylor College of Medicine, confirmed her commitment to the field.

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A post-doc at Stanford under Jure Leskovec deepened her expertise in adapting cutting-edge AI models to biological questions and shaped her approach to mentorship and scientific communication—skills she draws on daily as a PI. Her lab's current focus spans AI-driven drug discovery and repurposing, molecular modeling, and AI scientist systems capable of generating and refining research hypotheses. Honored by the award, Zitnik credits her mentors and students equally for making her contributions possible.

Read the full article here: https://doi.org/10.1093/bioinformatics/btag282

34th Conference on
Intelligent Systems for Molecular Biology
Washington, DC July 12–16

Can't join us live in Washington, DC?

You can still attend ISMB 2026 virtually!

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THE 2026 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.

ISCB proudly congratulates the 2026 Class of Fellows on this well-deserved recognition of their outstanding contributions to computational biology and bioinformatics!

ISCB will be honoring the 2026 Class of Fellows during the ISMB 2026 conference in Washington, DC.

Congratulations, 2026 Class of ISCB Fellows!

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Michelle D. Brazas, Ontario Institute for Cancer Research

Michelle Brazas is a driving force in bioinformatics education and community leadership, with a career dedicated to defining what the field should teach and proving that it works. As Scientific Director of Bioinformatics.ca hosted at the Ontario Institute for Cancer Research and the newly established Canadian Bioinformatics Hub, she has helped build training infrastructure that reaches researchers nationwide. Her peer-reviewed scholarship, including landmark work on bioinformatics core competencies and empirical evaluations of continuing education outcomes, has shaped curriculum design internationally. Within ISCB, she has served as Secretary, Executive Committee member, and Chair of the Nominations Committee, bringing the same rigor and generosity to governance that she brings to everything she does.

Tulio de Oliveira, Stellenbosch University

Tulio de Oliveira is a global leader in genomic surveillance, developing bioinformatic tools that have transformed how scientists track and respond to infectious disease outbreaks across HIV, Hepatitis B and C, Zika, Dengue, Chikungunya, and beyond. His work during the COVID-19 pandemic was pivotal. His group was central to the discovery and tracking of the Omicron variant, helping establish South Africa as a world leader in documenting viral mutations and informing containment strategies. Working across the University of KwaZulu-Natal, Stellenbosch University, the University of Washington, and the Wellcome Sanger Institute, he has built a research programme rooted in Africa and driven almost entirely by African scientists. A passionate advocate for African science, he has trained a generation of bioinformaticians across the continent and proven that world-class genomic epidemiology can be done locally.

Matthew Hahn, Indiana University

Matthew Hahn is a leader in molecular evolution, with wide-ranging contributions spanning population genetics, phylogenetics, gene family evolution, and transcriptional regulation. His lab's CAFE software has become a standard tool in genomic sequencing projects worldwide, enabling accurate inference of gene gain and loss across species, while his foundational work on introgression has reshaped our understanding of how gene flow shapes genomes. A methodological innovator, he was among the first in population genetics to apply machine learning approaches, and continues to push the boundaries of phylogenetic inference and evolutionary analysis. Beyond his research, Hahn has mentored 24 PhD students and postdocs and serves as President-elect of the Society for Molecular Biology and Evolution.

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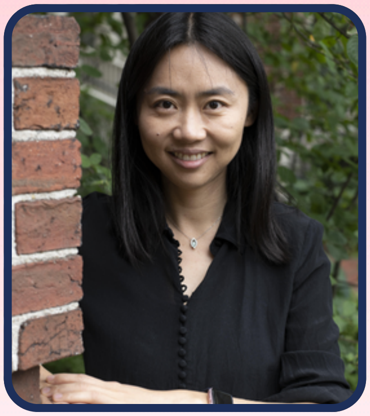
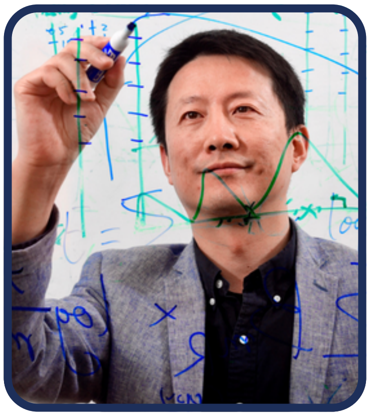
Daniel Huson, University of Tübingen

Daniel Huson is a foundational figure in evolutionary bioinformatics, whose algorithmically rigorous and biologically impactful tools have been adopted by researchers worldwide. His SplitsTree software transformed phylogenetic analysis by extending evolutionary inference beyond trees to networks, while MEGAN—the first interactive metagenomic analysis tool—revolutionized how scientists interpret microbiome data and earned the PLOS Computational Biology Research Prize. He further accelerated the field with DIAMOND, now the global standard for fast DNA-to-protein alignment, and contributed pioneering work demonstrating that closed bacterial chromosomes can be reconstructed from complex communities using long-read sequencing. With over 80,000 citations, more than 60 PhD students co-supervised, and decades of sustained innovation, Huson's career stands as a masterclass in turning mathematical rigor into biological discovery.



Jingyi Jessica Li, Fred Hutchinson Cancer Center, University of Washington

Jingyi Jessica Li is a pioneering statistician and computational biologist whose work has fundamentally elevated the standards of rigor, reproducibility, and interpretability in genomics. Her scDesign family of simulators has become foundational for benchmarking across single-cell and spatial omics, while her frameworks for false discovery rate (FDR) control and differential expression analysis have reshaped how the field approaches statistical inference. Her influential *Science* paper on the central dogma settled a decades-long debate in molecular biology by demonstrating that transcription, not translation, is the primary driver of protein abundance. A recipient of the 2023 ISCB Overton Prize, she is also a celebrated mentor whose trainees have gone on to become independent faculty and award winners across the field.



Wei Li, University of California, Irvine

Wei Li is a computational genomics leader whose work bridges statistics, epigenetics, and large-scale genomic data to drive discoveries with direct clinical impact. His group developed the TR-Atlas, the world's largest genetic reference map of tandem repeats across 340,000 individuals, opening a new frontier in understanding the missing heritability of complex diseases. In translating bioinformatics into patient care, he pioneered plasma cfDNA methylation-based liquid biopsies for cancer and neurodegenerative diseases, advancing clinically actionable biomarkers toward FDA approval.. With over 74,000 citations, an H-index of 105, and more than a dozen former trainees now serving as independent faculty, his influence on both the science and the scientists of computational biology is extraordinary.

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Xihong Lin, Harvard School of Public Health
Xihong Lin is a world-leading biostatistician whose methodological innovations have become cornerstones of modern statistical genetics, with tools like SKAT and STAAR now standard approaches for rare-variant and whole-genome sequencing association analyses used in studies sequencing over 500,000 genomes. During the COVID-19 pandemic, her team's landmark *Nature* analysis of 32,000 Wuhan cases directly informed public health intervention policies worldwide, and she played a key role in shaping test-trace-isolate strategies in Massachusetts and advising the UK Parliament. A member of both the National Academy of Sciences and National Academy of Medicine, she has supervised 45+ PhD students and 35+ postdoctoral fellows, and founded the ENAR Young Researcher Workshop, which has mentored over 500 junior faculty. Her career is a unique combination of transformative science, institutional leadership, and an enduring commitment to building the next generation of statisticians and computational biologists.

Jennifer Listgarten, University of California, Berkeley
Jennifer Listgarten is a computational biologist and machine learning innovator whose work spans a remarkable range of biological domains, from genetics and epigenomics to immunoinformatics, to CRISPR guide design and protein engineering. Her FaST-LMM methods transformed genome-wide association studies by elegantly addressing structured noise from population structure and relatedness, while her CRISPR guide design work mitigated the need to empirically test hundreds of guides per gene and revealed novel mechanistic insights in the process. More recently, her contributions to AI-driven protein engineering have set a rigorous standard for how machine learning should be applied under the practical constraints of real experimental settings. Her recent review article on AI for protein engineering in *Science* paints a coherent technical picture of the fast-moving field.

Kenta Nakai, The University of Tokyo
Kenta Nakai is a pioneer in computational sequence analysis, whose PSORT system became one of the field's most widely adopted resources, with its top papers accumulating over 10,000 citations. By combining knowledge of protein sorting signals with machine learning, he established subcellular localization prediction as a cornerstone of functional genomics, a contribution that has only grown in relevance as proteomics data has exploded. He later extended his expertise to transcriptional regulation, developing approaches to predict tissue-specific gene expression from genomic sequence. A long-standing leader in the Asia-Pacific bioinformatics community, he has served as President of the Japanese Society for Bioinformatics, held executive roles in APBioNet for over two decades, and is the inaugural recipient of both the JSBi Prize and the APBioNet Research Innovation Award.

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Gonzalo Navarro, University of Chile
Gonzalo Navarro is a world-leading algorithms researcher whose foundational contributions to sequence search and compressed indexing have quietly powered some of modern bioinformatics' most important tools. His early work on bit-parallel approximate string matching set the standard for efficient DNA and protein sequence analysis, while his co-invention of the r-index now underpins pangenome and population-scale genomic indexing worldwide. His two Cambridge University Press textbooks on pattern matching and compact data structures remain definitive references bridging theoretical computer science and biological sequence analysis. An ACM Fellow and decade-long Deputy Director of Chile's Centre for Biotechnology and Bioengineering, Navarro has built an enduring research community at the intersection of algorithms and genomics, with particular impact across Latin America.

Qing Nie, University of California, Irvine
Qing Nie is a world-leading computational and systems biologist whose CellChat tool—which has been cited nearly 7,400 times and named one of *Nature Communications*' Top 25 Life Sciences papers in 2021—has transformed how researchers decode cell-cell communication from single-cell data. His contributions span systems biology, multiscale modeling, and spatial omics, with foundational work on morphogen gradients, lineage trajectories, and tissue organization that has reshaped understanding of cell fate and development. Ranked #1 worldwide in single-cell transcriptomics over the past five years by ScholarGPS, he is equally distinguished as a builder of the field itself, directing NSF-Simons and NIH centers, creating interdisciplinary PhD programs at UC Irvine, and mentoring 34 postdocs and 26 PhD students. A Fellow of AAAS, SIAM, AMS, and APS, Nie exemplifies the rare combination of mathematical rigor, biological insight, and community investment that defines a truly transformative scientist.

Mihaela Pertea, Johns Hopkins University
Mihaela Pertea is the creator of StringTie, a transcriptome assembly tool that redefined the state of the art when it launched in 2015. StringTie not only outperforms existing methods in accuracy but does so 40 times faster and with dramatically lower memory requirements, turning days of computation into minutes. By ingeniously adapting maximum flow optimization to the problem of RNA-seq assembly, she introduced a mathematical framework that no one had previously applied to the field, and the impact has been extraordinary: her StringTie papers have accumulated over 18,000 citations and the software has been used by more than 75,000 researchers worldwide. Her contributions span 25 years, from developing the first computational gene finder for the malaria parasite early in her career to leading the CHESS human gene annotation database, which used StringTie to synthesize 10,000 RNA-seq experiments into a comprehensive human gene catalog. Pertea is a great example of a scientist who combines algorithmic innovation with the engineering rigor to turn theory into tools the whole world uses.

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Sylvia Plevritis, Stanford University
Sylvia Plevritis is a pioneering computational cancer biologist whose algorithms have defined how the field integrates multi-omics, imaging, and clinical data to uncover the biological underpinnings of the tumor microenvironment and its relationship to patient outcomes. Her work has led to widely used bioinformatics tools—including SPADE, PRECOG, MethylMix, TRACER, and CELESTA. At Stanford, she is serving as Chair of Biomedical Data Science, Director of the Biomedical Informatics Graduate Program, and inaugural Associate Director for Cancer AI, shaping both the science and the institutional infrastructure of the field. A devoted mentor, she has trained over 60 graduate-level researchers, more than 20 of whom are now faculty at leading universities.

Sophie Schbath, National Research Institute for Agriculture, Food and the Environment (INRAE)
Sophie Schbath is a distinguished statistical bioinformatician whose foundational work on DNA motif identification and genome analysis has made her one of the field's most respected references, crystallized in her co-authored book "DNA, Words and Models," described as one of a kind for its rare accessibility across disciplines. As head of the MaIAGE laboratory at INRAE and the Migale bioinformatics facility, she has built and sustained research infrastructure serving both her institution and the broader French scientific community. Her leadership of the French Society of Bioinformatics from 2010 to 2016—including co-organizing the landmark joint JOBIM-ECCB 2014 conference—helped shape computational biology as a discipline in France and across Europe. Equally celebrated as a mentor and community builder, she brings the same rigor and generosity to supporting younger researchers as she does to her science.

Eran Segal, Weizmann Institute of Science and Mohamed bin Zayed University of Artificial Intelligence
Eran Segal is a computational and systems biology leader whose work has connected sequence, regulation, and human physiology in ways that have reshaped multiple fields simultaneously. His landmark *Cell* 2015 study of 900 individuals produced the first predictive algorithm for personalized glycemic responses, launching personalized nutrition as a rigorous scientific discipline, while his microbiome research has delivered some of the field's most influential causal findings, from the effects of artificial sweeteners on glucose intolerance to the highly personal nature of probiotic colonization. His Human Phenotype Project, a large-scale deeply phenotyped prospective longitudinal cohort of over 35,000 participants, represents a bold vision for building a world model of human biology capable of predicting personalized health trajectories, simulating clinical trials in silico, and generating novel biological hypotheses. During the COVID-19 pandemic, he served as a senior scientific advisor to the Israeli government, translating computational biology into national policy in real time.

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Yun S. Song, University of California, Berkeley

Yun Song is a computational biologist of rare mathematical depth whose work has repeatedly opened new research directions, spanning rigorous population genomics to cutting-edge AI for biological sequences. His suite of tools—SMC++, momi2, diCal, pyrho, and SINGER—has become an essential resource for inferring complex population genetic models and ancestral recombination graphs from large-scale genomic data, while his CPT framework for variant effect prediction recently ranked as one of the top-performing methods among 97 predictors in an independent benchmark. His lab's genomic language models, GPN-MSA and GPN-Star, are setting a new standard for non-coding variant interpretation by leveraging evolutionary information across whole-genome alignments and phylogenetic structure. Currently serving as Director of the Center for Computational Biology at UC Berkeley, he has trained 35 PhD students and 13 postdoctoral scholars over his career, shaping both the science and the next generation of researchers with equal distinction.

Wing-Kin Sung, The Chinese University of Hong Kong

Wing-Kin Sung is a computational genomics pioneer whose contributions span over 30 years, from foundational algorithms to clinical applications that are improving lives today. His work on the Burrows-Wheeler Transform constructor became a cornerstone of NGS analysis through its role in BWA-MEM, while his chromatin interaction tools helped decode the 3D structure of the genome and his virus integration methods led to the landmark discovery that Hepatitis B Virus recurrently integrates into key cancer genes in nearly half of HBV-related liver cancer cases. Most recently, his structural variation and genome assembly tools are being used in Hong Kong to diagnose pathogenic mutations in rare disease patients, a powerful testament to the real-world impact of rigorous computational biology. A recipient of Singapore's National Science Award and author of two widely taught bioinformatics textbooks, Sung has shaped both the methods and the next generation of researchers in the field.

Haixu Tang, Indiana University

Haixu Tang is one of computational biology's most versatile pioneers, with foundational contributions spanning genomics, metagenomics, proteomics, glycomics, and genomic privacy. His co-development of the de Bruijn graph framework for genome assembly—recognized with the RECOMB Test-of-Time Award—became the algorithmic cornerstone of both short-read and long-read assemblers used worldwide, while his concept of "peptide detectability" transformed how computational proteomics accounts for the intrinsic biases of mass spectrometry. Perhaps most presciently, he pioneered the study of membership inference attacks in genomics, demonstrating that individual participation could be identified from aggregate study data, a discovery that seeded an entire field of privacy-preserving methods now central to both genomics and machine learning. As PI and Co-Director of the NSF Frontier Center for Distributed Confidential Computing and organizer of the annual iDASH Genome Privacy Challenges, he continues to bridge the worlds of biology and cybersecurity with rare breadth and impact.

John Weinstein, MD Anderson Cancer Center

John Weinstein is a true pioneer of multi-omic science, having initiated molecular profiling of the NCI-60 cancer cell line panel at the DNA, RNA, and protein levels as early as 1991, work that shaped landmark projects including TCGA, CCLE, and the PanCancer Atlas. His computational contributions, from Next-Generation Clustered Heat Maps now integrated into cBioPortal to the MBatch package used by over 60 NIH Analysis Working Groups, have become quiet workhorses of cancer genomics data quality and visualization. A Web of Science Highly Cited Researcher of the decade 2010–2019 with an H-index of 158, he has spent 17 years as department chair at MD Anderson while also directing its Bioinformatics Core and hosting over 130 sessions of his Data Science Forum, reaching more than 10,000 participants worldwide.

Eric Xing, Mohamed bin Zayed University of Artificial Intelligence, Carnegie Mellon University, and GenBio AI

Eric Xing is a visionary computational biologist and AI pioneer whose statistically rigorous machine learning methods gave the field mathematically grounded tools for uncovering causal genetic factors and personalized disease pathways that remain widely used today. More recently, he has pushed the frontier of AI for science with large-scale biological foundation models and "AI-Driven Digital Organism" frameworks that integrate genomics, transcriptomics, structure, imaging, and clinical data into unified predictive systems, opening a new paradigm in which complex biology can be explored through simulation. As founding President of the Mohamed bin Zayed University of Artificial Intelligence, he built a globally recognized AI research institution from scratch within five years, while his open-source LLM ecosystems have democratized access to advanced AI tools across the biomedical community. A rigorous mentor and tireless community builder, Xing has shaped not just the methods but the culture of computational biology.

Congratulations again to the ISCB 2026 Class of Fellows!

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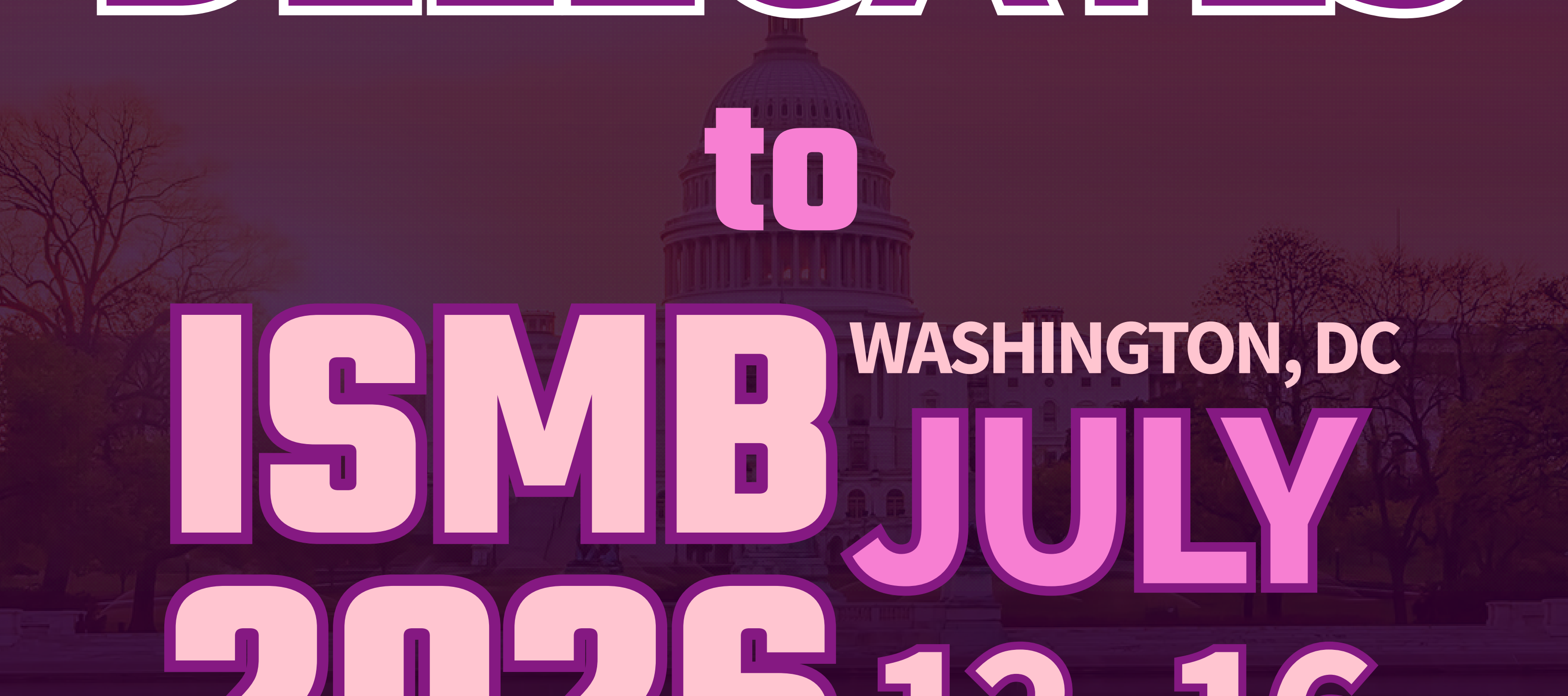

WELCOME DELEGATES

to

ISMB 2026

WASHINGTON, DC
JULY 12–16

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WELCOME TO ISMB 2026!

On behalf of the conference organizing committee, we wish you a warm welcome to ISMB 2026! Whether you're joining us in person or virtually, we're delighted you're here for a week of science, networking, and collaboration.

This year's conference marks a landmark moment: ISMB returns to Washington, DC, the very city where ISMB began. Over more than three decades, our field has evolved from a fledgling discipline to a cornerstone of modern biology. Returning to the DC area is both a celebration of that progress and a chance to deepen connections in a city that serves as a global hub for the life sciences—home to the NIH, NSF, FDA, and countless institutions shaping biomedical research worldwide.

We're sure you'll have an excellent time while in Washington, DC and attending ISMB. We encourage you to take full advantage of the conference and enjoy an amazing five days!

The scientific programme features exceptional keynote talks, thematic tracks showcasing cutting-edge research, plus tutorials, the Student Council Symposium, the Youth Bioinformatics Symposium, and nearly one thousand in-person and virtual posters.

Be sure to visit the Exhibit Hall in the Columbia Ballroom, where you can engage with the conference exhibitors while enjoying complimentary coffee during breaks. This year's exhibition brings together innovative bioinformatics platforms, leading academic and research institutions, publishing partners, and organizations advancing data science and healthcare.

For those joining us virtually through ISMB's virtual platform, you can view full daily schedules for each day of the conference, check out posters in the Poster section, and even contact exhibitors and sponsors with questions! While viewing a live-stream session, you can get involved by asking questions or chatting with other attendees using the live chat and Q&A features.

Highlights of the ISMB 2026 Programme include:

- 5 distinguished keynotes, including 3 ISCB 2026 Award winners
- Over 30 thematic tracks
- 16 Technology Track presentations
- 16 Tutorials (9 in-person, 7 virtual)
- The Career Fair
- The Success Circles networking event
- 900+ posters

There's a lot of science being shared throughout the conference, so if you miss something live, everything will be available via the ISMB 2026 virtual platform.

As Conference Chairs, we appreciate the support of the many volunteers who have helped guide the development of the conference and 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 these committees. Their dedication and leadership have been invaluable in bringing these five days of innovative, cutting-edge science to life.

Before we close, we wish to thank the Steering Committee for their efforts in planning and organizing the conference. We also want to thank our conference sponsors and exhibitors for their ongoing support.

Finally, as many of you know, without the highly skilled ISCB staff, there would be no ISMB 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 Programs), Seth Munholland (Lead Technologist), Diane Kovats (CEO), Justine Morris (Coordinator, Operations and Programs), Nína-Mari Grobler (Executive Assistant), and Mallory Wiper (Managing Director, Communications and Marketing).

We hope you take advantage of everything the conference offers, especially the endless opportunities to meet, network, and connect with your fellow computational biologists.
We wish you all a wonderful ISMB 2026!
Welcome to Washington, DC!

Yours sincerely,

Laxmi Parida,
Conference Co-Chair

Mihai Pop,
Conference Co-Chair

Judith Blake (Judy)

Judy Blake,
Honorary Chair

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GENOME SEQUENCE ANALYSIS

Tobias Marschall, Heinrich Heine University Düsseldorf, Germany

William Yu, Carnegie Mellon University, USA

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AREA CHAIRS, CONTINUED

MACROMOLECULAR SEQUENCE, STRUCTURE, AND FUNCTION

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David Koes, University of Pittsburgh, USA

Martin Steinegger, Seoul University, South Korea

PRIVACY AND SECURITY FOR COMPUTATIONAL BIOLOGY

Hoon Cho, Yale University, USA

Gamze Gursoy, Columbia University, USA

REGULATORY AND FUNCTIONAL GENOMICS

Kimberly Glass, Harvard Medical School, USA

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Mihai Pop, University of Maryland, USA

BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

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Qianwen Wang, University of Minnesota, USA

BOKR: BIO-ONTOLOGIES AND KNOWLEDGE REPRESENTATIONS

Tiffany Callahan, IBM Research, USA
Augustin Luna, NLM, USA
Robert Hoehndorf, KAUST

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TRACK & ABSTRACT AREA CHAIRS, CONTINUED

BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE

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Karsten Hokamp, Trinity College Dublin, Ireland
Jessica Maia, BD
Hervé Ménager, Institut Pasteur, France
Tazro Ohta, Chiba University
Monica Munoz-Torres, University of Colorado Anschutz Medical Campus, USA
Van Truong, University of Pennsylvania, USA
Deepak Unni, SIB Swiss Institute of Bioinformatics, Switzerland
Jason Williams, Cold Spring Harbor Laboratory, USA

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

Joaquin Dopazo, Fundación Progreso y Salud, Seville, Spain
David P Kreil, Boku University Vienna, Austria
Paweł P Łabaj, Austrian Academy of Sciences, and Jagiellonian University, Poland
Wenzhong Xiao, Stanford Genome Technology Center, and Massachusetts General Hospital, Harvard Medical School, USA

COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Wout Bittremieux, University of Antwerp, Belgium
Isabell Bludau, Heidelberg University Hospital, Germany
Marie Brunet, Sherbrooke University
Lindsay Pino, Talus Bio, USA
Timo Sachsenberg, University of Tübingen, Germany

COMPUTATIONAL BIOLOGY CAREERS SYMPOSIUM

Ben Busby, Nvidia, USA

CSI: COMPUTATIONAL AND SYSTEMS IMMUNOLOGY

Ferhat Ay, La Jolla Institute for Immunology, USA
Jishnu Das, University of Pittsburgh School of Medicine, USA

DREAM CHALLENGES: BENCHMARKING BENCHMARKING AI AND AGENTS ACROSS BIOLOGICAL DOMAINS

Kyle Ellrott, OHSU
Adi Tarca, Wayne University

EDUCATION: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS EDUCATION AND TRAINING

Russell Schwartz, Carnegie Mellon University, USA
Wai Keat Yam, International Medical University, Malaysia

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EQUITY AND DIVERSITY IN COMPUTATIONAL BIOLOGY RESEARCH

Larry Hunter, University of Chicago, USA
Farzana Rahman, Kingston University London
Nelly Salem, Langebio Cinvestav

EVOLCOMPGEN: EVOLUTION & COMPARATIVE GENOMICS

Lars Arvestad, Stockholm University
Dannie Durand, Carnegie Mellon University

FUNCTION: GENE AND PROTEIN FUNCTION ANNOTATION

Iddo Friedberg, Iowa State University, USA
Dukka KC, RIT, United States
Jason McDermott, PNNL, United States
Ana M. Rojas Mendoza, Centro Andauz de Biologica del Dessarrolo, Spain
Mark Wass, University of Kent, UK

GENCOMPBIO: GENERAL COMPUTATIONAL BIOLOGY

Ben Raphael, Princeton, USA
Simone Zaccaria, UCL Cancer Institute,UK

HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

Can Alkan, Bilkent University, Turkey
Christina Boucher, University of Florida, USA
Brona Brejova, Comenius University in Bratislava
Ana Conesa, Institute for Integrative Systems Biology
Francisco M. De La Vega, Stanford University; and Tempus Genomics, USA
Dirk Evers, Dr. Dirk Evers Consulting, Germany
Kjong Lehmann, RWTH Aachen
Kristoffer Sahlin, Stockholm University

INDUSTRY WORKSHOP

Xiaole Shirley Liu, Dana-Farber Cancer Institute
Tommy Tang, AstraZeneca

IRNA: INTEGRATIVE RNA BIOLOGY

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

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TRACK & ABSTRACT AREA CHAIRS, CONTINUED

MICROBIOME

Alice McHardy, Helmholtz Centre for Infection Research, Germany

Alexander Sczyrba, Forschungszentrum Jülich, Germany

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Elana Fertig, University of Maryland

David Knowles

NETBIO: NETWORK BIOLOGY

Jishnu Das, University of Pittsburgh School of Medicine

Deisy Morselli Gysi, Federal University of Paraná, Curitiba - Paraná

Martina Summer-Kutmon, Maastricht University, Netherlands

NIH/ODSS

Ishwar Chandramouliswaran, NIH

PATHOGEN DATA NETWORK FORUM

Jason Williams, Cold Spring Harbor Lab

PUBLISHING SESSION

Ragothaman Yennamalli, Jawaharlal Nehru University

QLS: QUANTUM FOR LIFE SCIENCES

Laxmi Parida, IBM

Filippo Utro, IBM

REGSYS: REGULATORY AND SYSTEMS GENOMICS

Marcel Schulz, Uniklinikum and Goethe University Frankfurt

Amin Emad, McGill University

Xiuwei Zhang, Georgia Tech University

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Andreas Dräger, Martin Luther University Halle-Wittenberg

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

Nantia Leonidou, German Cancer Research Center (DKFZ)

Reihaneh Mostolizadeh, University of Tübingen, Germany

Meghna Verma, AstraZeneca, USA

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TEXT MINING

Lars Juhl Jensen, University of Copenhagen, Denmark
Robert Leaman, NCBI/NLM/NIH, USA
Zhiyong Lu, NCBI/NLM/NIH, USA
Katerina Nastou, Statens Serum Institut

TRANSMED: TRANSLATIONAL MEDICINE INFORMATICS & APPLICATIONS

Irina Balaur, University of Luxembourg
Bosdriesz Evert, VU Amsterdamn, Netherlands
Irene Ong, Universtiyt of Wisconsin-Madison, USA
Heba Sailem, King's College London
Mansoor Saqi, Institute of Cancer Research, UK
Venkata Satagopam, University of Luxembourg
Maria Secrier, University College London

VARI: VARIANT INTERPRETATION

Emidio Capriotti, University of Bologna
Hannah Carter, University of California, San Diego
Julein Gagneur, Technical University of Munich
Tayo Obafemi-Ajayi, Missouri State University
Antonio Rausell, Imagine Institute for Genetic Diseases

WEB: WORKSHOP ON EDUCATION FOR BIOINFORMATICS

Dan Deblasio
Inimary Toby-Ogundeji

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ISMB
2026
WASHINGTON, DC
JULY 12–16

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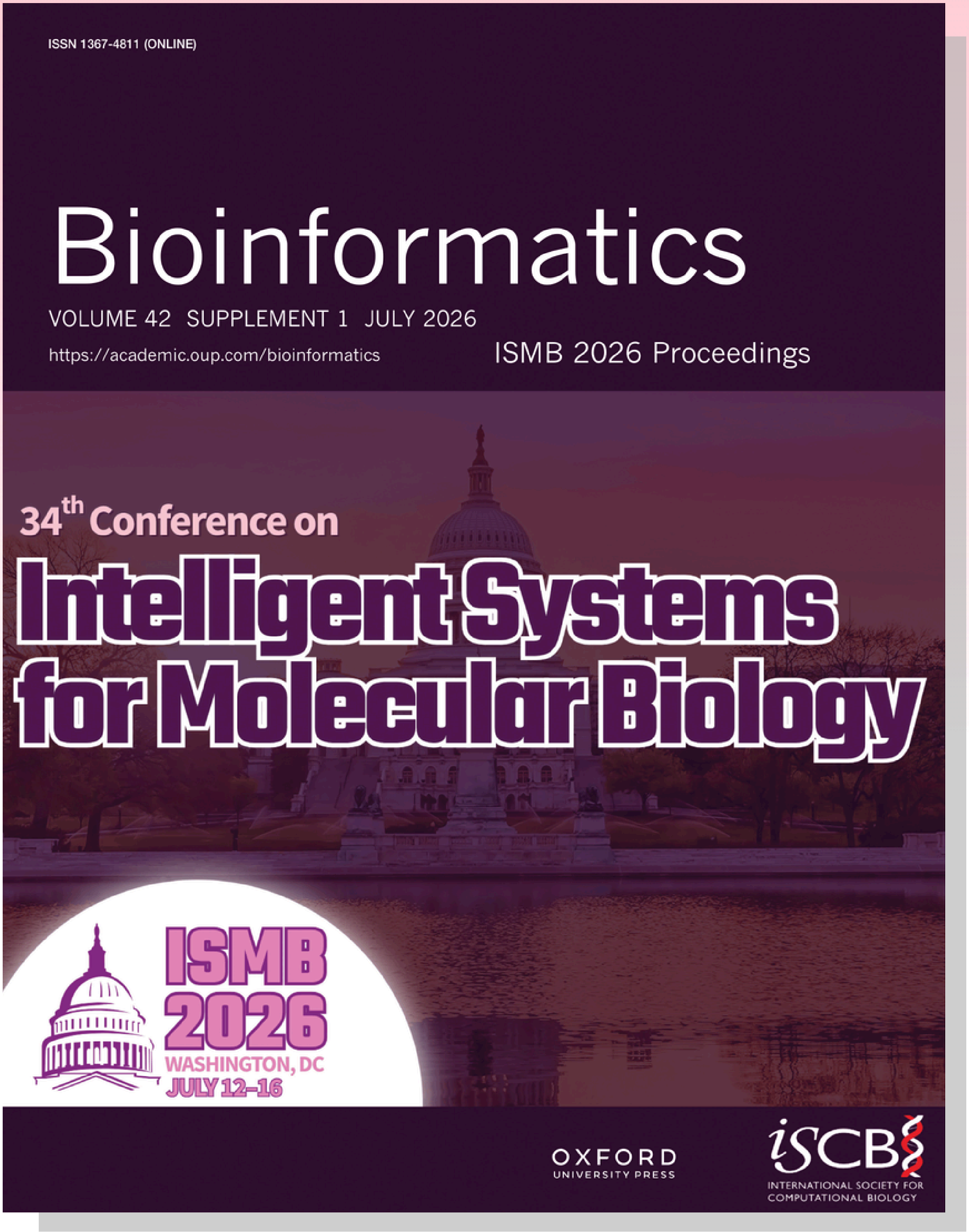

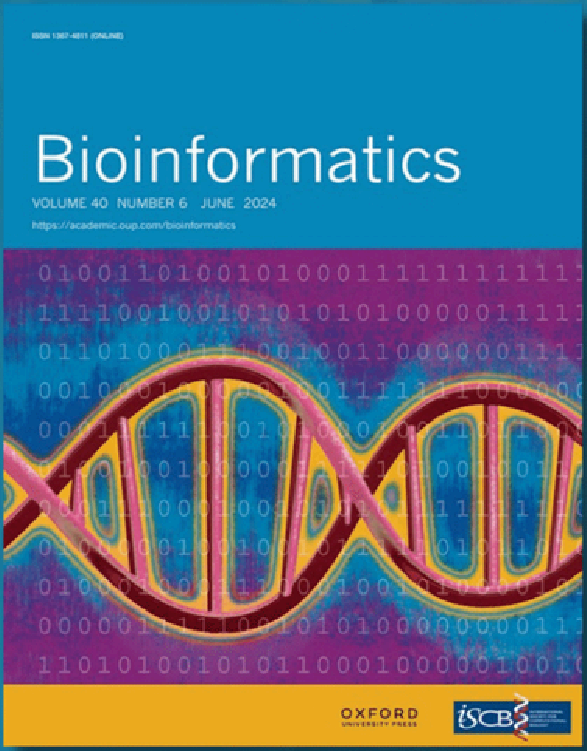
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DISTINGUISHED KEYNOTES

International Ballroom Center		
Day	**Time**	**Title and Speaker**
Sunday, July 12	**18:30**	More applications of the Burrows-Wheeler transform in computational genomics **Richard Durbin**
Monday, July 13	**9:00**	Toward Predictive Models of Human Biology and Disease **Olga Troyanskaya**
Tuesday, July 14	**9:00**	Enabling Precision Health at Scale for All **Carlos D. Bustamante**
Wednesday, July 15	**9:00**	Uncovering the Palimpsest of India's Population History Using Genome-Scale Analysis: Implications for Disease Epidemiology **Partha P. Majumder**
Thursday, July 16	**16:40**	Foundations of Human-AI Co-Science **Marinka Zitnik**

*Click here to visit the Distinguished Keynotes page.

Read on for a preview of the ISMB 2026 keynote abstracts!

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DISTINGUISHED KEYNOTES

RICHARD DURBIN

Time: Sunday, July 12, 2026 at 6:30PM

More applications of the Burrows-Wheeler transform in computational genomics

I will discuss a series of applications of the Burrows-Wheeler transform, based on suffix sorting, for sequence matching and compression in computational genomics. Initial applications, as in bwa with Heng Li, were for finding maximal exact matches as an alternative to fixed length seeds based on hashing for sequence read mapping. Next the Positional Burrows-Wheeler Transform (PBWT) incorporating run-length encoding gave both excellent compression and very fast maximal matching of haplotype sequences; this underlies most modern genotype imputation tools. More recently, the Graph Burrows-Wheeler Transform (GBWT) was introduced to provide path indices over pangenome graphs, again providing both compression and efficient search. Finally, I will describe a new dynamic GBWT framework based on doubly-linked skip lists that when implemented over a sparse de-Bruijn graph enables rapid O(log_N) time insertion and matching, supporting single-threaded pangenome graph construction and indexing at ~15 seconds per gigabase.

OLGA TROYANSKAYA

Time: Monday, July 13, 2026 at 9:00AM

Toward Predictive Models of Human Biology and Disease

A central goal of precision medicine is to develop predictive, mechanistic models of human health and disease that connect molecular processes to organismal physiology and clinical outcomes. Achieving this requires integrating information across scales—from genomic sequence and regulatory programs to cellular systems, organs, and longitudinal phenotypes—within models that are both mechanistically grounded and predictive. In this talk, I will describe AI frameworks that connect sequence, regulation, multi-omic networks, and biological context into unified representations of dynamic biological systems. These include models that interpret genomic variation through its biochemical and regulatory effects, network-aware approaches that perform in silico genetics by modeling how perturbations propagate through cellular circuits and pathways, and genetics-informed models of phenotype that link molecular programs to disease heterogeneity and trajectories. These purpose-built, multimodal, and multi-scale approaches integrate genomic, molecular, and clinical data to uncover drivers of disease, define biologically grounded subtypes, and predict outcomes across diverse contexts, including cancer, autism, and chronic kidney disease. The next frontier lies in combining these multi-scale models with verifiable, agentic AI systems that can reason over biological evidence, support hypothesis generation and testing, and enable transparent, reproducible scientific discovery.

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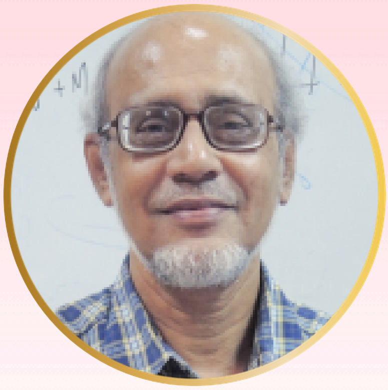
CARLOS D. BUSTAMANTE

Time: Tuesday, July 14, 2026 at 9:00AM

Enabling Precision Health at Scale for All

Advances in genomics, AI/ML, and large-scale health data are creating unprecedented opportunities to improve human health. Realizing the promise of precision health will require powering learning health systems that engage millions of people from diverse populations longitudinally.

In this keynote, I will share lessons from building large genomic resources, developing AI-driven approaches to genotype-to-phenotype discovery, and forging partnerships across academia, healthcare, industry, and government. I will discuss how these efforts are laying the foundation for a future in which precision health is scalable, equitable, and accessible to all.



PARTHA P. MAJUMDER

Time: Wednesday, July 15, 2026 at 9:00 AM

Uncovering the Palimpsest of India's Population History Using Genome-Scale Analysis: Implications for Disease Epidemiology

Robust reconstruction of human population history has been possible because of major advances in molecular, computational and statistical genetics. The ability to determine DNA sequences of a large number of humans and to study the sequence variation by calibrating the rate of accumulation of changes with evolutionary time has enabled robust inferences about our population history. These data indicate that (a) ancestors of all present-day people, i.e., modern humans and other humans, evolved in Africa about 600,000 years ago; (b) a large group of humans came out of Africa and evolved as Nearderthals, Denisovans and other archaic humans; (c) modern humans evolved in Africa and spread out within Africa, and (d) modern humans started to come out of Africa about 100,000 years ago, and admixed with both Neanderthals and Denisovans. After modern humans emerged out of Africa, one of the first waves of migration entered India. Contemporary India has a rich tapestry of cultures and ecologies. There are about 400 tribal and more than 4000 groups of castes and subcastes, all largely endogamous, speaking languages that belong to four major linguistic families. We shall provide genomic evidence of how India may have been peopled, the nature and extent of its genomic diversity, and genomic structure among the extant populations of India. We shall then provide a narrative, with evidence, of how the genomic diversity may have impacted on disease epidemiology – susceptibility to disease and response to treatment.

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MARINKA ZITNIK

Time: Thursday, July 16, 2026 at 4:40PM

Foundations of Human-AI Co-Science

AI scientists are AI systems that reason, hypothesize, and experiment alongside human researchers. In this talk, I will show how human-AI co-science is emerging through three capabilities: understanding disease, discovering interventions, and reasoning about treatments. Across these settings, we evaluate AI through discovery loops that pair AI with experiments in biological and clinical labs. I will begin with disease understanding. Foundation models trained on multimodal relational data predict disease mechanisms that are difficult to identify from any single dataset. Drawing on studies of Parkinson disease, bipolar disorder, and Alzheimer disease, I will show how these models generate hypotheses about disease mechanisms and therapeutic opportunities that are evaluated in vitro, in vivo, and through longitudinal health trajectories of five million patients. I will then turn to intervention discovery. AI scientists search large experimental spaces to identify therapeutic targets, predict synthetic lethal interactions in cancer, and model personalized responses to immunotherapy. Finally, I will discuss treatment reasoning. Therapeutic decisions require integrating disease context, comorbidities, medications, and biomedical evidence. I will present AI scientists that combine language models with biomedical tools to reason about treatments developed over the past century. We evaluate these systems through blinded expert assessments in rare diseases, real-world treatment decisions, and population-scale analyses of longitudinal health records. These systems define a foundation for human-AI co-science. They are powered by scientific environments that connect language models to an open universe of scientific tools, democratizing AI scientists.

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EXHIBITORS AT ISMB

We have several exhibitors to connect with at ISMB 2026! Make sure to stop by the Exhibit Hall in the Columbia Ballroom. To see the map of the exhibition area, visit the Exhibitors page.

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2026 GREEN CHALLENGES

SUN 12

Show your commitment to sustainability and greener computing by signing the ISCB Green Pledge. Start your commitment off strong by ditching single-use items. Share a photo of your reusable tote bag, water bottle, or coffee mug on socials using #greeniscb. Or show it off at the ISCB booth to grab a sticker!

MON 13

Go meatless for the day and enjoy plant-based meals! Share your favorite veggie dish from today on social media using #greeniscb on socials.

TUE 14

The most sustainable shirt is the one you already own! Dig out your oldest ISMB shirt, wear it proudly, and show it off on socials using #greeniscb.

WED 15

Take the green computing quiz to test your green computing knowledge. Show us your score at the ISCB booth and get a star sticker! Share your favorite piece of green computing advice with the community on socials using #greeniscb.

THU 16

Learn the impact you have on the environment by calculating the carbon footprint of your computational research! And, if you're able, consider donating to the ISCB Groves to plant trees and offset CO2 emissions.

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ABRIDGED AGENDA

Sunday, July 12	
9:00 - 16:00	Student Council Symposium and Poster Session
9:00 - 18:00	DREAM
9:00 - 18:00	Tutorials
13:00 - 17:15	Youth Bioinformatics Symposium and Scientific Challenge
16:00 - 18:00	Career Fair — Columbia
18:30 - 19:30	Keynote Speaker - Richard Durbin (2026 ISCB Accomplishments by a Senior Scientist Award Winner) — International Ballroom Center
19:30 - 21:00	Welcome Networking Reception — Columbia

Visit the Agenda at a Glance page,
or download the Abridged Agenda.

Click here for the ISMB dining guide!

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Monday, July 13

8:40 - 10:00	Morning Welcome and Distinguished Keynote – Olga Troyanskaya (ISCB 2026 Innovator Award Winner) – International Ballroom Center										
10:00 - 11:00	Caffeinate and Connect with Posters and Exhibitors – Columbia										
11:00 - 13:00	HitSeq	iRNA	RegSys	Comp MS	NIH/ ODSS	Microbiome	Text Mining	CSi	BOKR	Function	Tech Talks
13:00 - 14:20	Lunch Break – On Your Own										
14:20 - 16:00	HitSeq	iRNA	RegSys	Comp MS	NIH/ ODSS	Microbiome	Text Mining	CSi	BOKR	Function	Tech Talks
16:00 - 16:40	Caffeinate and Connect with Posters and Exhibitors – Columbia										
16:40 - 18:00	HitSeq	iRNA	RegSys		NIH/ ODSS	Microbiome	Text Mining	CSi	BOKR	Function	Tech Talks
18:00 - 19:30	President’s Reception (**Invite Only**)										

Click here for the ISMB dining guide!

Visit the Agenda at a Glance page,
or download the Abridged Agenda.

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Tuesday, July 14

8:40 - 10:00	Morning Welcome, Fellows Introduction, and Distinguished Keynote — Carlos D. Bustamante — International Ballroom Center										
10:00 - 11:00	Caffeinate and Connect with Posters and Exhibitors — Columbia										
11:00 - 13:00	HitSeq	iRNA	RegSys	Publication Session	BioInfo Core	Micro-biome	SysMod	BioVis	BOKR/ BOSC	Function	Tech Talks
13:00 - 14:20	Lunch Break — On Your Own										
14:20 - 16:00	HitSeq	iRNA	RegSys	Industry Workshop	BioInfo Core	NetBio	SysMod	BioVis	BOSC	BOKR/ Function	Quantum4 Life Sciences
16:00 - 16:40	Caffeinate and Connect with Posters and Exhibitors — Columbia										
16:40 - 18:00	HitSeq	iRNA	RegSys	Career Symposium	BioInfo Core	NetBio	SysMod	BioVis	BOSC	Function	BOKR
18:00 - 19:30	Success Circles — International Terrace										

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or download the Abridged Agenda.

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Wednesday, July 15

8:50 - 10:00	Morning Welcome and Distinguished Keynote — Partha P. Majumder — International Ballroom Center										
10:00 - 11:00	Caffeinate and Connect with Posters and Exhibitors — Columbia										
11:00 - 13:00	MLCSB	TransMed	3D	NetBio	WEB	GenCompBio	EvolComp Gen	VarI	BOSC	CAMDA	ICBO
13:00 - 14:20	Lunch Break — On Your Own										
14:20 - 16:00	MLCSB	TransMed	3D	NetBio	WEB	GenCompBio	EvolComp Gen	VarI	BOSC	CAMDA	ICBO
16:00 - 16:40	Caffeinate and Connect with Posters and Exhibitors — Columbia										
16:40 - 18:00	MLCSB	TransMed	3D	NetBio	WEB	GenCompBio	EvolComp Gen	VarI	BOSC	CAMDA	ICBO

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Thursday, July 16

8:40 - 10:00	MLCSB	3D	Bioninformatics in the USA	Education	GenComp Bio	EvolCompGen	Equity/ Diversity in CompBio Research		CAMDA	ICBO
10:00 - 11:00	Caffeinate and Connect with Posters and Exhibitors — Columbia									
11:00 - 13:00	MLCSB	3D	Bioninformatics in the USA	Education	GenComp Bio	EvolCompGen	Pathogen Data Network Event	Nvidia Workshop	CAMDA	ICBO
13:00 - 14:20	Lunch Break — On Your Own									
14:00 - 16:00	MLCSB	3D	Bioninformatics in the USA	Education	GenComp Bio	EvolCompGen			CAMDA	ICBO
16:00 - 16:40	Caffeinate and Connect with Posters and Exhibitors — Columbia									
16:40 - 18:00	Distinguished Keynote — Marinka Zitnik (ISCB 2026 Overton Prize Winner), and Closing Ceremonies — International Ballroom Center									

Visit the Agenda at a Glance page,
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POSTER SESSIONS

Posters will take place in the Columbia Ballroom.

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

- **Session A (odd numbers):** Monday, July 13, 10 – 11:00 AM and 16:00 – 16:40 PM
- **Session B (even numbers):** Tuesday, July 14, 10 – 11:00 AM and 16:00 – 16:40 PM
- **Session C (odd numbers):** Wednesday, July 15, 10 – 11:00 AM and 16:00 – 16:40 PM
- **Session D (even numbers):** Thursday, July 16, 10 – 11:00 AM and 16:00 – 16:40 PM

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

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

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

DISPLAY SCHEDULE

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

Poster set up: Monday, July 13 between 8:00 – 8:40
Poster dismantle: Tuesday, July 14 at 18:00

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

Poster set up: Wednesday, July 15 between 8:00 – 8:40
Poster dismantle: Thursday, July 16 at 18:00

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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TRACK SCHEDULES

3DSIG

Online schedule found here.

Wednesday, July 15; International Ballroom East

Time	Title and Speaker
11:00	Conformational dynamics and functional substates during enzyme evolution
12:00	A Unified Deep Learning Framework for Predicting DNA Structure **Jinsen Li**
12:20	BiMba: Predicting Protein Binding Sites using Vision Mamba **Azam Shirali**
12:40	Investigating the physiological substrates of a putative bacterial serotonin transporter in the gut
14:20	Deciphering Protein Mutation-Phenotype Linkages from CRISPR-based Tiling Mutagenesis Screens **Wei He**
14:30	Multiscale modelling and biophysical validation define a coiled-coil dimeric scaffold in FAZ10 from Trypanosoma brucei **Cleidy Mirela Osorio Mogollon**
14:40	Protein Language Models Capture Structural and Functional Epistasis **Ananthan Nambiar**
14:50	Generalizable and scalable protein stability prediction with SPURS **Ziang Li**
15:00	When Does Protein Structure Help? A Reliability Bottleneck in Mutation-Effect Prediction **Asher Moldwin**
15:20	Func2Seq and Func2Prot: Function-Conditioned Protein Generation for Variant-Effect Prediction and Controllable Design **Yihong Yang**

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3DSIG

Wednesday, July 15; International Ballroom East

Time	Title and Speaker
15:30	Simpatico: accurate and ultra-fast virtual drug screening with atomic embeddings **Jeremiah Gaiser**
15:40	Learning a PRECISE language for small-molecule binding **Kapil Devkota**
16:40	JointDiff: Simultaneous Generation of Sequence and Structure for Functional Protein Design **Yuxuan Liu**
17:00	Thermal Stability- and Binding Affinity-Guided Protein Design with ESM3 **Amitash Nanda**
17:20	AlloPep: A Pipeline for De Novo Design of Allosteric Peptides **Dibyajyoti Maity**
17:40	Machine Learning-Guided Engineering of Selective Protease Inhibitors by Deep Mutational Scanning **Yaron Orenstein**

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3DSIG

Thursday, July 16; International Ballroom East

Time	Title and Speaker
08:40	A Hybrid Deep Learning Pipeline for RNA 3D Structure Reconstruction from Cryo-EM Density Maps **Derek Peng**
08:50	RNAbpFlow: Base pair-augmented SE(3)-flow matching for conditional generation of RNA 3D structures
09:00	Using MutPred2 Predictions of Molecular Mechanisms to Identify Drug Repurposing Candidates for Genetic Disease **Matthew Neky**
09:20	An Integrative Biophysical Framework for Protein-Nucleic Acid Affinity Prediction from Structure and Sequence **Yafan Zhang**
09:30	LocAlign: Local Protein Structural Alignment with Geometric Deep Learning **Jérôme Tubiana**
09:40	Probabilistic RNA Designability via Interpretable Ensemble Approximation and Dynamic Decomposition **Liang Huang**
11:00	Structural bioinformatics and AlphaFold modeling of the human kinome and its interactions
12:00	Predicting the structural impact of human alternative splicing **Yuxuan Song**
12:20	DiSPA: Differential Substructure-Pathway Attention for Drug Response Prediction **Yewon Han**
12:40	Cross-attention protein language models infer partner-specific PPI interfaces complementary to AlphaFold3 **Alexey Porollo**

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3DSIG

Thursday, July 16; International Ballroom East

Time	Title and Speaker
12:50	DEPP: Dynamic Embedding Property-Based Predictor for Protein Conformational Ensembles and Drug-Protein Interactions **Dana Dayan**
14:20	AlphaFold Database expands to proteome-scale quaternary structures **Han Yewon**
14:40	MDRepo, a community-contributed open molecular dynamics data repository **Travis Wheeler**
15:00	NoisyFlow: Differentially Private Optimal Transport Using Neural Networks for Secure Biomedical Data Sharing across Multiple Institutions **Mark Gerstein**
15:20	ProMeta: A meta-learning framework for robust disease diagnosis and prediction from plasma proteomics **Sai Zhang**
15:40	Towards statistically valid protein structure search: revisiting E-values in Foldseek and Reseek **Yang Lu**
15:50	Unmasking Pathogen-Host Structural Mimicry in the AI era **Tung Nguyen**

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BIOINFO-CORE

Online schedule found here.

Tuesday, July 14; Cabinet

Time	Title and Speaker
11:00	The Payoff of FAIR: From Natural Language Queries to GEO Submissions and Nextflow Samplesheets in a Bioinformatics Core **Stuart Levine**
11:40	Agentic AI in cores
12:40	Less Code, More Biology: Carnation for Collaborative Multi-Omics Exploration **Apratim Mitra**
14:20	Panel 2 TBA
15:20	An R Package To Simplify The UK Biobank RStudio Experience **Nathan Kennedy**
15:30	Scaling up support for bioinformatics core facilities training **Patricia Carvajal-López**
15:40	A Hybrid-Cloud Nextflow NF-Core Compliant Framework for High-Throughput Bioinformatics Pipeline for Roche SBX Sequencing **Sabiq Chaudhary**
15:50	HuBMAP Workspaces: an integrated analysis environment for the Human BioMolecular Atlas Program Data Portal **Thomas C. Smits**
16:40	Telomere-to-Telomere Genome Assembly of Native Desert-Adapted Sheep Ovis aries Breed “Najdi” From Saudi Arabia **Muruj Tukruni**
16:50	Breakout Sessions

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BIOINFORMATICS IN THE USA

Online schedule found here.

Thursday, July 16; Room 9–10 Combo	
Time	**Title and Speaker**
08:40	Introduction to Bioinformatics in the USA
09:00	Spatial multi-omics of cancer **Ben Raphael**
09:40	Unavailability of experimental 3D structural data on protein folding dynamics and necessity for a new generation of structure prediction methods in this context **Tijana Milenkovic**
11:00	Advancing Bioinformatics and Computational Biology in the United States: Funding Priorities and Opportunities from the National Library of Medicine **Catherine Farrell**
11:20	NIGMS Funding Opportunities **Guoqin Yu**
11:40	F.O.R.E.S.T: Spatially Informed Deconvolution of Cell Type Composition in Spatial Transcriptomics **Ranojoy Chatterjee**
12:00	scAURA: Alignment- and Uniformity-based Graph Debiased Contrastive Representation Architecture for Self-Supervised Clustering of Single-Cell Transcriptomics. **Jubair Ibn Malik Rifat**
12:20	Differential prevalence study of dust microbiome from rural farming and non-farming homes in Wisconsin **Rene Welch**

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BIOINFORMATICS IN THE USA

Thursday, July 16; Room 9–10 Combo	
Time	**Title and Speaker**
12:40	U.S. Food and Drug Administration (FDA) and U.S. National Institute of Standards and Technology (NIST) Collaboration: Evaluation of Assays and Control Materials for Characterizing Animal Biotechnology Products Generated by Genome Editing **Ashley L. Cook**
14:20	Like a Chicken in the Corn: Bioinformatics in the Great Plains **Iddo Friedberg**
15:00	Quantum-enhanced attention improves expression prediction from cancer histopathology images with limited samples **Kahn Rhrissorrakrai**
15:20	AI Accelerates Biological Discovery. Are We Ready for the Risks? **Michelle Holko**
15:40	Integrating genomics and structural biology in one of the earliest computational biology programs in the USA **Remo Rohs**

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BIOVIS

Online schedule found here.

Tuesday, July 14; Jefferson East

Time	Title and Speaker
11:00	Opening Remarks
11:05	Keynote 1
12:00	Scalable cell population plots for single-cell data with scellop **Thomas C. Smits**
12:20	Interactive Visualization and Analysis of Genomic Data at NCBI using GDV, CGV, and MCGV **Vamsi Kodali**
12:40	SBGNFlow: An AI-Assisted & Interactive Workflow for Generation, Merging & Layout of Pathway Maps **Augustin Luna**
14:20	InterSCellar: Surface-Based Cell Neighborhood and Interaction Volume Analysis in 3D Spatial Omics **Eunice Lee**
14:40	How Do We Visualize Space in Molecular Biology? A Study of Spatial Transcriptomics Visualization Practices **Denisse Chacon-Ramirez**
15:00	Interactive Visual Exploration of Antibody Sequence Optimization: Bridging Machine Learning Predictions and Visual Analytics **Khushboo Jain**
15:10	Cluster stability in spatial transcriptomics: A method agnostic evaluation and visualization framework **Wenshan Wu**
15:20	Evaluating Agentic Schemes for Authoring Interactive Multiview Genomics Visualizations **Astrid van den Brandt**

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BIOVIS

Thursday, July 24; Room 4AB

Time	Title and Speaker
15:30	Introducing WWizNet, a fully interactive 3D web-based application for large-scale biomedical network visualization and analysis **Philipp Friedrich**
15:40	Interactive Exploration of Cancer Regulatory Landscapes with Reactive Notebooks **Vedat Yilmaz**
15:50	Hierarchical decomposition and visualization of metagenome assembly graphs with MetagenomeScope **Marcus Fedarko**
16:40	Keynote 2
17:35	Best Abstract Award Announcement & Ceremony
17:50	Closing Remarks

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Bio-Ontologies & Knowledge Representation

BOKR

Online schedule found here.

Monday, July 13; Lincoln West

Time	Title and Speaker
11:00	Automating subtype-specific cancer gene prioritization at the OncoTree ontology scale using large language models (LLMs) for exploration in cBioPortal **Suhasini Lulla**
11:20	Constrained LLM-Assisted Alignment of HPO Terms to Phecodes **Chenjie Zeng**
11:40	BiomarkerKB: A Knowledgebase Supporting a Standardized Biomarker-Centric Knowledge and Data Integration **Raja Mazumder**
12:00	Do Mice Speak Human? Cross-Species Semantic Alignment of Disease Metadata **Yuzhang Fu**
12:20	Signal Over Noise: Semi-Automated Relevancy Scoring for Biomedical Knowledge in Drug Repurposing **Shilpa Sundar**
12:40	Constraining Pathogenetic State Hypotheses in Synovial Sarcoma: A Neuro Symbolic Pipeline for SS18::SSX1 Characterization via TTT Linear and Z3 Based SMT Verification **George Anstey**
14:20	Bridging classical and transcriptomic cell types at scale: agentic AI workflows for the Cell Ontology **David Osumi-Sutherland**
14:40	Developing a Semantically Interoperable Knowledge Graph Schema to Support Single Cell Transcriptomics **Matthew Diller**
15:00	The critical role of human validation in the era of AI-assisted biocuration: Extending competencies and reflecting career progression in current frameworks **Patricia Carvajal-López**

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Bio-Ontologies &
Knowledge
Representation

BOKR

Monday, July 13; Lincoln West

Time	Title and Speaker
15:20	SomaModules:A Pathway Enrichment Approach Tailored to SomaScan Data **Julián Candia**
15:40	Bio-Ontologies and Knowledge Representation: Poster Madness
16:40	Keynote Lecture: AI and ontologies: The beginning of a beautiful friendship **Maryann Martone**
17:40	Bio-Ontologies and Knowledge Representation: Closing Day 1

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Bio-Ontologies &
Knowledge
Representation

BOKR

Tuesday, July 14; Lincoln West

Time	Title and Speaker
11:00	Welcome
11:05	MEDFORD in a Box: Demonstrating the Improvements and Future Directions for a Metadata Description Language **Noah Daniels**
11:05	Distributing standardized annotations of public transcriptomics samples and studies with MetaHQ and Meta2Onto **Parker Hicks**
11:20	KGXVal: Open-source quality control and curation support for biomedical knowledge graph harmonization. **Daniel Korn**
11:40	KG-Registry: the open registry of knowledge graphs and their provenance **J. Harry Caufield**
12:00	Scalable Representation of Categorical Genomic Variation Using Cat-VRS **Daniel Puthawala**
12:20	Curating Gene Symbol Relationships for the Resolution of Gene Symbol Ambiguity **Anastasia Bratulin**
12:20	FAIRSCAPE: Pre-model AI-Readiness and Interpretability for Biomedical Data **Timothy Clark**
12:20	A FAIR Framework for Structured Biomarker Representation, Discovery, and Hypothesis Generation **Maria Kim**
12:40	The OBO Foundry in 2026: Building Sustainable Ontology Infrastructure for Interoperable Life Science Data **James Balhoff**

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Bio-Ontologies &
Knowledge
Representation

BOKR

Tuesday, July 14; Lincoln East

Time	Title and Speaker
14:20	In a genAI world, does structured knowledge still have a role in science?
15:00	GO-CAM: thousands of curated pathways using GO, and new tools for using them **Paul Thomas**
15:20	STAR-GO: Improving Protein Function Prediction by Learning to Hierarchically Integrate Ontology-Informed Semantic Embeddings **Gökçe Uludoğan**
15:40	GIMME: Graph Inference for Microbial Metabolism Exploration using Knowledge Graphs **Winston Anthony**

Tuesday, July 14; Monroe

Time	Title and Speaker
16:40	DGLink: automated knowledge graph construction from biomedical data repositories **Woodward Galbraith**
17:00	Transforming PubChem BioAssay Data into Linked Open Data through the Resource Description Framework (RDF) and Standard Ontologies **Sunghwan Kim**
17:20	ImmPort: A Foundational Data Repository Facilitating AI-Enabled Immunology Research **Sanchita Bhattacharya**
17:40	Sage Brain: An AI-Powered Cross-Disease Knowledge Graph Connecting Neurodegenerative Research Communities **Orion Banks**

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BOSC

Online schedule found here.

Tuesday, July 14; Lincoln West

Time	Title and Speaker
11:00	MEDFORD in a Box: Demonstrating the Improvements and Future Directions for a Metadata Description Language **Noah Daniels**
11:00	Distributing standardized annotations of public transcriptomics samples and studies with MetaHQ and Meta2Onto **Parker Hicks**
11:20	KGXVal: Open-source quality control and curation support for biomedical knowledge graph harmonization. **Daniel Korn**
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12:40	The OBO Foundry in 2026: Building Sustainable Ontology Infrastructure for Interoperable Life Science Data **James Balhoff**

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BOSC

Tuesday, July 14; Lincoln West	
Time	**Title and Speaker**
14:20	Science for the People: Open science to engage and build trust with communities **Maryam Zaringhalam**
15:20	Policies and strategies for resilient open science
16:40	Designing CWL-Based Medallion Pipelines: A Spatial Aggregation Case Study for Climate and Air-Pollution Exposures **Michael Bouzinier**
17:00	WILDS WDL Library: Modular Bioinformatics Workflow Components for Researchers and Developers **Taylor Firman**
17:20	Raw Counts to Trusted References: A Reproducible QC Workflow Supporting the NLM Cell Knowledge Bases **Yun Zhang**
17:40	Where did the algorithms go? **Zebulun Arendsee**

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BOSC

Wednesday, July 15; Lincoln West

Time	Title and Speaker
11:00	From the Human Genome Project to the Realization of Genomic Medicine: A Scientific, Medical, and Societal Journey **Eric Green**
12:00	MuSAlS: Fast Multiple Sequence Alignment Using Hierarchical Clustering **Emily Light**
12:00	Combining RNA-seq and MS proteomics boosts sensitivity to detect differentially expressed genes by rpMeta **Matthew Wilkerson**
12:00	Generalized linear models for clustering of RNA-seq time series experiments **Jherson Medina Correa**
12:20	Large-scale Reference-Guided Cell Type Re-annotation of Single-Cell Brain Data **Rachel Schwartz**
12:20	Bridging the Metadata Gap: A Two-Stage Federated Learning Architecture and Visual Audit Tool (FedViz) for Global Biobank Consortia **Aditya Karna**
12:20	The AOP-Wiki EMOD Tool Suite: An Open Source Foundation for Enhanced Integration Between Adverse Outcome Pathways (AOPs), New Approach Methodologies (NAMs), AOP-Supporting Evidence, and Agentic Support for AOPs **Virginia Hench**
12:40	BOSC announcements
12:40	An Open-Source Platform for Quantitative Interactomics **Julian West**
12:40	The MoTrPAC Data Hub: An AI-Enabled, Open-Science Ecosystem for the Molecular Map of Exercise **Daniel H. Katz**

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BOSC

Wednesday, July 15; Lincoln West

Time	Title and Speaker
14:20	Canopy: An Open-Source Platform for FAIR Research Data Hubs **Marcos Martínez-Romero**
14:40	The Common Fund Data Ecosystem (CFDE) Incubator for Pan-NIH Resources: Enhancing Interoperability **Julie Jurgens**
14:40	Posters.science: Building Open Infrastructure for FAIR and AI-ready Scientific Posters **Bhavesh Patel**
14:40	Templated Collaborative Science Resources for Fostering and Sustainably Cataloging FAIR and Reproducible Digital AI Research Products **Hilmar Lapp**
15:00	Legal interoperability as infrastructure: Enabling computable licensing in biomedical knowledge graphs **Shilpa Sundar**
15:00	CTRL: A Dynamic open source e-Consent Platform **Sarah Kummerfeld**
15:00	As Open as Possible; As Closed as Necessary: Enabling Openness for Sensitive Human Data **Mallory Freeberg**
15:20	Toward domain-specific genomic AI agents: benchmarking sequencing library structure extraction **Chi-Lam Poon**
15:20	PosterSentry: a light-weight multimodal classification system for scientific poster quality assurance in open repositories **James ONeill**
15:20	Evaluating the Performance of LLMs in Drafting Data Management Plans **Nahid Zeinali**

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BOSC

Wednesday, July 15; Lincoln West

Time	Title and Speaker
15:40	Using AI to develop, maintain, and translate bioinformatics training materials **Geraldine Van der Auwera**
15:50	Learning in public, losing in private? How AI chatbots and LLMs are reshaping bioinformatics culture **Van Quynh Truong**
16:40	Open source in the age of AI

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CAMDA

Online schedule found here.

Wednesday, July 15; Lincoln East

Time	Title and Speaker
11:00	CAMDA Welcome
11:10	Strain-resolved metagenomics enables detection of bacterial genes associated with human traits **Katherine Pollard**
12:00	Introduction to CAMDA Challenges
12:20	Differential Connectivity Analysis of Integrated Gut Microbiome Networks for Disease Prediction **Yulin Li**
14:20	Metabolic Pathways as Ecological Niches: Topological Reorganization of Gut Microbiome Functional Networks Across Health and Disease **Jose Abel Lovaco-Flores**
14:40	A Dual-Layer Network Framework Reveals Hidden Functional Drivers of Gut Microbiome Dysbiosis **Safa Bushnaq**
15:00	Knowledge Graph-Guided Interpretation of Disease-Specific Taxon--Taxon Interaction Networks in the Gut Microbiome **Lucas Gillenwater**
15:20	Network-based optimal transport analysis of gut microbiome data in colorectal cancer **Jung Hun Oh**
15:30	Metabolite-centric functional annotation with context-specific starting points **Ivory Blakley**

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CAMDA

Wednesday, July 15; Lincoln East

Time	Title and Speaker
15:40	Predicting Resistance with ALPAR **Alper Yurtseven**
16:40	An Accurate Machine Learning Workflow for Inference of Antimicrobial Resistance from Bacterial Genomes **David Danko**
17:20	Quantifying uncertainty in protein representations across models and tasks **R. Prabakaran**
18:00	Closing remarks

Thursday, July 16; Lincoln East

Time	Title and Speaker
08:40	CAMDA Welcome
08:50	Towards Privacy-Preserving Genomics: Understanding and Mitigating Risks **Hoon Cho**
09:40	A rigorous benchmarking of alignment-based HLA typing algorithms for RNA-seq data **Serghei Mangul**
11:00	The Health Privacy Challenge

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CAMDA

Thursday, July 16; Lincoln East

Time	Title and Speaker
11:20	A Unified Weighted-Distance Framework for No-Box Membership Inference Attacks on Synthetic Gene Expression Data **Ruixuan Liu**
11:40	Privacy Auditing of Synthetic Single-Cell RNA-seq Data **Steven Golob**
12:00	Does Synthetic Bulk RNA-seq Data Protect Donors? Privacy Auditing through Membership Inference Attacks **Charlene Jarrell**
12:20	Privacy-Preserving Synthetic Single-Cell RNA-seq via NMF-Compressed Truncated Vine Copulas **Andrew Wicks**
12:40	From Graphical Models to Foundation Models: Synthetic Bulk RNA-seq Data Generation **Elias Chaibub Neto**
12:50	Two-Stage P-PGM + Beta-CVAE Pipeline for Differentially Private Synthetic RNA-seq Generation **Ahmet Yiğit Doğan**
14:20	Harmonization and Integration of Pharmacogenomics Screens **Aleysha Chen**
15:00	Adapting Mamba 2 For EHR Data Using Continual Learning **Conrad Testagrose**
15:20	Insights from a Large Community Challenge Benchmark Applicable to AI/ML-based Complex Biomarkers **Wendell Jones**
15:50	CAMDA Trophy and closing

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COMPMS

Online schedule found here.

Monday, July 13; Room 9–10 Combo

Time	Title and Speaker
11:00	Introduction to CompMS
11:10	Data-Driven Modeling of TLR4 Signaling Identifies Missing Negative Feedback Underlying Prolonged Inflammatory Outcomes **Aleksandra Nita-Lazar**
11:50	mzPeak - A new cloud-native community format for mass spectrometry data **Oliver Kohlbacher**
12:00	Detecting brain cancer-specific proteoforms from peptide-level proteomics using the ProteoPy framework **Ian Dirk Fichtner**
12:10	MiRROR: fast and accurate de novo peptide sequencing by aligning mirror symmetries in spectrum subgraphs. **George Glidden-Handgis**
12:20	Benchmarking Fine-Tuned Large Language Models for Tandem Mass Spectrum Prediction: Competitive In-Distribution but Limited Cross-Dataset Generalization **Dongyeop Jang**
12:30	A threshold-free replacement for prevalence filtering in untargeted LC-MS metabolomics **Chiraag Gohel**
12:40	SHINE: Decoding transcriptional-metabolic microenvironments through higher-order spatial integration **Bingxue Du**
14:20	Foundation Model Enables Interpretable Open and Error-Tolerant Searching for Mass Spectrometry-Based Proteomics **Tom Altenburg**

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CompMS
Computational Mass Spectrometry

COMPMS

Monday, July 13; Room 9–10 Combo

Time	Title and Speaker
14:40	Using Proteome Priors to improve De Novo Peptide Sequencing performance without constraining the search space **Samuel Khan**
15:00	Advancing Proteomic Discovery through Optimized Multi-stage Scoring and Deep Learning-Enhanced Open Search **Chen Qian**
15:20	JMod: Enabling increased multiplexing and throughput for sensitive proteomics **Kevin McDonnell**
15:40	SPRINT-MS: A high-throughput platform for identifying protein-protein interactions using pooled IP-MS and sparse signal recovery **Tomas Rube**

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COMPUTATIONAL BIOLOGY CAREERS SYMPOSIUM

Online schedule found here.

Tuesday, July 14; Room 9–10 Combo	
Time	**Title and Speaker**
16:40:00	Computational Biology Career Opportunities in Industry and How to Prepare for Them! **Moderator: Ben Busby**

Career Fair Jobs Board

If you're looking for the next step in your career, check out the ISMB 2026 Jobs Board!

Start your job search here!

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CSI

Online schedule found here.

Monday, July 13; Jefferson East

Time	Title and Speaker
11:00	Defining context-specific molecular mechanisms from human autoimmune disease loci: Application to the CD40 locus **Soumya Raychaudhuri**
11:40	Using Interpretable Latent Representations of Spatial Transcriptomic Datasets to Identify Molecular Mechanisms of Immunomodulation **Hanxi Xiao**
12:00	Segmentation-free discovery of spatial niches in image-based spatial transcriptomics **Tamjeed Azad**
12:20	Hist2Pheno enables nuclei-resolved phenotypic prediction from histological images in esophageal squamous cell carcinoma **Lingyu Li**
12:40	Single-cell spatial transcriptomics of archived colitis biopsies uncovers cellular neighborhoods defining two distinct archetypes of vedolizumab resistance **Alexis Combes**
12:50	A multimodal foundation model for single-cell immune profiling **Xu Liao**
14:20	Keynote — **Golnaz Vahedi**
15:00	Comprehensive Mapping of Immune Nanobody Repertoires with NanoMAP **William White**

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CSI

Monday, July 13; Jefferson East

Time	Title and Speaker
15:20	Deep learning TCR-pMHC structure prediction differentiates epitope specific interactions **Michael Robben**
15:40	Scalable Unmutated Common Ancestor Inference of Paired B Cell Receptor Ancestors Across Immune Repertoires **Cole Jensen**
16:40	A signaling-informed sequence-to-function model identifies mechanisms of cytokine-specific gene regulation **Anamarie Martinez**
17:00	TyCHE enables time-resolved lineage tracing of B cells, tumors, and other heterogeneously evolving cell populations **Kenneth Hoehn**
17:20	Agentic AI for screening ligand–target binding affinity **Simona Rabinovici-Cohen**
17:40	Systems Vaccinology Reveals Shared and Distinct Early Transcriptional Predictors of High Antibody Responses Across Vaccines **Stephanie Hao**
17:50	scTRP: a clonotype-aware single-cell contrastive model for predicting antitumor-reactive T cells **Li Su**

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DREAM CHALLENGES

Online schedule found here.

Sunday, July 12; International Ballroom East	
Time	**Title and Speaker**
09:30	Opening Remarks. Introducing BEACON: A Benchmarking, Evaluation, and Assessment Consortium for scientific rigor
09:45	Biologically Grounded AI Models and Agents Across Molecular and Cellular Scales
11:00	SEA-Alzheimer Disease Challenge
11:15	Olfactory Mixtures Prediction Challenge **Pablo Meyer**
11:30	Target2035-DREAMQ Challenges
11:45	Digital Pen Feature Extraction Challenge **Solveig Sieberts**
12:05	Benchmarking Automated Scientific Enquiry
12:40	BioAgentBench: Reliable LLM Agents for End-to-End Omics Workflow Orchestration
12:50	Evidence Agents: evaluating a multi-agent framework for evidence-based scientific discovery **Joao Bettencourt-Silva**

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DREAM CHALLENGES

Online schedule found here.

Sunday, July 12; International Ballroom East	
Time	**Title and Speaker**
14:00	A Framework for Benchmarking Artificial Intelligence Agents on Crowdsourced Computational Biology Competitions **Nikolaos Kalavros**
14:20	Prospective Benchmarking of Generalist AI Agents Across Biological Prediction Challenges **Gaia Andreoletti**
14:35	The MecCog open science challenge: Discovering mechanism in preclinical biology **John Moult**
14:50	BioAgentBench: Reliable LLM Agents for End-to-End Omics Workflow Orchestration
15:00	DREAMx: Deploying Federated DREAM Challenges Behind Institutional Firewalls to Evaluate Cross-Institution Generalizability of Computational Models **Arushi Shrivastava**
15:20	GA4GH AI Workstream
15:40	Benchmarking large language models for predictive modeling in biomedical research with a focus on reproductive health **Reuben Sarwal**
15:50	OpenChallenges: A FAIR-Aligned, Centralized Platform for Crowdsourcing in Biological Research

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EDUCATION

Online schedule found here.

Thursday, July 16; Cabinet

Time	Title and Speaker
08:40	Keynote: Challenges and Opportunities of Bioinformatics in the Global South **Prashanth N Suravajhala**
09:20	Empowering African Life Scientists Through R: Outcomes of a Community-Led Bioinformatics Training Initiative
09:40	Hackathons as a Scalable Model for Training and Community Engagement **Allissa Dillman**
11:00	Teaching biological data science with generative and agentic artificial intelligence **Steven Brenner**
11:20	From Survey to Syllabus: Evidence-Informed Integration of Bioinformatics into Required Undergraduate Biology Courses **Adena Collens**
11:40	Enhancing Computational Biology Education in Pharmacy Students through a Structured Training Program in Drug Discovery **Sara Munir**
12:00	Navigating Career Pathways with the EMBL-EBI Competency Hub **Daria Sokolova**
12:20	Ethical and Integrity Issues in using AI in the Classroom

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EDUCATION

Wednesday, July 23; Room 11A

Time	Title and Speaker
14:20	Quantifying domain-specific relevance of computational biology Wikipedia articles using TF-IDF and cosine similarity **Dan DeBlasio**
14:40	Leveraging a hybrid cross-disciplinary training model to accelerate global bioinformatics capacity **Serghei Mangul**
15:00	BiotrAIn: development and implementation of a training program on artificial intelligence focused on biosciences for Latin America **Rebeca Campos-Sánchez**
15:20	Keynote: Growing bioinformatics capacity through mentorship and community in Peru and Latin America **David Requena**

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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.**

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EQUITY-FOCUSED RESEARCH

Online schedule found here.

Thursday, July 16; Jefferson East	
Time	**Title and Speaker**
08:40	A Systematic Fairness Evaluation of Racial/Ethnic Bias in Alzheimer's Disease Diagnosis Using Machine Learning Models **Neha Goud Baddam**
08:50	Large-scale automated detection reveals pervasive sex bias in biomedical research **Lydia Valtadoros**
09:00	Keyboard accessibility of biomedical data portals and visualization tools **Thomas C. Smits**
09:20	Exploring the Human Gut Microbiome Diversity in Latin America: Focus on Populations at Nutritional Risk **Rebeca Campos**
09:30	Open-Source Enablers: Infrastructure, Good Practices & Reproducibility for students and young researchers in Bioinformatics in Mexico **Jose Abel Lovaco Flores**
09:40	Generalization Performance of RNA-Based Predictors of Homologous Recombination Deficiency in Diverse Populations **Samantha Lopez Alvarez**

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EVOLCOMPGEN

Online schedule found here.

Wednesday, July 15; Jefferson West

Time	Title and Speaker
11:00	Comparative Genomics in the Open Ocean **Casey Dunn**
12:00	Topology-Based Analysis of Gene Tree Heterogeneity with Applications to Incomplete lineage Sorting and Introgression **Tanjeem Zaman**
12:20	Leveraging horizontal gene transfer networks to predict the host of Staphylococcus aureus isolates **Katerina Terwelp**
12:30	Machine learning identifies the fingerprints of host adaptation in bacterial genomes
12:40	AmpliPhy improves gene trees by adding homologous sequences without affecting alignments **Dongwook Kim**
14:20	Phlag: Scalable detection of genomics regions with unexplained phylogenetic heterogeneity **Ali Osman Berk Şapcı**
14:40	To peel the pangenome **David Sankoff**
15:00	PINNOU: Physics-Informed Neural Networks for Ornstein–Uhlenbeck Inference in Phylogenetics **Soumitra Pal**
15:20	What is the best strategy for building gene trees and species trees? **Erik Wright**
15:40	The Impact of Species Tree Shape on Method Performance **Yunzhuo Liu**

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Wednesday, July 15; Jefferson West

Time	Title and Speaker
16:40	ADAMIXTURE: Adaptive First-Order Optimization for Biobank-Scale Genetic Clustering **Joan Saurina-i-Ricos**
17:00	Phylogenetic Placement Achieves Near-Haplotype Resolution in Wastewater-Based Epidemiology using WEPP **Pranav Gangwar**
17:20	Ok-k-mer: Integrating multiple k-mers for calculating genomic distance **Stephen Hwang**
17:40	Recombination on genotype representation graphs: toward fast forward-time genetic simulation with arbitrary complexity **Sahana Senthilkumar**

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EVOLCOMPGEN

Thursday, July 16; Jefferson West

Time	Title and Speaker
08:40	LAML-Pro: Joint Maximum Likelihood Inference of Cell Genotypes and Cell Lineage Trees **Gillian Chu**
09:00	Bounding mutations for a subsampling-placement strategy to reconstruct clonal lineage trees for somatic evolution **Nishat Anjum Bristy**
09:40	New evolutionary dynamics emerge from phenotypic uncertainty **Anna Sappington**
11:00	CAMUS: Scalable Phylogenetic Network Estimation **James Willson**
11:20	DO-tanglegrams for phylogenetic trees and networks **Daniel Huson**
11:40	Tracing Input Trees Inside PhyloFusion Network **Banu Cetinkaya**
12:00	Structure-Aware Reinforcement Learning for Reconstructing Duplication Event Histories in Gene Families **Jeonghoon Choi**
12:20	In Pursuit of Forbidden Protein Domain Architectures **Yu-Hsiang Chen**

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Thursday, July 16; Jefferson West

Time	Title and Speaker
12:40	BATH2: splice-aware translated search of protein sequences or profile HMMs against genomic DNA **Genevieve Krause**
14:20	Systematic inference of mutation rates and spectra across the tree of life via a scalable read-based framework **Yosef Efraim Maruvka**
14:40	Identifying Coevolution in Multiple Sequence Alignments with Machine Learning Anomaly Detection Methods **Matthieu Vilain**
15:00	A Unified Substitution–Mutation Rate Ratio (c/μ) Framework and Near-Neutral Selectionist Theory for Molecular Evolution: Insights from SARS-CoV-2 **Chun Wu**
15:20	Evolution and Comparative Genomics: The state of the field

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FUNCTION

Online schedule found here.

Monday, July 13; Lincoln East

Time	Title and Speaker
11:00	AI-Driven Protein Functional Annotation and Biomedical Discovery
11:40	AMR-Fold: Structure-Aware Deep Learning for Antibiotic Resistance Gene Discovery and Classification **Sergio Sánchez Carrillo**
12:00	Leveraging phenomic variation and knowledge graphs to elucidate molecular functionality **Yannick Mahlich**
12:20	Enhancing Protein Function Annotation through Explainable Reasoning with LLM **Huiying Yan**
12:40	Protein embeddings to address functional specificity in protein families **Ana Rojas**
14:20	Knowledge-guided Contextual Gene Set Analysis with Large Language Models **Zhizheng Wang**
14:40	Alpha&ESMhFolds: An updated database for the comparison and functional annotation of predicted structural models for the human proteome **Matteo Manfredi**
15:00	A Deep Positive-Unlabeled Learning Approach to Cell-Penetrating Peptide Discovery **Jérôme Tubiana**
15:20	PUFFIN: Protein Unit Discovery with Functional Supervision **Gökçe Uludoğan**
15:40	Poster flash talks

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FUNCTION

Monday, July 13; Lincoln East	
Time	**Title and Speaker**
16:40	How Not to be Seen: Predicting Unseen Enzyme Functions using Contrastive Learning **Xiang Ma**
17:00	Improving protein function annotation with balanced representations and evolutionary profiles **Jiaqi Luo**
17:20	Learning Protein Post-Translational Modification Sites Prediction via Spatially-Aware Local Conditioning of Embeddings on Proximal Evidences **Pawel Pratyush**
17:40	nail: high-speed sequence annotation with profile hidden Markov models **Travis Wheeler**

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FUNCTION

Tuesday, July 14; Lincoln East

Time	Title and Speaker
11:00	Critical Assessment of Protein Function Annotation algorithms: CAFA6 preliminary results and CAFA Forever **An Phan**
11:40	Extending CAFA to Natural Language: Towards Evaluating Free-Text Protein Function Descriptions **M. Clara De Paolis Kaluza**
12:00	The Variation-leveraged phenomic Foundation Model (VFM): A novel multi-omic AI model for understanding biological systems context **Jason McDermott**
12:20	Agentic evaluation of AI function prediction pipelines **Harry Caufield**
12:40	PU-GRAIL: residue-level graph learning for identifying protective bacterial antigens under positive–unlabeled supervision **Jaemin Jeon**
14:20	In a genAI world, does structured knowledge still have a role in science?
15:00	GO-CAM: thousands of curated pathways using GO, and new tools for using them **Paul Thomas**
15:20	STAR-GO: Improving Protein Function Prediction by Learning to Hierarchically Integrate Ontology-Informed Semantic Embeddings **Gökçe Uludoğan**
15:40	GIMME: Graph Inference for Microbial Metabolism Exploration using Knowledge Graphs **Winston Anthony**
16:40	Function annotation and prediciton: new standards for a new era?

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GENCOMPBIO

Online schedule found here.

Wednesday, July 15; Georgetown	
Time	**Title and Speaker**
11:00	Long-read sequencing of single cell-derived melanoma sublines reveals divergent and parallel genomic and epigenomic evolutionary trajectories **Anton Goretsky**
11:20	CN-SigBench: A benchmarking pipeline for pan-cancer copy-number signature analysis **Keshav Gandhi**
11:40	Benchmarking sample mispairing detection tools in complex cancer datasets **Emma Lathouwers**
12:00	Super-silencers safeguard cell identity and are repurposed as super-enhancers in cancer metastasis. **Di Huang**
12:20	Phasing Tumor Clones By Timing Somatic Mutations In Bulk Long-Read Sequencing **Ataberk Donmez**
14:20	Bridging Ancestry Gaps in Genomic Risk Prediction with Tabular Foundation Models **Anirban Das**
14:40	A disentangled transformer-based transfer learning framework to predict patient drug response from tumor single-cell transcriptomics **Xinliang Sun**
15:00	SAD-DRP: A Subspace-Aware Domain Adaptation Model with Explicit Prototype-Based Local Alignment for Cancer Drug Response Prediction **Ruisheng Wang**

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GENCOMPBIO

Wednesday, July 15; Georgetown	
Time	**Title and Speaker**
15:20	Sex-dependent and cell-type specific transcriptional responses to sleep deprivation caused by mutations in the autism gene Shank3 in early development **Caitlin Ottaway**
16:40	Accurate detection of mosaic mutations at short tandem repeats from bulk sequencing data **Weixiang Wang**
17:00	inSTRbility: a computational framework for quantifying somatic mosaicism at tandem repeat loci **Akshay Kumar Avvaru**

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GENCOMPBIO

Thursday, July 16; Georgetown	
Time	**Title and Speaker**
08:40	SIVA: Diagonal Integration of Spatial Multi-omics Data via Spatially-Informed Variational Autoencoders and Anchor Guidance **Peng Jiang**
09:00	Meta-CCC: Deciphering Cell–Cell Communication through Integrative Single-Cell **Jia-Jun Liu**
09:20	CLEAR-ST: Physics-informed probabilistic decontamination of spatial transcriptomics by modeling mRNA lateral diffusion **Kun Ma**
09:40	SpaReg: Sparsity-based scalable reconstruction of three-dimensional microenvironments at subcellular resolution **Rajdeep Pawar**
11:00	Is a Win-Win Possible? Achieving Pareto-Optimal Privacy-Utility Balance in Fine-Tuned Genome Language Model Embeddings Against Embedding Reconstruction Attacks **Reem Al-Saidi**
11:20	Deciphering Key Factors of Active Learning Performance in Biomolecular Design **Yixuan Zhi**
11:40	Optimizing Protein Tokenization: Reduced Amino Acid Alphabets for Efficient and Accurate Protein Language Models **Ella Rannon**
12:00	Fairness-aware Supervised Hierarchical Contrastive Semantic Learning for Sexual Dimorphism Analysis **Euiseong Ko**
12:20	ATTNSOM: Learning Cross-Isoform Attention for Cytochrome P450 Site-of-Metabolism Prediction **Hajung Kim**

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GENCOMPBIO

Thursday, July 16; Georgetown	
Time	**Title and Speaker**
12:40	Improving Hit Discovery by Integrating Activity Cliff Sensitivity into Active Learning **Junha Kim**
14:20	PIMO: Pathway-based Interpretable Multi-Omics interactions for multi-omics integration **Sai Phani Parsa**
14:40	Attention-driven accurate deconvolution of bulk transcriptomes using population-scale single-cell references **Xing Zheng**
15:00	Qombucha identifies distinct developmental methylation programs and cell type compositions in Glioblastoma **Xuan Li**
15:20	STEP2h: Detecting transposable element exonization with multi-task deep learning **Liliana Florea**
15:40	absuite: A Package in R for Antibody Repertoire Profiling and Clonotype Analysis **Favour Igwezeke**

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HITSEQ

Online schedule found here.

Monday, July 13; International Ballroom Center

Time	Title and Speaker
11:00	Welcome
11:05	TBD
12:00	Scalable computation of ultrabubbles in pangenomes by orienting bidirected graphs **Corentin Moumard**
12:20	RLBWT-Based LCP Computation in Compressed Space for Terabase-Scale Pangenome Analysis **Ahsan Sanaullah**
12:40	ImpuT2T: Pangenome-Based Patching for Human Genome Assemblies **Mao-Jan Lin**
14:20	Optimizing sparse and skew hashing: faster k-mer dictionaries **Rob Patro**
14:40	10-minimizers: a promising class of constant-space minimizers **Yaron Orenstein**
15:00	The gift of novelty: repeat-robust k-mer-based estimators of mutation rates **Haonan Wu**

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HiTSeq

HITSEQ

Monday, July 13; International Ballroom Center

Time	Title and Speaker
15:20	Incorporating indel channels into average-case analysis of seed-chain-extend **Spencer Gibson**
15:40	ORION: A High-Performance Barcode and UMI Correction Tool for Oxford Nanopore Single-Cell Sequencing **Dohun Yi**
16:20	SpatiaXen: An Open-Source Interactive Platform for Cell-Type-Resolved Spatial Transcriptomics Analysis **Anirban Chakraborty**
16:40	Detecting and reconstructing breakage-fusion-bridge cycles from long-read sequencing using BFBArchitect **Chaohui Li**
17:00	TBD

Tuesday, July 14; International Ballroom Center

Time	Title and Speaker
11:00	TBD
12:00	scVarSim: A Unified Simulator for Benchmarking Genetic Variant Calling and RNA Editing Detection in Single-Cell RNA-seq Data **Weijian Wang**
12:20	Spatiotemporal cell type deconvolution leveraging tissue structure **Xiuwei Zhang**

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HITSEQ

Tuesday, July 14; International Ballroom Center

Time	Title and Speaker
12:40	MethylSeg: Context-Aware Methylome Segmentation Enables Robust PMD Detection in Array and WGBS Data **Jacob Tye**
14:20	Amaranth: Enhanced Single-Cell Transcript Assembly via Discriminative Modeling of UMI Reads and Internal Reads **Xiaofei Carl Zang**
14:40	Minerva: Breakpoint-Guided Allele-Specific Copy Number Inference in Long-Read Cancer Genomes **Ayse Keskus**
15:00	Unravelling genome-wide mosaic microsatellite mutations at single-cell resolution **Yanmei Dou**
15:20	SQANTI-epi: Functional and Quality Annotation of Single-Molecule Epigenomic Data **Tianyuan Liu**
15:40	Likelihood-based optimization enables accurate copy number estimation for paralogous genes using exome data **Sang Yoon Byun**
16:40	Seqwin: Ultrafast identification of signature sequences in microbial genomes **Michael X. Wang**
17:00	pHapCompass: Probabilistic Assembly and Uncertainty Quantification of Polyploid Haplotype Phase **Marjan Hosseini**
17:20	Pilot discovery of allele-specific modification QTLs from long-read RNA sequencing **Michael Goneos**
17:40	CRANE: Correcting Errors in Raw Nanopore Signals Using Hidden Markov Models **Simon Ambrozak**

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INDUSTRY WORKSHOP

Online schedule found here.

Tuesday, July 14; Room 9–10 Combo	
Time	**Title and Speaker**
14:20	CEO
14:50	Director of Bioinformatics
15:20	Venture Partner

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IRNA

Online schedule found here.

Monday, July 13; International Ballroom West

Time	Title and Speaker
11:00	Introduction
11:10	Rules for 3' splice site choice inferred from high-throughput in silico mutagenesis **Steve Mount**
11:20	Expanding RNA Biology with XNAs: In Vitro Evolution of Non-natural Nucleic Acids for Recognition and Catalysis **Lijun Zhou**
12:00	Deep Learning to Accelerate Discovery of Functional Synthetic Nucleic Acids **Jiatao Liang**
12:20	RNA Language Model learns structure prediction of Internal Ribosome Entry Sites despite sequence only training **Adam Sychla**
12:40	RNA Design with Language Models **Milan Gautam**
12:50	Sampling-based Continuous Optimization for Messenger RNA Design **Wei Yu Tang**
14:20	Nuclear speckles enable processing of RNA from GC-rich isochores **Ferhat Ay**
14:40	ERV-Seq: Revealing The Hidden Transcriptome of Human Endogenous Retroviruses **Lan Lin**

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Monday, July 13; International Ballroom West	
Time	**Title and Speaker**
15:00	Statistical guarantees for identifying RNA-binding protein interaction sites **Young-suk Lee**
15:20	Nearest Neighbor Parameters for Estimating the Folding Stability of RNA Sequences Including Pseudouridine **Thandolwethu Shabangu**
15:40	Deciphering Fusion Transcript Complexity Using Targeted RNA Sequencing **Paweł P. Łabaj**
15:50	Systematic identification and multi-omic characterization of human chromatin-associated long non-coding RNAs **Zhao Li**
16:40	modulator: Fragment-Specific Modification Calling for Nanopore Direct-RNA Sequencing Data **Theodore Nelson**
17:00	Beyond the known genome: expanding the vertebrate lncRNA universe through targeted full-length RNA sequencing **Barbara Uszczynska-Ratajczak**
17:20	Decoding the temporal landscape of mRNA modifications at single-molecule resolution **Eduardo Eyras**

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IRNA

Tuesday, July 14; International Ballroom West

Time	Title and Speaker
11:00	Decoding the Cancer Splicing Landscape: From Aging Associated Isoforms to Regulatory Networks and Therapeutic Targets **Olga Anczuków**
11:40	ASPECT: Alternative Splicing Event Classification with Transformers for Cancer Transcriptomics **Sahil Thapa**
12:00	An integrative framework links cryptic splicing to neoantigen generation and candidate splicing factor regulation in lupus neutrophils **Ning Wang**
12:20	Alternative RNA processing-informed deep learning models boost gene expression-based patient outcome prediction and reveal novel prognostic indicators **Zachary Wakefield**
12:40	predNMD: prediction of nonsense-mediated mRNA decay for enhanced clinical variant pathogenicity classification **Yaqi Su**
12:50	scPTR: Decomposing Post-Transcriptional Regulation at Single-Cell Resolution **Bryan Cheng**
14:20	Charting the Axes of Isoform Variation using Long Read Single-cell Transcriptomics with Allos **Eamon Mcandrew**
14:40	Spatial isoform sequencing at single-cell resolution reveals novel patterns of spatial isoform variability in brain cell types **Lieke Michielsen**
15:00	BenchDrop-seq: a microfluidics-free platform for benchtop single-cell long-read RNA sequencing **Avi Srivastava**

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IRNA

Tuesday, July 14; International Ballroom West	
Time	**Title and Speaker**
15:20	Three-Dimensional RNA Spatial Mapping Reveals Microcircuit Organization of the Nucleus Accumbens **Lauren Wills**
15:40	Single-cell RNA editing identifies aggressive and favorable cellular states in chronic myelomonocytic leukemia **Tongjun Gu**
16:40	Leveraging Long-Read Transcriptomics and Ribo-seq to Expand the Noncanonical Proteome **Nuo Xu**
16:50	seq2ribo: Structure-aware integration of machine learning and simulation to predict ribosome location profiles from RNA sequences **Gün Kaynar**
17:10	An Integrative Approach to Predictive Modeling of Translation **Can Cenik**
17:50	Concluding remarks and poster prizes

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MICROBIOME

Online schedule found here.

Monday, July 13; Georgetown

Time	Title and Speaker
11:00	The Genome Taxonomy Database and identification of new stop codon reassignments **Donovan Parks**
11:40	PhageMind: Generalized Strain-level Phage Host Range Prediction via Meta-learning **Yanni Sun**
12:00	Metagenomic Strain-Resolved DNA Modification Patterns Link Extrachromosomal Elements to Host Strains **Shuai Wang**
12:10	UniqSketch: sensitive and resource-efficient strain-level detection in metagenomes **Bonnie Hurwitz**
12:20	ICICLE: Transformer-Based Detection of Integrative and Conjugative Elements from Genomic and Metagenomic Sequences **Christina Boucher**
12:30	Phylogenetic Placement Enables Near-Haplotype Resolution of Metagenomic Samples using metaWEPP **Pranav Gangwar**
12:40	Quantifying classification stability under reference database perturbation **Elizabeth Hunter**
12:50	Medival Can Detect Mobile Genetic Elements Without a Reference Database **Grace Oualline**
14:20	VirBinn improves viral genome binning from metagenomic Hi-C through graph diffusion **Yuxuan Du**
14:40	Comparative metagenomics using pan-metagenomic graphs **Tal Korem**

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MICROBIOME

Monday, July 13; Georgetown

Time	Title and Speaker
14:50	Modeling Scale Uncertainty Improves Microbiome Analysis **Maxwell Konnaris**
15:00	Inferring gut butyrate resilience from sparse longitudinal metabolomics via effective landscapes **Javad Aminian Dehkordi**
15:10	LaBay: Scalable Bayesian Modeling of Longitudinal Microbiome Dynamics After Sleeve Gastrectomy **Ali Reza Taheriyoun**
15:20	Creation and validation of LIMON - Longitudinal Individual Microbial Omics Networks **Beatriz Penalver Bernabe**
15:30	Semi-supervised Genome Annotation Using a Mixture-of-Experts Genome Foundation Model **Junho Hong**
15:40	Limousia bacteria encode mucinolysome for mucin utilization in animal gut microbiomes **Yanbin Yin**
15:50	dbcan-nf: a scalable Nextflow pipeline for CAZyme annotation in metagenomes **Xinpeng Zhang**
16:40	RAmpSim: A Thermodynamic Simulator for Hybridization Capture in Metagenomic Sequencing **Aidan Zhang**
17:00	The Kenyan Human Gut Virus Catalogue Reveals Extensive Virome Diversity
17:10	WWBio: Control-Calibrated Multi-Evidence Inference for Robust Marker Detection in Long-Read Wastewater Metagenomics **Ayesha Wasim**

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MICROBIOME

Monday, July 13; Georgetown

Time	Title and Speaker
17:20	The gut microbiome and mycobiome landscape of treatment-naïve lymphoma **Andrey Zaznaev**
17:30	End-to-end evaluation of pipelines for metagenome-assembled genomes reveals hidden performance gaps **Izaak Coleman**
17:40	RECAST: A Reproducible Workflow for Updating Taxonomic and Functional Classifications for Metagenome Analysis **Julia U. B. Fischer**
17:50	Multi-sample binning increases MAG recovery from Empty Quarter desert soils with minimal benefit from geographic sample grouping **Alejandra Lopez-Velazquez**

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MICROBIOME

Tuesday, July 14; Georgetown	
Time	**Title and Speaker**
11:00	A Novel Transformer Model of Protein Domains for Viral Taxonomy Classification **Jihye Shin**
11:20	MetaKSSD: boosting the scalability of the reference taxonomic marker database and the performance of metagenomic profiling using sketch operations **Huiguang Yi**
11:30	Perseus: Lineage-Aware Refinement of Kraken2 Taxonomic Classification for Long Read Metagenomes **Matthew Nguyen**
11:40	Improving Metagenomics Classification with Kmask: Entropy-Based Masking of Low-Complexity Regions **Peter Ge**
11:50	Integrating cross-platform metagenomics studies - high taxonomic concordance and functional analysis challenges **Paweł P. Łabaj**
12:00	Launching CAMI III: Critical Assessment of Metagenome Interpretation **Alice McHardy**
12:20	Structure-guided approaches to discover novel human-microbiome interactions **Ilana Brito**

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MLCSB

Online schedule found here.

Wednesday, July 15; International Ballroom Center

Time	Title and Speaker
11:00	Benchmarking AI scientists for omics data-driven biological discovery **Erpai Luo**
11:20	Agentomics: An Agentic System that Autonomously Develops Novel State-of-the-art Solutions for Biomedical Machine Learning Tasks **Vlastimil Martinek**
11:40	Data-driven AI system for learning how to run transcript assemblers **Yihang Shen**
11:50	The Virtual Biotech: A Multi-Agent AI Framework for Therapeutic Discovery and Development **Harrison Zhang**
12:00	A Conversational Multi-Agent AI Framework for Integrated Multi-Omics Analysis and Biomedical Discovery **Pankaj Rajdeo**
12:10	Transfer learning from datasets with unshared features for detecting Autism Spectrum Disorder using AutDB **Ruslan Kurmashev**
12:20	Enabling direct nanopore sequencing of non-canonical bases using bootstrapped learning and signal splicing **Mauricio Lisboa Perez**
12:30	Linear-time prediction of proteome-scale microbial protein interactions **Andre Cornman**
14:20	Learning from evolutionary trajectories **Yun Song**
15:20	TBD

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MLCSB

Wednesday, July 15; International Ballroom Center	
Time	**Title and Speaker**
15:25	SpatioVelo: Spatial RNA velocity inference by integrating scRNA-seq and spatial transcriptomics **Guan-Ting Chen**
15:30	Characterizing Functional Microniches with SpaceTravLR **Alyson Wang**
15:35	Correcting cell count bias improves perturbation effect estimates and virtual cell models **Bence Czakó**
15:40	Topographical Archetypes of Somatic Mutagenesis in Cancer **Doga C. Gulhan**
16:40	Toward an In Silico Tissue Laboratory: From Virtual Staining to Executable Tissue Modeling **Young Hwan Chang**
17:40	Spatial-ZEDNet: A Unified Spatial Transcriptomics Framework for Detecting Differential Gene Activation and Expression **Osafu Egbon**
17:50	Spatiotemporal Modeling with ATLIS: Anchored Tissue Landscapes in an Interpretable Space **Wenjun Zhao**

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MLCSB

Thursday, July 16; International Ballroom Center

Time	Title and Speaker
08:40	From Learning to Leveraging Graphs in Biomedicine
09:40	Interaction-aware multitask deep learning reveals cross-species receptor compatibility landscapes across sarbecoviruses **Kritika Prasai**
09:45	Multimodal spatial alignment and morphology mapping with MOSAICField **Hongyu Zheng**
09:50	Domain-Aware Enzyme Classification via Multiple Instance Learning **Qingyang Xiao**
11:00	CROP: A feature-independent context-aware method for CRISPR-Cas9 frameshift prediction **Yaron Orenstein**
11:20	PertAdapt: Unlocking Single-Cell Foundation Models for Genetic Perturbation Prediction via Condition-Sensitive Adaptation **Ding Bai**
11:40	A Palma Ratio–Driven Graph-Fusion Approach for Detecting Ultra-Rare Cell Types in scRNA-seq Data **Shibiao Wan**
11:50	Bridging the negative data gap in bioactivity prediction using InertDB **Seungchan An**
12:00	ChromCodes: interpretable discrete representations enable controllable design of cell-type-specific regulatory DNA sequences **Luca Pinello**
12:10	CPS: Mapping Physical Coordinates to High-Fidelity Spatial Transcriptomics via Privileged Multi-Scale Context Distillation **Kai Cao**

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MLCSB

Thursday, July 16; International Ballroom Center	
Time	**Title and Speaker**
12:30	Riemannian Metric Learning for Alignment of Spatial Multiomics **Peter Halmos**
14:20	Opportunities and challenges in sequence-based deep learning **Katie Pollard**
15:20	Diffusion-based Representation Integration for Foundation Models Improves Spatial Transcriptomics Analysis **Tuan M. Pham**
15:40	Striping artifact removal in VisiumHD data through nuclear counts modeling **Paola Malsot**

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NETBIO

Online schedule found here.

Tuesday, July 14; Georgetown

Time	Title and Speaker
14:20	NetBio Opening
14:30	Taming the complexity of large-scale metabolic networks **Zoran Nikoloski**
15:20	A Novel Network Approach to Identify Sample-Specific Context-Informed Metabolic Signatures During Developmental Processes **Emma Lee**
15:40	Bayesian Likelihood-based Inference of Metabolic Modules for Prokaryotes (BLIMMP) **Neha Sontakke**
16:40	Rawk: Metabolic pathway local enrichment analysis via random walks on metabolic reaction network **Yuanchao Zhang**
17:00	DyGraphTrans: A temporal graph representation learning framework for modeling disease progression from Electronic Health Records. **Most Tahmina Rahman**
17:20	Genetic Interaction-based Machine Learning Models for Disease Risk Prediction **Mathew Fischbach**
17:30	PICDGI: Dynamic Gene Interaction Network Modeling Reveals Cancer Driver Genes from Single-Cell Data **Benedict Anchang**
17:40	Sample-Specific Differential miRNA Network Rewiring Associated with Asthma Exacerbation Using LIONESS **Parham Hadikhani**
17:50	BIRDccNEST: Interpretable single cell characterization with inferred cell networks **Gizem Cicekli**

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NETBIO

Wednesday, July 15; Room 9–10 Combo

Time	Title and Speaker
11:00	From Spatial Transcriptomics to Network Biology in Health and Disease **Helder Nakaya**
11:40	Spatially Varying Gene Regulatory Network Inference from Spatial Transcriptomics **Yurui Li**
12:00	Inferring and Evaluating Network Medicine-Based Disease Modules with Nextflow **Johannes Kersting**
12:20	EPIC: Event Prototyping via Information Constrained graph learning for personalized cancer driver gene prediction **Sang-Pil Cho**
12:40	Single-Cell Multiome Analysis Links Genetic Risk to a Cell-Type–Specific Regulatory Program in L6 IT Car3 Neurons Following Opioid Exposure **Fengge Chang**
12:50	Deep integrative multiplex network-based analysis of rare neuromuscular disorders reveals overlapping multiscale endotypes involved in cardiac and skeletal muscle myopathies **Iker Núñez Carpintero**
14:20	GATSBI: Improving context-aware protein embeddings through biologically motivated data splits **Gowri Nayar**
14:40	The NIH Common Fund Data Ecosystem Data Distillery Knowledge Graph: A Scalable Framework for Multimodal Integration and Network-Based Biomedical Discovery **Deanne M. Taylor**
15:00	Predicting Phosphatase-Substrate Association using a Heterogeneous Knowledge Graph **Marzieh Ayati**

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NETBIO

Wednesday, July 15; Room 9–10 Combo

Time	Title and Speaker
15:20	From General-Purpose to Disease-Specific Features: Aligning LLM Embeddings on a Disease-Specific Biomedical Knowledge Graph for Drug Repurposing **Suman Pandey**
15:40	drGT: Attention-Guided Gene Assessment of Drug Response Utilizing a Drug-Cell-Gene Heterogeneous Network **Yoshitaka Inoue**
15:50	Challenges and Opportunities in Single-Sample Network Modeling **Kimberly Glass**
16:40	VDJ-REMIX: Repertoire Module Identification and eXploration **Sakina Amin**
17:00	Traditional machine learning vs. deep learning from dynamic graph representations of proteins' 3D folds in the task of protein structure classification **Aydin Wells**
17:10	stem.MAP: A mouse embryonic stem cell specific protein complex map **Akshaya Rajaraman**
17:20	The AI Revolution in Protein Science: From Prediction to Discovery and Cure **Qian Cong**

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NIH/ODSS:
SOCIAL AND TECHNICAL INFRASTRUCTURE TO ADVANCE HEALTH RESEARCH

Online schedule found here.

Monday, July 13; Cabinet	
Time	**Title and Speaker**
11:00	Leaderhip Remarks
11:10	ADAPTS - Autoimmune Disease Analysis Platform Testing Space using a Trusted Federated Platform for Research Data Interoperability **Richard Scheuermann**
11:30	The NIAID Discovery Portal: A federated ecosystem for finding infectious and immune-mediated disease resources **Chunlei Wu**
11:50	AnVIL: A Federated Cloud Ecosystem for Scalable, Secure, and Reproducible Genomic Data Science and Clinical-Genomic Harmonization **Jonathan Lawson**
12:10	Seven Bridges Core Infrastructure (SB-CI): A public–private model for secure, interoperable, and reusable data science with NIH stewardship **Surya Saha**
12:30	FAIR Knowledge Graphs On-Demand **Chris Bizon**
12:50	Open Q&A
14:20	Extended Break
14:25	Leadership Remarks

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NIH/ODSS:
SOCIAL AND TECHNICAL INFRASTRUCTURE TO ADVANCE HEALTH RESEARCH

Monday, July 13; Cabinet	
Time	**Title and Speaker**
14:35	Clinical Dataset Structure: A Universal Framework for Structuring Clinical Research Datasets **Bhavesh Patel**
14:45:00	Assessing Infrastructure Readiness for Standardized Categorical Variant Representation in CIViC **Daniel Puthawala**
14:55:00	CEDAR: A platform to drive standardization of metadata for FAIR data sharing and reuse **Mark Musen**
15:05:00	Enabling Recognition and Reward of Artificial Intelligence Research Objects
15:15:00	A Blueprint for FAIR Data Sharing Across a Distributed Biomedical Data Ecosystem **Lisa Mayer**
15:25:00	Discussion
16:40:00	Extended Break
16:45:00	Leadership Remarks
17:05:00	Building Sustainable Infrastructure for Multimodal Biomedical AI Annotation and Validation

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NIH/ODSS: SOCIAL AND TECHNICAL INFRASTRUCTURE TO ADVANCE HEALTH RESEARCH

Monday, July 13; Cabinet

Time	Title and Speaker
17:15	Accelerating Research Across the Biosciences Using Experimentally-Determined 3D Biostructures and Computed Structure Models of Proteins Generated using Artificial Intelligence/Machine Learning **Stephen K. Burley**
17:25	EMAI: A Universal Computational Framework to Develop Ethics-Aware Multimodal Disease Foundation Models **Farnoush Banaei-Kashani**
17:35	Governing Controlled-Access Data Reuse in the LLM Era: Policy-Aligned Frameworks and Technologies for Secure Model Sharing **Jonathan Lawson**
17:45	spatiAlytica: A Viewer-Coupled Multi-Sub-Agent System with Agentic Memory for Conversational Spatial-Biology Analysis by Non-Coding Biomedical Researchers **Arun Das**
17:55	Closing Remarks

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NVIDIA WORKSHOP

Online schedule found here.

Thursday, July 16; Lincoln West	
Time	**Title and Speaker**
11:00	Building AI Scientist Workflows with BioNeMo: From Accelerating Genomics Analysis to Protein Design using Agents **Angel Pizarro**

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PATHOGEN DATA NETWORK FORUM

Online schedule found here.

Thursday, July 16; Jefferson East	
Time	**Title and Speaker**
11:00	Opening Remarks
11:10	Pathogen Data Network, Platforms for Data, Discovery, and Learning **Christophe Dessimoz**
11:20	Overview of Data and Analysis Resources with Enhanced Usability in the BV-BRC **Maulik Shukla**
11:30	Data to Discovery: AI-Powered Analysis in BRC Analytics **Michael Schatz**
11:40	AI Best Practices for Pathogen Data - Applying the NIST AI Risk Framework to Bioinformatics Workflows **Sam Halabi**
11:50	Challenges and Opportunities for Infectious Disease Data
12:20	Closing remarks

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PUBLISHING SESSION

Online schedule found here.

Tuesday, July 14; Room 9–10 Combo	
Time	**Title and Speaker**
11:00:00	Welcome and Introductions
11:02:00	AI in scientific publishing and peer review **Jessica Miles**
11:10:00	Clinical ML: Utility, development, validation, and real-world evaluation **Kenneth Kehl**
11:20:00	Rigorous Benchmarking for Bioinformatics Methods: From Universal Rankings to Context-Specific Evaluation **Jingyi Jessica Li**
11:30:00	ML development and benchmarking in academia and industry **Bill Lotter**
11:40:00	Data analysis for organoid intelligence **Brian Caffo**
12:00:00	Panel Discussion

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QUANTUM FOR LIFE SCIENCES

Online schedule found here.

Tuesday, July 14; Monroe	
Time	**Title and Speaker**
14:20	Welcome & Introduction
14:25	NIH Quantum Biomedical Innovation and Technologies **Geetha Senthil**
14:35	Applications of Quantum Computing in Biomedical Data Science **Mark Gerstein**
15:00	Quantum Hamiltonian-Based Generative Modeling of Gene Regulatory Networks: Inference algorithms and sample complexity analysis. **Arvind Rao**
15:20	Quantum Computing Approaches for Biological Network Inference and Analysis **Mhaned Oubounyt**
15:40	RotorMap and Quantum Fingerprints of DNA Sequences via Rotary Position Embeddings **Sergii Strelchuk**

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REGSYS

Online schedule found here.

Monday, July 13; International Ballroom East

Time	Title and Speaker
11:00	When Regulators Become Mutagens: Transcription Factor-Induced Mutagenesis **Raluca Gordan**
11:40	REGA: an interpretable hierarchical network representation learning framework for reference regulatory element–guided gene expression analysis **Lixin Ren**
12:00	STORMI: Inference of mechanistic gene regulation dynamics from multimodal and interventional data **Alexander Aivazidis**
12:20	MiRformer: a dual-transformer-encoder framework for predicting microRNA-mRNA interactions from paired sequences **Jiayao Gu**
12:40	NEXIS: Disentangling Cell-Autonomous and Intercellular Gene Regulation from Spatial Transcriptomics **Wenjun Zhao**
12:40	SpiderNet reveals a meta-interaction basis for cell-cell communication in tissues **Junjie Tang**
12:40	Chromatin-informed inference of cell-type-specific regulatory programs in Alzheimer’s disease using single-cell multi-omics **Jiahui Hou**
14:20	TFScope: Learning the DNA-binding specificity of transcription factors from protein sequence **Lei Huang**
14:40	NPBIP: Predicting binding preferences of uncharacterized nucleic-acid-binding proteins **Noam Shimshoviz**
15:00	Multi-modal functional mapping of non-coding sequences regulating fetal hemoglobin **Basheer Becerra**

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REGSYS

Monday, July 13; International Ballroom East

Time	Title and Speaker
15:20	ExoShorkie: Predicting RNA-seq coverage of exogenous genomes in yeast by transfer learning **Yaron Orenstein**
15:40	Developing a methylation and SNP-aware DNA large language model **Dante Bolzan**
15:40	Chorus: An Agentic Framework for Comparative Regulatory Genomics with Sequence-to-Function Oracles **Luca Pinello**
15:40	FIREFate: Functional and Interpretable Regulatory Encoding of Fate determination **Swapnil Keshari**
16:40	Sequence basis of heterogenous and dynamic single-molecule chromatin states **Jian Zhou**
17:20	An Expanded Registry of cis-Regulatory Elements Enables Systematic Analysis of Transcriptional Regulation **Jill Moore**
17:40	Unlocking the Microglial Storm: The Genetic “Off-Switch” Failure in Alzheimer’s Disease. **Ivan Ovcharenko**

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REGSYS

Tuesday, July 14; International Ballroom East

Time	Title and Speaker
11:00	Interpreting deep learning models via concept attribution **Shaun Mahony**
11:40	Cherimoya: Lightweight Sequence-to-Function Models For Large-Scale Regulatory Element Design **Jacob Schreiber**
12:00	When Less Is Enough: Low-rank Structure in DNA Sequence-to-Function Models **Elizabeth Gilfeather**
12:20	Sequence-to-function modeling uncovers the context-specific grammar of Drosophila chromatin insulation **Yuri Pritykin**
12:40	DNA-aware evaluation and debiasing of sequence-to-function models **Doruk Cakmakci**
14:20	stORCA: Correspondence-aware differential spatial expression analysis across biological conditions **Yeojin Kim**
14:40	Integrative Inference of Spatially Resolved Cell Lineage Trees using LineageMap **Xiuwei Zhang**
15:00	CellPace: a generative framework for modeling continuous single-cell dynamics **Chen Su**

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REGSYS

Tuesday, July 14; International Ballroom East

Time	Title and Speaker
15:20	An interpretable model of the cell-type-specific Protein-RNA regulatory relationship **Donglu Bai**
15:40	R4ST: A Reference-guided Graph-generative Model for Robust Reconstruction of Spatial Transcriptomic Profiles **Mingyue Wei**
16:40	TBD
17:20	MARCA: Detecting Micro-compartment Anchors in 3D Genome utilizing Spatial Relationships **Ferhat Ay**
17:40	HiC-LEGO: A Modular Graph-Based Architecture for High-Resolution 3D Genome Reconstruction from Hi-C Data **Abhishek Pandeya**

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iSCB Student COUNCIL
SYMPOSIUM 2026
12 July 2026, Washinghton, DC, USA

STUDENT COUNCIL SYMPOSIUM

Online schedule found here.

Sunday, July 12; Room 9–10 Combo

Time	Title and Speaker
09:00	Opening Remarks
09:15	TBD
10:15	Similarity-based counts weighting improves differential T cell clonotype abundance analysis **Thomas C. Smits**
11:00	3R-Fold: Enhancing RNA Secondary Structure Prediction via Retrieval-Augmented Self-Representation **Chaimae Toubali**
11:15	Benchmarking LLMs on SMILES-Based Metabolite Property Prediction and Identifying Structural Determinants of Prediction Success **Youngchan Kim**
11:30	EMBL-EBI Competency Hub as a Tool to Navigate Career Pathways **Daria Sokolova**
11:45	Sex-dependent cell-type specific transcriptional responses to sleep deprivation caused by mutations in the autism gene Shank3 in early development **Caitlin Ottaway**
11:50	The Shank3ΔC mutation differentially impacts the molecular response to sleep deprivation across development **Elliot Wald**

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ISCB Student Council
SYMPOSIUM 2026
12 July 2026, Washinghton, DC, USA

STUDENT COUNCIL SYMPOSIUM

Sunday, July 12; Room 9–10 Combo

Time	Title and Speaker
11:55	Therapeutic Target Discovery for Rare Diseases via Machine Learning Integrating GWAS and TWAS
12:00	Bioinformatics Analysis of Circulating Tumour DNA Sequencing Data: A Promising Approach to Monitor Prostate Cancer Progression **Samira Rahimirad**
12:05	DrugAgent: Explainable Multi-Agent Large Language Model-based Reasoning for Aggregating Heterogeneous Biomedical Evidence **Yoshitaka Inoue**
12:20	Group Photo
12:30	Poster Session
14:00	drGT: Interpretable Drug Response Prediction with Attention-Guided Gene Attribution on a Drug-Cell-Gene Heterogeneous Graph **Yoshitaka Inoue**
14:15	Hypothesis-Driven Analysis of Gut Microbiome in Subclinical ASCVD **Shreya Chindepalli**
14:20	Using Large Language Models to Automate Cancer Gene Prioritization for 898 Cancer Subtypes from the OncoTree Ontology for Exploration in cBioPortal **Suhasini Lulla**
14:25	Role of Genomics and Proteomics in disease diagnosis **Sara Munir**

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ISCB Student COUNCIL
SYMPOSIUM 2026
12 July 2026, Washinghton, DC, USA

STUDENT COUNCIL SYMPOSIUM

Sunday, July 12; Room 9–10 Combo	
Time	**Title and Speaker**
14:30	ISCB-SC Talk
15:00	Panel Discussion
16:15	TBD
17:15	Closing Remarks

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SYSMOD

Online schedule found here.

Tuesday, July 14; Jefferson West

Time	Title and Speaker
11:00	Welcome and introduction to SysMod COSI
11:20	From Single-Cell Decisions to Tissue-Scale Disease: A Multiscale Modeling Framework **Shayn Peirce-Cottler**
12:10	VAPOR: A variational autoencoder with transport operators to disentangle latent dynamics in single-cell and spatial transcriptomics data **Daifeng Wang**
12:30	Mechanistic ODE Modeling of MAPK/AKT Signaling Reveals Scheduling-Dependent Control of Persister Dynamics in BRAF-Mutant Melanoma **Ethan Wang**
12:40	Computational pipeline elucidates how single-cell, lymphocyte motility behaviors drive B-T interactions that mediate the antibody response. **Nikita Sivakumar**
14:20	Predicting microbial metabolic function for therapeutic development **Jason Papin**
15:10	Metabolic signatures of immune checkpoint inhibitor response in gynecologic cancers: Insights from flux balance analysis **Gideon Idumah**
15:30	SPECIMEN powered by refineGEMs for streamlined automated high-quality genome-scale modeling **Andreas Dräger**
15:50	Temporal competence windows govern four discrete phases of neural progenitor fate commitment in a multi-layer ODE framework of CNS development **Batuhan Safa Kar**

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SYSMOD

Tuesday, July 14; Jefferson West

Time	Title and Speaker
16:40:00	Decoding Anti-TNF Therapy Outcomes from Pre-Treatment Single-Cell Data via Network-Based Perturbation Modeling **Matthew Leipner**
17:00:00	PIMENTO: a Physics and bIology-inforMed Neural network for dynamic inference of gene regulatory networks to model plant response to biotic stresses **Silvia Bottini**
17:20:00	Mechanistic Modeling of rTMS-Mediated Quiescent Cell Targeting in Glioblastoma **Chitransh Dave**
17:40:00	Closing Remarks and Poster Awards

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TECH TRACK

Online schedule found here.

Monday, July 13; Monroe	
Time	**Title and Speaker**
11:00	Targeted genomic language models paired with multi-agent AI for biomedical discovery **Ali Rahnavard**
11:20	Leveraging LLMs for accurate and confidence calibrated cell type and state identification **Parashar Dhapola**
12:00	Decoding IBD Risk: A Transformer-Based approach to Predict Allelic Regulatory Impact of IBD associated Variants Across Multiple Cell Lines
12:20	dkNET Computational Core — Cloud-native, Collaborative AI/ML and Literature Intelligence for Biomedical Research **Chen Li**
14:20	AI and Quantum Computing for Healthcare and Life Sciences **Filippo Utro**
14:40	Integrated Pathway/Genome/Omics Informatics in Pathway Tools and BioCyc **Peter Karp**
15:20	Genome-wide detection of human 5′ UTR variants that impact protein translation **Matthieu Chaldebas**
15:40	Scaling Protein Domain Classification: Advances in CATH and TED **Christine Orengo**
16:40	Seqera Co-Scientist: The Intelligent, Collaborative Partner for Scalable Bioinformatics **Esha Joshi**
17:00	Nucleotide Transformer v3: A Scalable AI Engine for Precision Agriculture and Genomic Design **Gurnek Singh**
17:40	Burak Multiomics: A Sovereign Bio-Computational Framework for Predicting Metabolic Failure via the 8-Layer Sovereign Logic

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TECH TRACK

Tuesday, July 14; Monroe	
Time	Title and Speaker
11:00	Pathogene-on-FHIR: Making Pathogen Genome Data Interoperable with Patient Health Records **Sonika Tyagi**
11:20	The NIAID Data Ecosystem: A centralized platform for discovering infectious and immune-mediated disease resources **Chunlei Wu**
11:40	10x Genomics: Building Scalable, open analysis for the next-generation in situ platforms **Roger Zhu**
12:00	An interactive R/Shiny Single Cell Visualization Application **Geetha Priyanka Yerradoddi**
12:20	Enabling Agentic Systems for Life Science Discovery

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TEXT MINING

Online schedule found here.

Monday, July 13; Jefferson West

Time	Title and Speaker
11:00	Reading Science at Scale: AI for Biomedical Discovery and Trustworthy Knowledge **Halil Kilicoglu**
11:40	eGoT: Enhanced Graph-of-Thoughts for Multi-Hop Knowledge Retrieval and Hypothesis Generation in Biomedicine **Nihar Sanda**
12:00	DrugAgent: Explainable Multi-Agent Reasoning for Aggregating Heterogeneous Biomedical Evidence **Yoshitaka Inoue**
12:20	MedHopQA: Benchmarking Multi-Hop Reasoning in LLM-Based Biomedical Question Answering with a Disease-Centered Corpus **Rezarta Islamaj**
12:30	Outcome-aware feature generation from unstructured metadata using LLMs for cross-study transcriptomic analysis **Christine Hou**
12:40	KLaR: Fusing Knowledge Graphs and Language Models for Biomedical Target Discovery **Yinghui Jiang**
14:20	FAIR-SMART: Enabling FAIR Access to Supplementary Materials for Biomedical Text and Data Mining **Chih-Hsuan Wei**
14:40	Temporally annotated textual time series from PubMed Open Access clinical case reports **Sayantan Kumar**

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TEXT MINING

Monday, July 13; Jefferson West

Time	Title and Speaker
15:00	Transferring semantic knowledge from scientific literature to metadata for comprehensive annotation of hundreds of thousands of public human and mouse biomedical datasets **Mansooreh Ahmadian**
15:20	GenPTM: A Generalizable Framework for Protein Post-Translational Modification Information Extraction from the Scientific Literature **Shovan Bhowmik**
15:30	Optimizing transformer-based language model performance for named entity recognition of cell phenotypes in literature. **LaToya McDonald**
15:40	Poster teasers
16:40	AutoPCR: Automated Phenotype Concept Recognition by Prompting **Yicheng Tao**
17:00	Trustworthy literature agents for biomedical discovery: grounding, reproducibility, and evaluation

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TRANSMED

Online schedule found here.

Wednesday, July 15; International Ballroom West

Time	Title and Speaker
11:00	TransMed Opening
11:10	How can AI agents help you advance biomedicine? **Kuan-lin Huang**
11:50	Large-scale clinical sequencing reveals the pan-cancer genetic and clinical landscape of telomere maintenance mechanisms **Harshit Sahay**
12:10	Routine Clinical Time Series Predict Cancer Adverse Events **Chenlian Fu**
12:30	Validating PREDICT Breast v4.1.1 across racial groups and genomic risk strata in a Southern California cancer registry **Devanshi Pratiher**
12:50	Surveying alternative splicing in non-small cell lung cancer identifies unique histological and population-specific differences
14:20	PORTALS: Integrating Plasma Proteomics and Clinical Features via Tabular Foundation Models for ALS Survival Prediction **Yurui Chen**
14:30	Brain Ontology Expression (BRONTE) graph neural network model uncovers disease-linked spatial variation in gene regulation across the human brain **Rachel Melamed**
14:50	Computational prediction of ARSA variant severity to support newborn screening: advances revealed in the CAGI 7 ARSA challenge **Steven Brenner**

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TransMed

TRANSMED

Wednesday, July 15; International Ballroom West

Time	Title and Speaker
15:10	Discovering new molecular targets directly from electronic health records in neurology and oncology, using network models of drug off-target effects **Jennifer Wilson**
15:30	From Variants to Therapy: A Multi-Agent Framework for Traceable Genomic and Regulatory Reasoning in Precision Medicine **Maaly Nassar**
15:50	FIG: Fairness through Intersectional Grouping, A Post-Processing Framework for Domain-Specific Bias Mitigation **Yang Dai**
16:40	Drug-wide association studies as a tool for drug discovery and methodological improvement **Sonja Kleper**
16:50	Integration of eye imaging with multi-omics data to explore targets for eye rejuvenation **Roberto Bonelli**
17:00	Integrative Single-Cell and Spatial Omics Reveal Temporal-Spatial Dynamics of Fibroblast Subtypes during AKI-to-CKD Transition **Mengying Xia**
17:10	TBD
17:50	TransMed closure

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VARI

Online schedule found here.

Wednesday, July 15; Jefferson East

Time	Title and Speaker
11:00	VarICOSI Session Introduction
11:10	Advances in computational variant impact prediction: findings from the Critical Assessment of Genome Interpretation, seventh edition (CAGI 7) **Steven Brenner**
11:20	Mapping, manipulating, and modelling regulatory DNA to link disease variants to functions **Jesse Engreitz**
12:00	PPI-seq: A Massively Parallel System to Decode Genetic Variant Impacts on Protein Interactions **Justin Delano**
12:20	High content phase separation profiling of genetic variants reveals principles of complex heredity in disease **Nidhi Sahni**
12:40	Deconvolving mutation effects on protein stability and function with disentangled protein language models **Kerr Ding**
12:50	Position-dependent variant effects reveal importance of context in genomic regulation **Sambina Islam Aninta**
14:20	TBD
15:00	Machine Learning-Based Deconstruction of Polygenic Risk Scores for Identification of Age-Dependent Genetic Effects **Frederick Kamanu**

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VARI

Wednesday, July 15; Jefferson East

Time	Title and Speaker
15:20	Genetic data-driven prioritization of druggable transcription factors in Alzheimer's Disease **Alena Orlenko**
15:30	Short-Context gLM Training for Long-Range Variant Effect Prediction **Megha Hegde**
15:40	Resolving Variants of Uncertain Significance at Scale with Calibrated Computational and Experimental Evidence **Predrag Radivojac**
16:40	Interpreting indel mutational signatures in 6,975 tumors based on more informative indel classification schemes **Steven G. Rozen**
16:50	Allele-aware spatial RNA-seq simulator enables comprehensive benchmarking of copy number variation analysis across methods and spatial patterns **Jiamu Qiao**
17:00	PGViS: Personal Genome Variant interpretation Score for lung cancer genomes **Pallavi Surana**
17:10	Panel Discussion: Current challenges and opportunities for computational variant interpretation
17:50	Closing Remarks

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WEB:
WORKSHOP ON EDUCATION FOR BIOINFORMATICS

Online schedule found here.

Wednesday, July 15; Cabinet	
Time	**Title and Speaker**
11:00	AI in Bioinformatics Training Hackathon Masterclass
12:00	Breakout Session 1
14:20	Breakout Session 2 Peer Share & Test Drive
15:30	Implementing AI-Driven Curriculum with Rigor:
16:40	Audience share/Wrap-up Session - Finalizing a set of “Best Practices”

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OTHER ACTIVITIES AT ISMB

SUNDAY, JULY 12, 2026

Welcome Networking Reception with Exhibitors

Time: 19:30 – 21:00

Location: Columbia

MONDAY, JULY 13, 2026

Embassy Row Morning Walk/Run

Time: 6:15

Location: Meet on Terrace Level

Cost: $15 per person

TUESDAY, JULY 14, 2026

Rock Creek Trail Morning Walk/Run

Time: 6:15

Location: Meet on Terrace Level

Cost: $15 per person

Success Circles

Time: 18:00 – 19:30

Location: International Terrace

Cost: $10

WEDNESDAY, JULY 15, 2026

Beetlejuice!

Time: 19:30

Location: The National Theatre

Cost: $46.75 Balcony or $63.75-$89.25 Mezzanine

⚡ Grab your discounted tickets here!

Social Networking for Network Biologists

Time: 19:00 – 21:00

Location: City Tap House - Dupont

Cost: $25

SOLD OUT

THURSDAY, JULY 16, 2026

The Conference of Super-Errors

Time: 13:00 – 14:20

Location: Lincoln West

Cost: Free

SOLD OUT

ISMB 2026
WASHINGTON, DC
JULY 12–16

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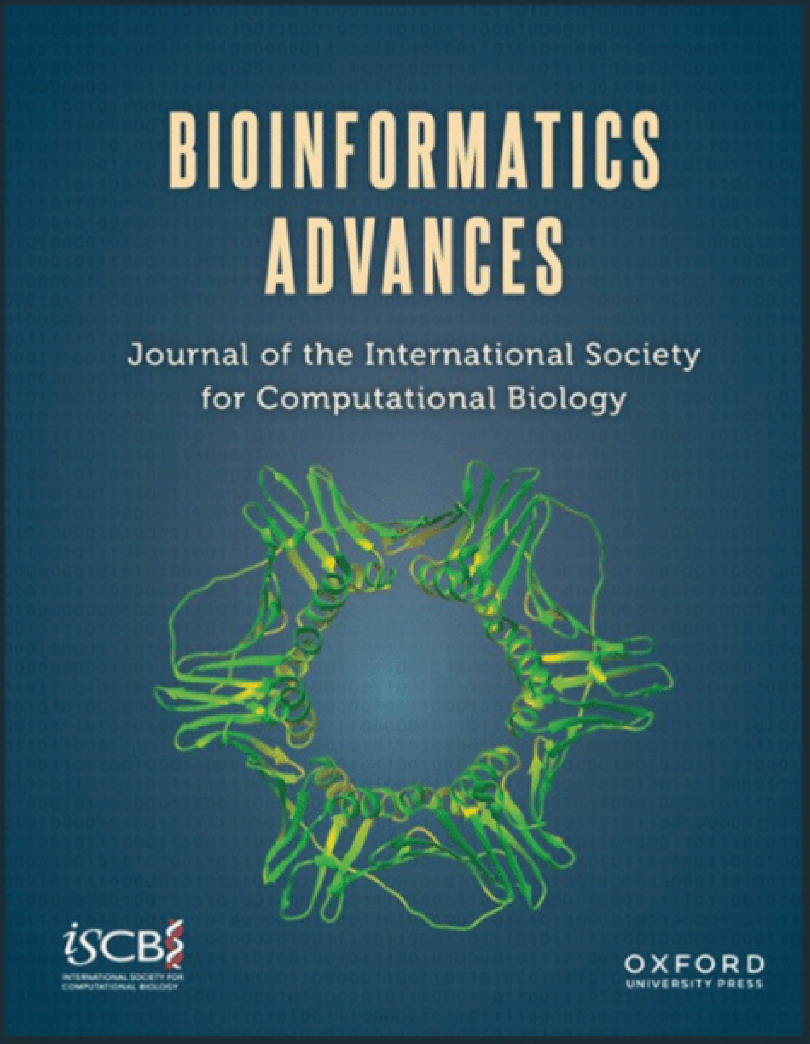
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Sep 28 – 30
Omaha, Nebraska
20% Discount

NOV 2026

ISCB-LATAM SOIBIO SPBBC 2026

November 9 – 11
Lima, Peru
20% Discount

BIOINFO/GIW ISCB-ASIA 2026

November 17 – 20
Seoul, Korea
15% Discount

3DBIOINFO 2026

November 25 – 27
Rome, Italy
Discount TBD

JAN 2027

PSB 2027

January 3-7, 2027
Kohala Coast, HI
$50 USD Discount

MORE EVENTS

Click *here* to view the full upcoming events calendar!

ISCB MEMBERS GET DISCOUNTS ON THESE CONFERENCES!

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SAVE THE DATE

ISMB
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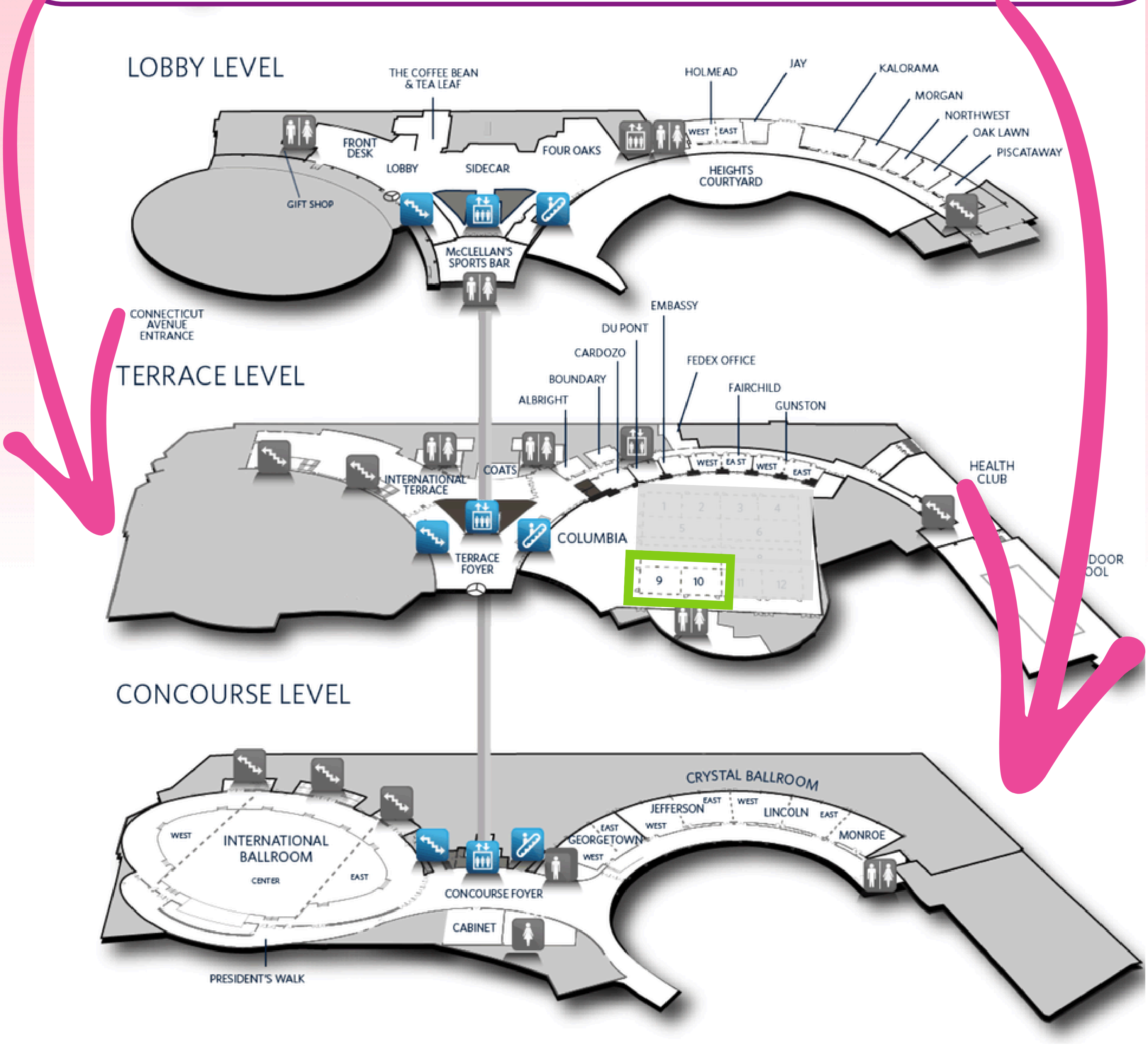
2027

July 18–22 Copenhagen

ISMB 2026 VENUE MAP

All ISMB 2026 sessions and activities will take place in the Terrace and Concourse Levels



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Sustainability Initiatives

Hilton

OUR MISSION

At Washington Hilton, our team has a vested interest in operating efficiently while delivering an exceptional experience for our guests. Living sustainably is imperative to our business, and a cornerstone of our commitment to guests, partners and our community. We are proud members of Destination DC's Sustainability District.

U.S. DEPARTMENT OF ENERGY SEP® PLANTINUM RATING

In 2015, Washington Hilton achieved the U.S. Department of Energy's Superior Energy Performance (SEP) certification. Hilton Worldwide is the first hospitality company to achieve the certification.

LIGHTSTAY

Washington Hilton is able to measure and analyze sustainability data across multiple utility and operational indicators:

Energy
Water
Waste

Sustainability Calculator

The Lightstay Sustainability Calculator allows planners to input meeting details to measure the impact of a meeting or an event.

FOOD & BEVERAGE

ORCA Food-Waste Disposal

- First Hilton Hotel to implement ORCA as an on-site waste management system. ORCA can "digest" up to 2,400 pounds of food waste per day and turns food waste into environmentally-safe water within 24 hours. The hotel disposes 68,000 lbs. per year.

Food Donation

- Washington Hilton donates approximately $100K of food per year.

CONSERVE, REUSE, & RECYCLE

CONSERVE

- Building Automation System for Public Space AC/Heating system.
- Low consumption shower heads, faucets, and toilets.
- Guest rooms utilize Compact Fluorescent Light (CFL) and LED bulbs.
- All meeting room LED lights are turned off when vacant.

REUSE

- Guest communication that provides the option to keep bed linens and bath towels for the length of their stay.

RECYCLE

- Clean the World soap recycling.
- Recycle program for paper, plastic, tin, glass, and aluminum.
- Cardboard compactor utilization.

Washington Hilton

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