# ISCBNEWSLETTER

SUMMER 2023 | ISSUE 02

## NEWSLETTER

## CONFERENCE PROGRAMME

## COSI SCHEDULES

***Featuring the ISMB/ECCB 2023 Conference Programme***

# A NOTE FROM
# ISCB'S CEO, DIANE KOVATS

*Dear ISCB Members & Colleagues ,*

I am thrilled to welcome you all to Lyon, France and through these pages of our latest ISCB Newsletter and ISMB/ECCB 2023 Conference programme. If you are joining us virtually, welcome to the ISCB Nucleus platform that allows us to connect, inform, and collaborate with 2400+ of your fellow attendees.

2023 has shaped up to be a year for the record books. As we enter ISCB's 26th year, we do so marking our highest membership on record, closing this month with over 3,600 members and the forecast is for continued growth. Members are the building blocks of scientific societies so it is with great appreciation for all that I say a sincere thank you for being a part of ISCB.

Throughout the year, ISCB has been steadfast in its mission to provide valuable resources and opportunities to our members. In order to do so we need to gain a better understanding of our community at large and members. To do this, we released our membership survey to help us improve our services and better understand the needs of our members. If you have not filled out the survey, please visit the link below. Your opinion matters to us, and we want to ensure that we are meeting your expectations and providing the best possible experience.

Click here to take the survey

Pulling from lessons learned and feedback from members and conference attendees, 2023 saw the continued improvement of the ISCB Nucleus, the center for science, collaboration, and training. We continued its reach and saw an increase in global participation. In 2023, to date, 22 webinars and trainings have been hosted live on ISCB Nucleus, a now fully open access resource. Please take a moment to visit ISCB Nucleus to see the dynamic and vibrant platform hosting webinars, trainings, networking, collaboration, and so much more, all available at your fingertips. This one stop shop offers regular updates and fresh information to keep you engaged and informed. The constantly evolving platform and content provides you with the latest developments, cutting-edge research, insightful interviews, thought-provoking webinars, and much more. Please check it out, and of course, I welcome your feedback.

Looking ahead, ISCB remains committed to supporting and nurturing the next generation of computational biologists. Our education and training initiatives, including webinars, workshops, and mentorship programs, are designed to equip aspiring scientists with the knowledge, skills, and networks needed to thrive in this dynamic field. Together, we will continue to foster an environment that encourages curiosity, innovation, and excellence.

As we navigate the future, we are also keenly aware of the need to address issues of equity, diversity, and inclusion within our community. ISCB is dedicated to promoting a welcoming and inclusive environment that values and embraces individuals from all walks of life. We are actively working to ensure that opportunities and resources are accessible to everyone, regardless of their background or circumstances.

## WELCOME BACK TO OUR MEMBERSHIP!

## ISCB'S CEO, DIANE KOVATS

ISMB/ECCB 2023 continues to offer a hybrid experience for those unable to attend Lyon in person. It is our goal and hope that you find both in person and hybrid experiences fully immersive, easy to navigate and unbeatable. Whether you attend in-person or virtually, conference attendees get exclusive access to the content well beyond the conference days!

As always, thank you for your continuous support of our Society. I would like to extend my deepest gratitude to the ISCB leadership, staff, volunteers, and members for their unwavering support and dedication. It is through your collective efforts that ISCB remains at the forefront of computational biology, driving the scientific advancements that shape our world. We continue to grow, supporting one another as we work towards our goal to be the leading professional society for participants in the field of computational biology and bioinformatics, serving researchers, practitioners, technicians, students, and suppliers worldwide. Thank you for sticking with us and we hope you enjoy everything ISMB/ECCB 2023 has to offer, especially in Lyon, the Gastronomy hub of France!

Whether you are attending ISMB/ECCCB 2023 in-person or virtually, we hope you will attend the ISCB Town Hall, Monday, July 24 (12:45PM - 1:45PM CEST). During this session, you will get to learn about all programs as well as new plans and initiatives at ISCB! We will also celebrate some of our Society achievements. I hope to see you there!

I invite you all to actively engage with ISCB, share your ideas, and take advantage of the diverse opportunities available to you. Together, we will continue to push the boundaries of the field, and make a lasting impact on this society.

I look forward to meeting many of you here in Lyon and having an exemplary ISMB/ECCB 2023.

Sincerely,

Diane E. Kovats, CAE, CMP
Chief Executive Officer

## HOW YOU CAN SUPPORT ISCB

Dontate Now!

### ANNA TRAMANTANO FUND

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

### STUDENT FELLOWSHIP CAMPAIGN

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

### GENERAL RESOURCES FUND

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

### SPONSOR MEMBERSHIP DUES OF MEMBERS FROM DEVELOPING COUNTRIES

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

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

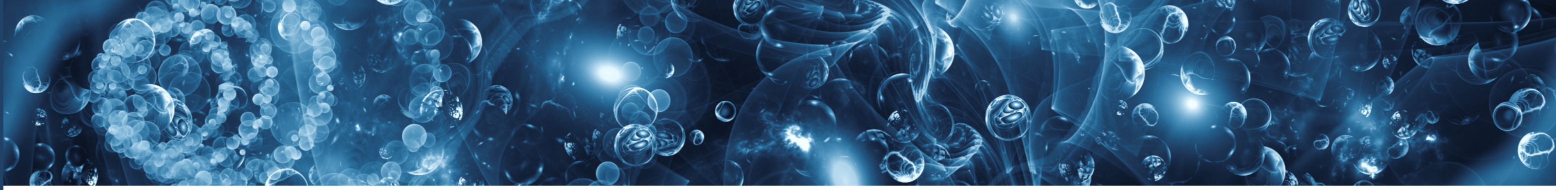
# 2023 ISCB INNOVATOR AWARD
# DANA PE’ER

*The annual ISCB Innovator Award recognizes a scientist who is within two decades of completing her or his graduate degree and has made profound contributions to the field of computational biology or bioinformatics. The 2023 ISCB Innovator Award winner is Dr. Dana Pe’er, Chair and Professor of Computational and Systems Biology at the Sloan Kettering Institute and Howard Hughes Medical Institute Investigator. She will receive her award and deliver a keynote address at the 2023 Joint ISMB/ECCB meeting.*

## Dana Pe’er:
## *From Mass Cytometry to Plasticity*

Dana Pe’er has cultivated her love of mathematics since her childhood in Israel, recalling lessons from her father that revealed the beauty of mathematical logic[1]. As a high school student, she had her first hands-on experience in the lab of Idan Segev at the Hebrew University of Jerusalam, where she used mathematical modeling to understand subthreshold oscillations in neurons. This project exposed Pe’er to mathematical applications for biological questions, planting seeds for her future research interests. Although Pe’er had contemplated a degree in neurobiology, her curiosity in genomics and bioinformatics was kindled after listening to a mesmerizing talk by Eric Lander describing the onset of the human genome project. She completed her bachelor’s degree in mathematics and master’s and Ph.D. degrees in computer science at Hebrew University. Pe’er’s Ph.D research mentor Nir Friedman revealed to her the power of statistical machine learning in interpreting complex biological data. Pe’er also came to appreciate the importance of having a strong foundation in abstract biological concepts through her collaboration with fellow graduate student Aviv Regev. After graduate school, Pe’er pursued her postdoctoral studies in the lab of George Church at Harvard University, where she learned to wrestle with the ambiguities of wet lab biology. Her perspective also shifted from asking, “What type of computation can I do for this data?” and learned to ask instead, “What data do I need to answer a biological question I am passionate about?”1 Pe’er also gained invaluable informal mentorship during her PhD and postdoc from Daphne Koller, who not only instructed her in the importance of good modeling assumptions, but also provided critical career advice as she prepared to become an independent researcher. Pe’er launched her own lab in 2006 at Columbia University in the Department of Biological Sciences and Systems Biology.

During her postdoc, Pe’er realized the power of single cells and that inter-cell variability can be exploited for regulatory circuit reconstruction. Single cell approaches accelerated as she launched her own lab at Columbia University in part through pioneering research with Garry Nolan, for which she developed critical aspects of the computational foundation for single-cell data analysis. These studies opened the floodgates of data science to immunologists and Pe’er was uniquely positioned to take on these studies at the juncture of computational biology and immunology. Pe’er introduced the single-cell field to large-scale analysis with the conceptual framework in which cell phenotypes are constrained to geometric manifolds corresponding to landscapes of possible cell states. This established a now-dominant paradigm that models cell state transitions in development and disease as continuous processes rather than discrete toggles. By leveraging asynchrony in cell states, she demonstrated that it is possible to infer continuous pseudotime trajectories, which provide dynamics from a single sample and generated fundamental knowledge



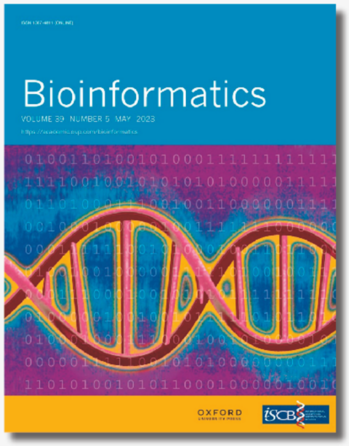
in numerous development, immunology, cancer, and regenerative medicine studies. Pe'er also developed the neighbor-graph-based representation of the phenotypic manifold that serves as the field standard, and guided her development of widely used methods for identifying cell types, visualizing the manifold, deriving pseudotime trajectories, identifying lineage bifurcations and quantifying developmental potential.

As Pe'er became an established PI, she was more involved in the greater computational biology community, including serving as a founding member of the Human Cell Atlas (HCA) Project. She played pivotal roles in formulating the vision of the HCA and has been a key driver of the computational direction of the HCA, especially through her role as co-chair of the Analysis Working Group within the HCA. In 2016, Pe'er moved her lab to the Sloan Kettering Institute (SKI), where she became Chair of the Computational and Systems Biology Program and Scientific Director of the Alan and Sandra Gerry Metastasis and Tumor Ecosystems Center. In this new home, she said, "My focus on biology completely changed. I was in a new environment with great peers, like Sasha Rudensky and Scott Lowe, who also became my teachers." Pe'er was also given the responsibility of developing the Single Cell Research Initiative at SKI, which has flourished by harnessing the power of single cell analysis to address fundamental cancer and immune system questions. Pe'er's own team has published seminal findings in cancer research that revealed the complexity of the tumor immune microenvironment and has nurtured her fascination with cell plasticity. She said, "I want to understand how cells work in tissues. Plasticity helps cells respond to their neighbors, and during development, cells lean on their plasticity to form tissues." Some of Pe'er's most recent work has shown how the plasticity of tumor cells allow them to hijack and mimic programs of embryonic organogenesis, which ultimately drives metastasis. Although Pe'er gets excited about tackling biology questions, she still loves being in the trenches of algorithm development and troubleshooting technical problems. She considers questions related to plasticity to be particularly well-suited to computational approaches and said gleefully, "These questions require so much math, and math is my playground."

In 2022, Pe'er was awarded an appointment as an HHMI investigator in recognition of fundamental studies on cellular plasticity and how it shapes many biological processes. This recognition validates the broader impacts of single cell studies and solidifies Pe'er's role as a leader of the field. Pe'er's impressive publication record and numerous awards further highlight the many contributions she has made to computational biology, including her recognition with the 2014 ISCB Overton Prize. Pe'er feels deeply honored to be recognized with the 2023 ISCB Innovator Award, particularly because it comes from her computational biology peers. Pe'er's infectious enthusiasm for current research projects is certain to lead to many new algorithms and insights in the future.

# Discover the ISCB Journals at OUP

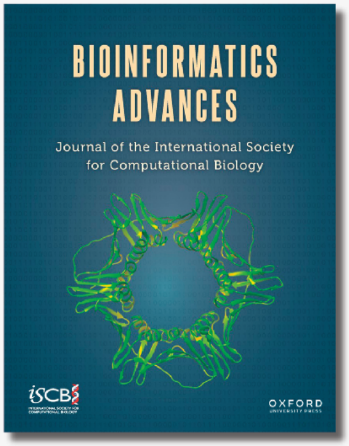
## Bioinformatics



*Bioinformatics* is now a fully open access journal that publishes scientific papers and review articles on new developments in bioinformatics and computational biology. ISCB members will enjoy a discount on publishing fees. The journal now accepts Application Notes of 4 pages in length.

**academic.oup.com/bioinformatics**

## Bioinformatics Advances



*Bioinformatics Advances* is a fully open access, peer-reviewed journal published jointly by OUP and by the International Society for Computational Biology. ISCB members will enjoy a 20% discount on publishing fees. The Editors-in-Chief, Alex Bateman and Thomas Lengauer, are at ISMB/ECCB and would be happy to talk about your research with you.

**academic.oup.com/bioinformaticsadvances**

OXFORD
UNIVERSITY PRESS

iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

# MARK GERSTEIN

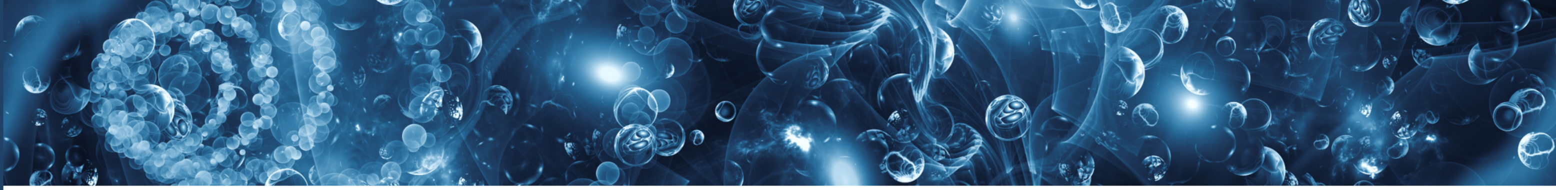
*ISCB recognizes the outstanding contributions by a leader in the fields of computational biology and bioinformatics annually with the Accomplishments by a Senior Scientist Award. This award is the highest recognition conferred by ISCB to a scientist who has made notable research, education, and service contributions to the field and to ISCB. Mark Gerstein, Albert L. Williams Professor of Biomedical Informatics, Molecular Biophysics and Biochemistry, Computer Science and Statistics and Data Science at Yale University, New Haven, CT, is the 2023 recipient of the ISCB Accomplishments by a Senior Scientist Award. He will be presented his award and deliver a keynote address at the 2023 ISMB/ECCB conference in Lyon, France.*

## Mark Gerstein:
## *From Hacker to Architect of Computational Biology*

Mark Gerstein was born in New York City and recalled a childhood where his interests in science and mathematics were nurtured and encouraged. As a young child, he fondly remembers becoming engrossed in a science project constructing a model of the DNA double helix, foreshadowing his future interest in biological macromolecules. Gerstein's intellectual curiosity led him to double major in physics and the history of science at Harvard College. Although he enjoyed physics and was curious about the nascent field of computer science, Gerstein ultimately wanted to pursue a PhD in a growth area of science. He recalled, "I really wanted to look at the confluence of biological science and computation." This was at a time when the structures of large macromolecules were just beginning to be resolved using computers. Gerstein was encouraged to pursue these interests at Cambridge University through his conversations with Martin Karplus and Don Wiley at Harvard. Their recommendation connected to his ongoing fascination with Cambridge given its storied place in scientific history, including Watson and Crick's discovery of the DNA double helix and the development of the theory of computation by Cambridge alumnus Alan Turing. Gerstein was given a Herschel-Smith Scholarship to pursue his PhD at the Chemistry Department and the Medical Research Council (MRC) in Cambridge, during which time he worked with computational chemist Ruth Lynden-Bell and protein biophysicist (and 2015 ISCB Accomplishments by a Senior Scientist Award Winner) Cyrus Chothia. His project involved developing computer simulations of liquids, including water, and their interaction with proteins, which laid the foundation for his future postdoctoral studies. Gerstein also came to appreciate that his time at MRC brought him into contact with many gifted scientists, including future Nobel Prize winners such as Venkatraman Ramakrishnan and Richard Henderson.

Gerstein moved on to postdoctoral studies in 1993 under the mentorship of future Nobel laureate Michael Levitt at Stanford University, where he used his newly minted skills in modeling to study macromolecular geometry and simulate water surrounding proteins. Gerstein tapped into his computer hacking passion and brought LINUX to Levitt's lab. He recalled, "Not only was Levitt a gifted scientist, but he was also a computer hacker." Levitt's mentorship helped Gerstein realize that working at the interface of biology and computation was an exciting and viable career path. He also got to know Russ Altman during his post-doc and ultimately attended the first ISMB in 1993. Gerstein said, "I started to see there were a lot of things you could do with these large biological datasets."

Gerstein's productive postdoc years were critical to launching his career as an independent investigator. He was hired in 1997 as an assistant professor at Yale University. He was one of the first computational biology faculty members hired by a large research



university, and he had anticipated building a lab that studied macromolecular modeling. Early projects included simulation and classification of protein motions using a database framework.  He was also intrigued by the emerging area of genome sequencing. This led Gerstein to study structural genomics and build up his research program with collaborators at numerous institutions.  After receiving tenure, Gerstein became interested in human genome annotation and later became deeply involved with ENCODE and related large-scale projects, such as psychENCODE. These interests evolved into several high-impact publications demonstrating that multi-omics data can be reframed as control networks and can be compared to networks in other contexts - for instance, in social relations. These studies have been critical to identifying regulatory sites in genomes and in finding pseudogenes and improving our understanding of genome evolution. Gerstein and his lab were also involved in the 1000 Genomes Project and applied concepts developed from this work to develop tools for more accurate variant interpretation with respect to risks for cancer or neuropsychiatric diseases. His lab now examines many aspects of data science, including the large-scale integration of genomic and phenotypic data, collected by biosensors and images, and the attendant privacy concerns

Gerstein considers his efforts to develop undergraduate and graduate computational biology programs at Yale to be one of his most lasting contributions to the field. He said, “Computational biology is important, and part of making it a field is education.” He has taught his introductory undergraduate computational biology class since 1998, when it began as a ten-student course called “Genomics and Bioinformatics.” He has made every set of lecture slides available online, toward his mission to educate the world more broadly about computational biology.  The course in its current form, called “Biomedical Data Science,” provides students with a range of immersive experiences, including the culminating project in which students analyze a chromosome from the science writer Carl Zimmer’s genome and present their findings to Zimmer in person. Gerstein was also integral to co-founding the Computational Biology Graduate Program at Yale with his colleague Perry Miller over 20 years ago and has watched many of the program’s graduates move into their own faculty positions. Gerstein himself has mentored more than 125 trainees, of which nearly 40 have gone on to start their own labs. Gerstein sees his work as a mentor within and beyond the lab as integral to advancing the field of computational biology. His prestigious publication record reflects the efforts of Gerstein and his trainees, including over 650 publications and 189,000 citations. He is an ISCB and AAAS Fellow and has served on numerous editorial boards, working groups and committees. Gerstein is also a frequent contributor to Op-Ed columns, using his voice to communicate the nuances of data science in various contexts to a wider audience.

Gerstein still gets very excited about computational biology and considers the field to hold a unique place among the data sciences. He said, “In the future, computational biology has an important role for how we go forward with data science. Now people are seduced by big data, but computational biology is a bridge between big data, physical modeling, and a mechanistic description of how biology is actually carried out on a molecular scale.” The same cannot be said yet for big data applications in political or social sciences, and computational biology uniquely feeds human curiosity as to how living things work.

Gerstein is deeply honored to be recognized with the 2023 ISCB Senior Scientist Accomplishment Award, as it is a recognition of his contributions from his peers, and it serves as further validation that the field of computational biology has matured to stand alone and guide the future of data science.

# 2023 OUTSTANDING CONTRIBUTIONS TO ISCB AWARD
## SHOBA RANGANATHAN

*The Outstanding Contributions to ISCB Award recognizes an ISCB member annually for notable service contributions toward the betterment of ISCB through exemplary leadership, education, and service. The 2023 Outstanding Contributions to ISCB Award recipient is Shoba Ranganathan. She will be recognized with this award at the 2023 ISMB/ECCB conference in Lyon, France.*

### Shoba Ranganathan

Shoba Ranganathan is Professor of Bioinformatics at Macquarie University in Sydney, Australia. Ranganathan's research interests include immunoinformatics, transcriptomics, and biodiversity informatics. She is a long-standing ISCB member and has served the greater bioinformatics community for over 20 years. Ranganathan was born and raised in India and received her PhD from the Indian Institute of Technology in Delhi. Her bioinformatics career has spanned the globe through academic and industry positions in India, France, the United States, Singapore, and Australia, which has given her a unique and valuable insight into bioinformatics research and education activities in diverse settings.

Shoba first became a member of ISCB in 1999 when she had a paper accepted at the Pacific Symposium of Biocomputing (PSB). It was here she met some of the pioneers of computational biology, including Russ Altman, Larry Hunter, Subramanian Subbiah, and Keith Dunker, among others. This led to her getting involved with the Asia-Pacific Bioinformatics Network (APBioNet), which was the first regional affiliate of ISCB. Shoba has held numerous leadership roles in APBioNet, including Vice-President (2000-4), President (2005-16), Advisory Board (since 2020), and Board of Directors (honorary) (2016-Present). She has also built ISCB's connections with other international scientific networks, including serving as a founding co-chair of CompMS (joint initiative of ISCB community of special interest (COSI), Human Proteome Organization, and the Metabolomics Society). Shoba is a founding president (2003-2005) of the Association for Medical and Bio Informatics Singapore (AMBIS),ISCB regional affiliate, and a founding member of GOBLET (Global Organization for Bioinformatics Learning, Education and Training) (2012-Present), and hosted their annual meeting at the International Conference of Bioinformatics (InCoB) 2019. She has also been instrumental in facilitating the peer review of InCoB papers in BMC Bioinformatics (2006-present), followed by the addition of BMC Genomics, BMC Medical Genomics, BMC Systems Biology and BMC Cell and Molecular Biology.

Ranganathan has directly served ISCB in various roles, including as a member of the ISCB Board of Directors (2002-2006), on the Education Committee as Co-Chair (2003-4), Chair (2004-5), and current member, and as a Co-Chair of Affiliates Committee (2004-6). She campaigned for parallel sessions at ISMB, which was adopted from 2004, switching from the single session program until 2003. Her service has been pivotal to realizing ISCB's role in promoting bioinformatics education. She recalled, "I moved to Singapore in August 2000, where I put forward a proposal for a Workshop on Education in Bioinformatics (WEB) for ISMB2001, organized by Søren Brunak. I kissed my bank account away signing a personal guarantee for the entire cost of this Special Interest Group meeting. It is gratifying to note that WEB is still on the agenda (as a COSI now), and fortunately, all SIG meetings are underwritten by the ISCB nowadays."

Shoba's service has been driven by a desire to better connect the global bioinformatics community. She still sees a "digital divide" among the bioinformatics communities in the Asia-Pacific, especially in under-resourced areas. Ranganathan has worked to connect these groups through activities with APBioNet, Bioinformatics Australia/ABACBS, ICSB, and other societies, which has been critical to improving bioinformatics education and supporting newly formed bioinformatics societies. Her work in this area has been pivotal in building bioinformatics education and infrastructure in Australia. Her work has been recognized with multiple awards, including the 2018 ABACBS Honorary Senior Fellowship, and as first UNESCO Chair of Biodiversity Informatics in 2006.

Shoba remains deeply involved with the bioinformatics community, especially as she anticipates the global reach of bioinformatics to expand to applications including environmental and health research, synthetic biology and gene modifications, and artificial intelligence for biological knowledge integration and analysis. She is honored and grateful for her recognition with the 2023 Outstanding Contributions to ISCB Award and encourages junior scientists and trainees to seek out varied service opportunities to expand their knowledge and give back to their scientific community.

thank you

*Thank you, Steven Leard, for your many years of leadership as the Director of ISMB.*

*We wish you all the best in your future endeavors.*

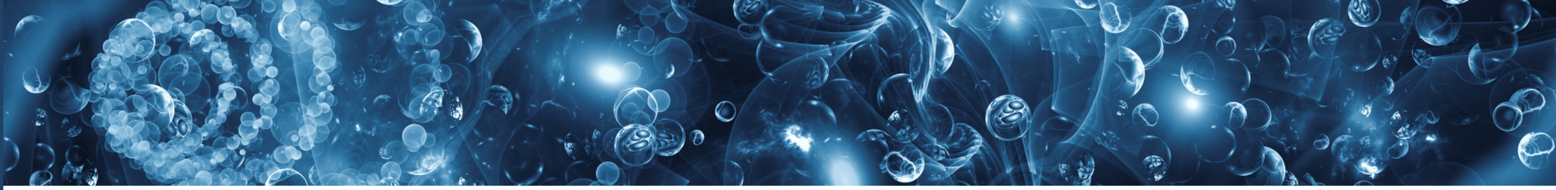
*THE ISCB TEAM*

*The ISCB Overton Prize recognizes early or mid-career scientists as emerging leaders in computational biology or bioinformatics who have made significant research, education, and service contributions to the field. In 2001, the Overton Prize was established to honor the untimely loss of G. Christian Overton, a leader in the field of bioinformatics and a founding member of the ISCB Board of Directors. The 2023 Overton Prize winner is Dr. Jingyi Jessica Li, Professor in the Department of Statistics (primary), Department of Human Genetics and Department of Biomathematics (secondary) at the University of California, Los Angeles (UCLA). She will receive her award and a give a keynote talk at the Joint ISMB/ECCB conference.*

# Jingyi Jessica Li:
## *At the Junction of Biology and Statistics*

Jingyi Jessica Li grew up in Chongqing, China immersed in mathematics. Both of her parents were math majors and went on to become math teachers. Her mother in particular fostered Li's mathematical curiosity, as she believed everyone can learn and grow in mathematical understanding. She said, "My mom thought that math is like exercising. Everyone should do some exercise, even though we are not all top athletes going to the Olympics." Although Li was exposed to math at a young age, she considered it a mature field and wanted to pursue studies in an area that could feed her curiosity. She entered Tsinghua University in China in 2003 and pursued a degree in biology, which was stoked by her interest in the Human Genome Project. She recalled, "It was a very exciting period with all these new technologies that could discover unknown things. I knew that to analyze this data we would need math, so I thought I should use my skills to approach biological questions. That's why I decided to learn more statistics."

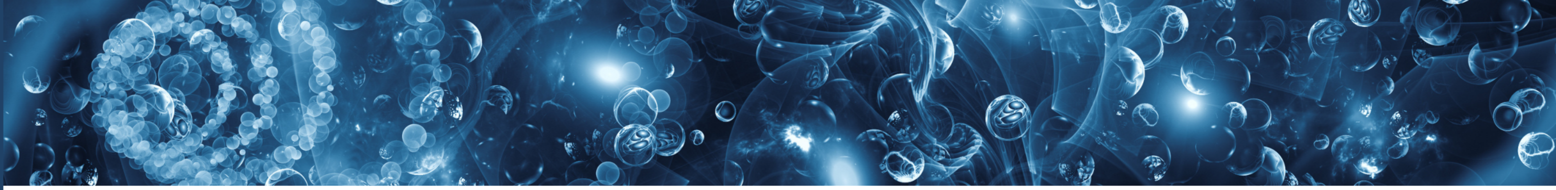
Li pursued her interests in biology and statistics through her Ph.D. studies at the University of California, Berkeley under the joint mentorship of Professors Peter J. Bickel and Haiyan Huang. Bickel is a world-renowned theoretical statistician and Huang is a statistician with expertise in bioinformatics. Bickel and Huang collaborated on bioinformatics projects, which offered Li the benefits of observing and learning from different perspectives in tackling research questions. When she joined their teams, they were both involved in the Encyclopedia of DNA Elements (ENCODE), which was developed as follow-up to the Human Genome Project to identify functional elements of the human genome. These studies generated enormous amounts of data due to the emergence of next-generation sequencing (NGS), leading to technologies including ChIP-seq (combining chromatin immunoprecipitation (ChIP) with NGS) and RNA-seq (using NGS to reveal the presence and quantity of RNAs). Li was interested in how to convert this type of raw data into numbers. She said, "We had not encountered this kind of data in statistics. How do we formulate this information into statistical questions? Sequence data are not numbers, so that forces the question to be important. It was very fun but challenging because we had to gain consensus on how to analyze those data. Everything was open and new." She also recalled that statistics was a more rigid field set in dogma and theorems. Bioinformatics was more open and flexible, and she could use different approaches, such as computer algorithms or statistical models, so long as a biologically interesting question was being addressed.



Li’s fruitful Ph.D. research honed her skills to identify important bioinformatics problems and provide rigorous statistical solutions. Her work was published in high profile journals and resulted in a faculty position in 2013 in the Department of Statistics, with a joint affiliation in the Department of Human Genetics, at UCLA. She was embraced by her new colleagues who mentored her through her first grant proposals, which yielded funding of an NIH RO1 grant on her first attempt. She was also the recipient of an NSF CAREER Award and Sloan Research Fellowship, serving as further recognition of her research contributions and potential as an independent investigator. Li attributes the early success of her young lab to her first graduate student, Wei Vivian Li, who is currently an Assistant Professor in the Department of Statistics at University of California, Riverside. She considered working with (Vivian) Li like a mutual learning process as she was a new PI with a new Ph.D. student. They worked together through the early stages of establishing a research program, including gaining funding, and publishing papers. The success of this relationship set a very high benchmark for future graduate students in Li’s lab and helped Li grow as a mentor. She considers the most critical elements of successful mentorship to be transparency, open communication, finding a suitable project for a trainee, and pairing up students to encourage collaboration and mutual support.

Li’s intellectual curiosity has brought about her interest in improving the statistical rigor of genomic data analysis. She has had a long-standing interest in this area, and as a PI, she has more experience in developing more rigorous and computationally efficient and transparent solutions.  One area where she has improved rigor is the control of false discovery rates (FDRs) in the differential expression (DE) analysis using RNA-seq data, in which a gene’s expression levels measured by RNA-seq are compared between two conditions, and the genes found as differentially expressed are “discoveries” of potential biological interests. Traditional DE analysis assigns a p-value to every gene by assuming every gene’s expression levels follow a negative binomial distribution under each condition. However, this assumption has not held up well when the RNA-seq samples under each condition are not experimental replicates, leading to invalid p-values and an inflated FDR—a co-discovery Li and her postdoc Dr. Xinzhou Ge made in a collaboration with Dr. Wei Li and his postdoc Dr. Yumei Li at UC Irvine. Li was inspired to look at the DE analysis in a different way after she heard a talk by a renowned Stanford statistician Professor Emmanuel Candes who developed the “knockoff filter” to control for false discovery rates when performing variable selection. This ultimately led Li and her team to develop the Clipper, which is a p-value free false discovery rate control method that is generally applicable to high-throughput data (such as NGS data) analysis, including the DE analysis.

Li is deeply involved in serving the fields of bioinformatics and statistics in many capacities, including work as a journal reviewer and editor, grant reviewer, and meeting organizer. She has developed both undergraduate and graduate courses featuring the use of statistics in computational biology, and her use of statistics to quantitate the Central Dogma is so widely recognized that it has been incorporated into the undergraduate textbook Molecular Cell Biology. Li is currently a Helen Putman Fellow at the Harvard Radcliffe Institute writing a statistical methods textbook focused on the selection of methods that are seemingly similar but have fundamental differences. She hopes this book will be a useful tool to genomics researchers as they develop bioinformatics tools. She is also working on a statistical framework to address the evergreen question of whether cells belong to a single continuous trajectory or are discrete types.



Li’s publication record is diverse and highly cited, highlighting her strong record of outstanding interdisciplinary research at the nexus of statistics and biology. Her many awards and grants from the NIH, NSF and other institutions highlight her visionary research, but she is truly grateful for the Overton Prize as it comes from her peers who also work at this unique juncture of science.

## THANK YOU TO OUR GENEROUS DONORS

**Alan Berger**
**Kayode Adeyemi**
**Peter Ebert**
**Donna Slonim**
**Bertrand Marchand**
**Natalie Davidson**
**Stanley Pounds**
**ANUPAM PANDEY**
**Antonio Miguel de Jesus Domingues**
**William McLaughlin**
**Andrew Hill**
**Khalid Mahmood**
**Riccardo Percudani**
**Jeffrey Fisk**
**Mark Mammel**
**Andrew MacBride**
**Andreas Zanzoni**
**Pier Luigi Martelli**
**Jennifer Weller**

## Christian Schoenbach

***1965 - 2023***

It is with great sadness that we share the passing of Dr. Christian Schoenbach with the ISCB community. Schoenbach was a Professor and Chair of the Department of Biology at Nazarbayev University in Kazakhstan at the time of his unexpected passing on April 15, 2023. Schoenbach was also a member of the ISCB Board of Directors, member of the ISCB Affiliates Committee, and past President of the Asia Pacific Bioinformatics Network (APBioNet).

Schoenbach was born on March 10, 1965 in Starnberg, Germany and was the son of Walter Erwin and Anna (Karl) Schoenbach. He completed his undergraduate degree at the State University of New York, Albany, and then completed his Master of Science (Dipl. Biol.) in Biology at Julius-Maximilians University Würzburg, Germany and his Doctoral degree (Dr. rer. nat.) in Genetics (magna cum laude) at Eberhard-Karls University Tübingen, Germany. During his doctoral studies, he focused on the origin , evolution and function of MHC (major histocompatibility complex) genes, in primates. His early career as an independent researcher brought him to Japan in 1993 as a fellow through a special exchange program offered by the Japanese-German Center in Berlin. It was during his time as a postdoc at the University of Tokyo that his interest in human MHC molecules (aka HLA or human leukocyte antigen), with a particular focus on identifying and characterizing peptides that bind to HLA molecules. In the late 1990’s, Schoenbach became a research scientist in the Bioinformatics and Gene Discovery Program at the Chugai Research Institute for Molecular Medicine in Japan.

Schoenbach was born on March 10, 1965 in Starnberg, Germany and was the son of Walter Erwin and Anna (Karl) Schoenbach. He completed his undergraduate degree at the State University of New York, Albany, and then completed his Master of Science (Dipl. Biol.) in Biology at Julius-Maximilians University Würzburg, Germany and his Doctoral degree (Dr. rer. nat.) in Genetics (magna cum laude) at Eberhard-Karls University Tübingen, Germany. During his doctoral studies, he focused on the origin , evolution and function of MHC (major histocompatibility complex) genes, in primates. His early career as an independent researcher brought him to Japan in 1993 as a fellow through a special exchange program offered by the Japanese-German Center in Berlin. It was during his time as a postdoc at the University of Tokyo that his interest in human MHC molecules (aka HLA or human leukocyte antigen), with a particular focus on identifying and characterizing peptides that bind to HLA molecules. In the late 1990’s, Schoenbach became a research scientist in the Bioinformatics and Gene Discovery Program at the Chugai Research Institute for Molecular Medicine in Japan. During this period, Schoenbach’s interest in immunology exposed him to the nascent field of bioinformatics, and he worked on several projects developing algorithms and databases for molecular immunology. He became a Principal Investigator in the Computational Immunology group at Kent Ridge Digital Labs in Singapore and then went on to be a Research Scientist, and eventually, a Team Leader of the Immunoinformatics Research Team, Advanced Genome Information Technology Research Group; Biomedical Knowledge Discovery Team, Group; Biomedical Knowledge Discovery Team, Bioinformatics Group, at the RIKEN Genomic Sciences Center, Japan. Here, Schoenbach made seminal contributions to large scale genomic projects, including the functional annotation of the full-length mouse cDNA collection as part of the Mouse Gene Encyclopedia Project and the FANTOM Consortium for functional annotation of the mouse transcriptome.

As Schoenbach became a leader in the emerging field of immunoinformatics, he took a position as an associate professor in the Division of Genomics and Genetics, School of Biological Sciences, Nanyang Technological University, Singapore in 2009, and then became a professor at the Department of Bioscience and Bioinformatics, School of Computer Science and Systems Engineering, Kyushu Institute of Technology, Japan in 2010. Throughout his time in Japan and Singapore, Schoenbach became more engaged with the greater computational biology community and led efforts to organize APBioNet's annual flagship conference, International Conference on Bioinformatics (InCoB), in Tokyo in 2010, from when he was elected to the APBioNet Executive Committee, serving as Vice-President (Conferences) from 2012-16 and as President 2016 to 2018. His leadership contributed significantly to making InCoB one of the leading bioinformatics conferences in Asia.

Following the passing of his Kyushu Institute of Technology mentor and guide, Prof. Akinori Sarai in 2013, Schoenbach accepted a Professorship of Systems Biology and Bioinformatics at the Nazarbayev University, Kazakhstan.

He returned to Japan as Professor at the International Research Center of Medical Sciences, Graduate School of Medical Sciences, Kumamoto University, Japan, but returned to Nazarbayev University in 2018 as Chair of the Department of Biology in the School of Science and Technology and remained there until his death. He was instrumental in bringing bioinformatics research and instruction to Nazarbayev University and elevating the university's research program.

Throughout his career as an established scientist, Schoenbach worked with various scientific publishers to ensure that research presented at bioinformatics conferences was published in peer-reviewed journals. He considered this a critical aspect of disseminating research findings and worked tirelessly with publishers, editors, and reviewers for many years to publish such bioinformatics materials. His major contributions include serving as Editor of the 1stvolume of Immunomics Reviews, Immunoinformatics in 2008 and Editor-in-Chief of the 1st edition of Elsevier's 2019 Encyclopedia of Bioinformatics and Computational Biology (The A to Z of Bioinformatics) in 2019.

Christian Schoenbach is remembered by his colleagues for his extraordinary work ethic and willingness to work in culturally diverse settings, especially in Kazakhstan, where he launched the first genomics facility. He was extremely dedicated to the development of the bioinformatics community in Asia and made a lasting impact in the field of immunoinformatics and bioinformatics through his unique contributions in research, education, and service to the community.

## IN MEMORIAM
## FROM THE COMMUNITY

**Michael Ashburner**

"We are deeply saddened by the loss of Michael Ashburner, a pioneering co-founder and former Head of Research at EMBL-EBI.

His contributions to bioinformatics have been immeasurable. Our thoughts are with his family, colleagues and all those whose lives were enriched by his work."
*EMBL-EBI*
*@emblebi*

**Alma Dal Co**

“Alma embodied the ideals of interdisciplinary science, and was a true modern polymath,” according to a statement from the UNIL Department of Computational Biology. “She loved to connect concepts, ideas, and techniques and people across disciplinary and institutional boundaries.”
*TheScientist*

To continue reading: https://www.the-scientist.com/news-opinion/microbial-ecologist-alma-dal-co-dies-in-diving-accident-70780

**The European Nucleotide Archive** (ENA) is currently running an ENA Data Use Survey which is designed to gain better understanding of ENA users on the data retrieval side and their experience using their services.

They hope this survey will provide some great insight into the tools users use, the training they receive and the issues they encounter when looking for and downloading data. Take the survey to assist in helping them reach their goals.

**https://docs.google.com/forms/d/e/1FAIpQLScCAv31_tKiNUwBog1Cm46ibArgtF2ufNoF0Nwm3lsgcYrWjg/viewform**

# CONFERENCE PROGRAMME

# ISMB ECCB 2023

# LYON FRANCE

July 23-27

iSCB

INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

# Welcome to ISMB/ECCB 2023

On behalf of the organizing committee of ISMB/ECCB 2023 and the Board of Directors of the International Society for Computational Biology (ISCB), we wish you a very warm welcome to the conference and the beautiful city of Lyon or if you are joining us virtually, welcome to this hybrid conference experience! ISMB/ECCB 2023, in collaboration with French Society for Bioinformatics will spike your curiosity, deliver the latest research in the field, and allow you to connect, collaborate, and engage with over 2,000 attendees. This conference has shaped up to be the must attend event of the year!

Starting off the conference with a bang is the new ISMB/ECCB 2023 Virtual Posterpalooza, an open-access virtual event, focusing on highlighting the posters being presented at the conference. The Posterpalooza features flash talks from our poster presenters as well as the opportunity to connect with the authors. Each day thereafter the conference's scientific programme includes outstanding keynote speakers including 3 ISCB Award Winners, special tracks, technical talks, and thematically organized Communities of Special Interest (COSI) tracks. In addition, there are workshops, special sessions, Career Fair, and poster sessions. And of course, we cannot forget about our Exhibit Hall - Forum 3 in the Centre de Congrès de Lyon, where you can meet with our 18 conference exhibitors while grabbing a coffee during breaks. From equity focused research to Bioinformatics in France special session, ISMB/ECCB 2023 will provide an intense multidisciplinary forum for disseminating the latest developments in computational tools for data driven biological research, fostering fresh dialogues and perspectives to learn about and shape the future of the field.

ISMB/ECCB 2023 Programme Overview:

- 5 Distinguished Keynote presentations, including our 2023 ISCB Award Winners
- 22 community-led COSI Tracks and workshops
- 3 Special Sessions (Bioinformatics in France, Human Frontier Science Program (HFSP) Symposium, Large Language Models - Are these the next pocket calculators?)
- Special Track: NIH ODSS/ELIXIR
- 17 Technology Track presentations
- Virtual Posterpalooza
- 13 Pre-conference Tutorials (6 virtual & 7 in person)
- Career Fair
- More than 1,200 posters

For those joining us online via ISCB's Nucleus platform, you also have the opportunity to interact with all of the ISMB/ECCB 2023 participants within the collaboration hub. In the forums section, you can chat with your fellow colleagues and friends in designated forum space or even start a conversation of your own. While viewing a live session, you can chat and ask questions. Poke around the exhibit hall where you too can learn about the commercial and non- profit providers of bioinformatics tools, technologies, and publications.

Equally important, there are more than 1,200 posters, presented by their authors in three sessions throughout the conference, both in-person and virtual.. Discussions directly with authors can be so much more revealing than just hearing a presentation, so make sure to add a poster session to your conference scheduler and attend a poster session.

We hope you take advantage of everything the conference has to offer, especially the endless opportunities to meet, network, and connect. We wish you a stimulating and productive time in Lyon or virtually.

As Conference Chairs, we appreciate the support of the very many volunteers who have helped guide the development of the conference and of course all the reviewers who have played an essential role towards forging the scientific program of the conference. We want to acknowledge all the chairs of the COSI Tracks & Abstracts, Proceedings, Special Sessions, Technology Track, and Tutorials. Their dedication and leadership during this time has been invaluable in offering to you an insightful, relevant, and cutting-edge program.

As many of you know, without Diane Kovats, ISCB Chief Executive Officer, and Steven Leard, the ISMB Conference Director, there would be no ISMB/ECCB meeting! We are immensely grateful to Diane, Steven and their teams for the dedication and effort that they put into organizing all the logistics of this very complex meeting while enabling a hybrid experience for those unable to attend in-person.

We also want to take this opportunity to thank our conference sponsors and exhibitors for their ongoing support. We hope you take advantage of everything the conference has to offer, especially the endless opportunity to meet, network, and connect with your fellow computational biologists.

Finally, we thank the city of Lyon for its welcoming hospitality and wish you all a great conference experience!

Let’s have a great ISMB/ECCB 2023!

Yours sincerely,

Alessandra Carbone
Conference Co-chair

Lim Soon Wong
Conference Co-chair

ISMB
ECCB
2023

LYON
FRANCE
July 23-27
iSCB

# BE OUR GUEST!

## NETWORK:

**ISMBECCB 2023**

## PASSWORD:

**Lyon2023**

## *WIFI IS ON US!*

# Scientific Organizing Committee

## CONFERENCE CHAIRS

CONFERENCE CO-CHAIR
**Alessandra Carbone**
CNRS - Sorbonne Université
France

CONFERENCE CO-CHAIR
**Lim Soon Wong**
National University of Singapore
Singapore

## ISMB/ECCB 2023 STEERING COMMITTEE

**Alessandra Carbone, CNRS - Sorbonne Université France**

**Lim Soon Wong, National University of Singapore Singapore**

**Janet Kelso,** ISCB Treasurer; ISCB Conferences Advisory Council Chair, Max Planck Institute for Evolutionary Anthropology
Germany

**Anna-Sophie Fiston-Lavier,** SFBI President (French Society of Bioinformatics)University of Montpellier - Computational Departement, Institute of Evolutionary Sciences of Montpellier (ISEM), France

**Diane E. Kovats,** ISCB Chief Executive Officer, United States

**Steven Leard,** ISMB Conference Director, Canada

**Christine Orengo,** ISCB President, University College London, United Kingdom

**Pat Rodenburg,** Conference Administrator, Canada

**Sushmita Roy,** University of Wisconsin-Madison, United States

**Yann Ponty,** Proceedings Co-chair, CNRS; Laboratoire d'Informatique de l'Ecole Polytechnique, France

**Torsten Schwede,** ECCB Steering Chair, University of Basel, Switzerland

## PROCEEDINGS COMMITTEE

### PROCEEDINGS CO-CHAIRS

**Yann Ponty, CNRS;** Laboratoire d'Informatique de l'Ecole Polytechnique, France
**Sushmita Roy,** University of Wisconsin-Madison, United States

### *AREA CHAIRS*

### BIOINFORMATICS EDUCATION

**Nicola Mulder, University of Cape Town, South Africa**
**Jérôme Waldispühl, McGill University, Canad**

### BIOINFORMATICS OF MICROBES AND MICROBIOMES

**Robert Beiko, Dalhousie University, Canada**
**Hélène Touzet, CNRS; Université de Lille, France**

### BIOMEDICAL INFORMATICS

**Zhiyong Lu, National Institutes of Health, United States**
**Marinka Zitnik, Harvard University, United States**

### EVOLUTIONARY, COMPARATIVE, AND POPULATION GENOMICS

**Lars Arvestad, Stockholm University, Sweden**
**Céline Scornavacca, CNRS; Université de Montpellier, France**

### GENOME PRIVACY AND SECURITY

**Hyunghoon Cho,** Broad Institute of MIT and Harvard, United States
**Gamze Gursoy,** Columbia University and New York Genome Center, United States

### GENOMIC SEQUENCE ANALYSIS

**Rayan Chikhi, CNRS; Institut Pasteur, France**
**Rob Patro, University of Maryland, United States**

### MACROMOLECULAR SEQUENCE, STRUCTURE, AND FUNCTION

**David H Mathews, University of Rochester Medical Center, United States**
**Sergei Grudinin, CNRS; Université Grenoble Alpes, France**

### REGULATORY AND FUNCTIONAL GENOMICS

**Jian Ma, Carnegie Mellon University, United States**
**Marcel Schulz, University of Frankfurt, Germany**

### SYSTEMS BIOLOGY AND NETWORKS

**Tijana Milenkovic, University of Notre Dame, United States**
**Bo Wang, University Toronto, Canada**

### EQUITY-FOCUSED RESEARCH

**Ran Blekhman, University of Chicago, United States**
**Casey Greene, University of Colorado's Anschutz Medical Campus, United States**

### GENERAL COMPUTATIONAL BIOLOGY

**Mohammed El-Kebir, University of Illinois, United States**
**Lenore Cowen, TUFTS University, United States**

# Scientific Organizing Committee

## COSI TRACK LEADS & ABSTRACT CHAIRS

### 3D-SIG: STRUCTURAL BIOINFORMATICS AND COMPUTATIONAL BIOPHYSICS

Douglas Pires, Exscientia, United Kingdom
Rafael Najmanovich, University of Montreal, Canada

### BIOINFO-CORE

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

### BIO-ONTOLOGIES

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

### BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE

Nomi L. Harris (Chair), Lawrence Berkeley National Laboratory, United States
Karsten Hokamp, Trinity College Dublin, Ireland
Radhika Khetani, Harvard T.H. Chan School of Public Health, United States
Hervé Ménager, Institut Pasteur, France
Monica Munoz-Torres, University of Colorado Anschutz Medical Campus, United States
Deepak Unni, SIB Swiss Institute of Bioinformatics, Switzerland
Jason Williams, Cold Spring Harbor Laboratory, United States
Peter Cock (ex officio, Open Bioinformatics Foundation (OBF), United Kingdom

### BIOVIS: BIOLOGICAL DATA VISUALIZATIONS

Jan Byška, Masaryk University, Czech Republic
Katarína Furmanová, Masaryk University, Czech Republic
Helena Jambor, TU Dresden, Germany
Michael Krone, University of Tübingen, Germany
Aditeya Pandey, Regeneron Genetics Center, United States
Qianwen Wang, Harvard Medical School, United States

### CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

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

### COMPMS: COMPUTATIONAL MASS SPECTROMETRY

Wout Bittremieux, University of Antwerp, Belgium
Isabell Bludau, Max Planck Institute of Biochemistry, Germany
Lindsay Pino, University of Pennsylvania, United States
Timo Sachsenberg, University of Tübingen, Germany

### EDUCATION: COMPUTATIONAL BIOLOGY AND BIOINFORMATICS EDUCATION AND TRAINING

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

### EQUITY-FOCUSED RESEARCH

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

### EVOLCOMPGEN: EVOLUTION & COMPARATIVE GENOMICS

Edward L. Braun, University of Florida, United States
Dannie Durand, Carnegie Mellon University, United States
Nadia El-Mabrouk, University of Montreal, Canada
Wataru Iwasaki, University of Tokyo, Japan
Giltae Song, Pusan National University, Korea

### FUNCTION: INCORPORATING CAFA 4: GENE AND PROTEIN FUNCTION ANNOTATION

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

### HITSEQ: HIGH THROUGHPUT SEQUENCING ALGORITHMS & APPLICATIONS

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

### IRNA: INTEGRATIVE RNA BIOLOGY

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

### MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

Su-In Lee, University of Washington, United States
Oznur Tastan, Sabanci University, Turkey

### MICROBIOME

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

### NETBIO: NETWORK BIOLOGY

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

### REGSYS: REGULATORY AND SYSTEMS GENOMICS

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

# Scientific Organizing Committee

## COSI TRACK LEADS & ABSTRACT CHAIRS

### SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

Shaimaa Bakr, Stanford University, United States
Matteo Barberis, University of Surrey, United Kingdom
Chiara Damiani, Università degli Studi di Milano-Bicocca, Italy
Reihaneh Mostolizadeh, University of Tübingen, Germany
Bhanwar Puniya, University of Nebraska-Lincoln, United States
Meghna Verma, AstraZeneca, United States

### TEXT MINING

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

### TRANSMED: TRANSLATIONAL MEDICINE INFORMATICS & APPLICATIONS

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

## SPECIAL SESSIONS

### SPECIAL SESSION: BIOINFORMATICS IN FRANCE

Sandra Dérozier, SFBI member, France
Anna-Sophie Fiston-Lavier, SFBI president, France
Guy Perrière, former SFBI president, France
Marie-France Sagot, SFBI member, France

## TRAVEL FELLOWSHIPS COMMITTEE

Wisdom Akurugu, University of Cape Town, South Africa
Priscila Grynberg, Embrapa, Brazil
Anne-Christin Hauschild, University Medical Center Goettingen, Germany
Kana Shimizu, Waseda University, Japan

### VARI: VARIANT INTERPRETATION

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

### GENERAL COMPUTATIONAL BIOLOGY

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

## TECHNOLOGY TRACK COMMITTEE

Chair: Kristen Beck, IBM Almaden Research Center, United States
Co-chair: Edgardo Ferran, EMBL-EBI Industry Programme External Consultant, France

## TUTORIALS

Chair: Annette McGrath, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
Co-chair: Madelaine Gogol, Stowers Institute for Medical Research, United States
Co-chair: Patricia M. Palagi, SIB Swiss Institute of Bioinformatics, Switzerland

# Distinguished Keynote Presentations

### SUNDAY JULY 23, 6:30 PM - 7:30 PM

**Janet Kelso**

Max Planck Institute for Evolutionary Anthropology

***Unraveling the Human Past: Insights from Ancient DNA***

Introduced by: Anna-Sophie Fiston-Lavier, SFBI President, French Society of Bioinformatics

### MONDAY, JULY 24, 8:45 AM - 9:45 AM

***ISCB Innovator Award Keynote***

**Dana Pe'er**

Sloan Kettering Institute and Howard Hughes Medical Institute

***Machine learning meets single-cell biology: Cellular dynamics and gene programs***

Alessandra Carbone, Conference Co-chair, CNRS - Sorbonne Université France

### TUESDAY, JULY 25, 8:45 AM - 9:45 AM

***ISCB Overton Prize Keynote***

**Jingyi Jessica Li**

University of California, Los Angeles

***Using Synthetic Controls to Enhance the Statistical Rigor in Genomics Data Science***

Introduced by: Martin Vingron, Chair, ISCB Awards Committee

### WEDNESDAY, JULY 26, 8:45 AM - 9:45 AM

**Hanah Margalit**

The Hebrew University of Jerusalem, Israel

***Insights from RNA-seq experiments into post-transcriptional control mechanisms***

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

### THURSDAY, JULY 27, 4:30 PM - 5:30 PM

***ISCB Accomplishments by a Senior Scientist Award Keynote***

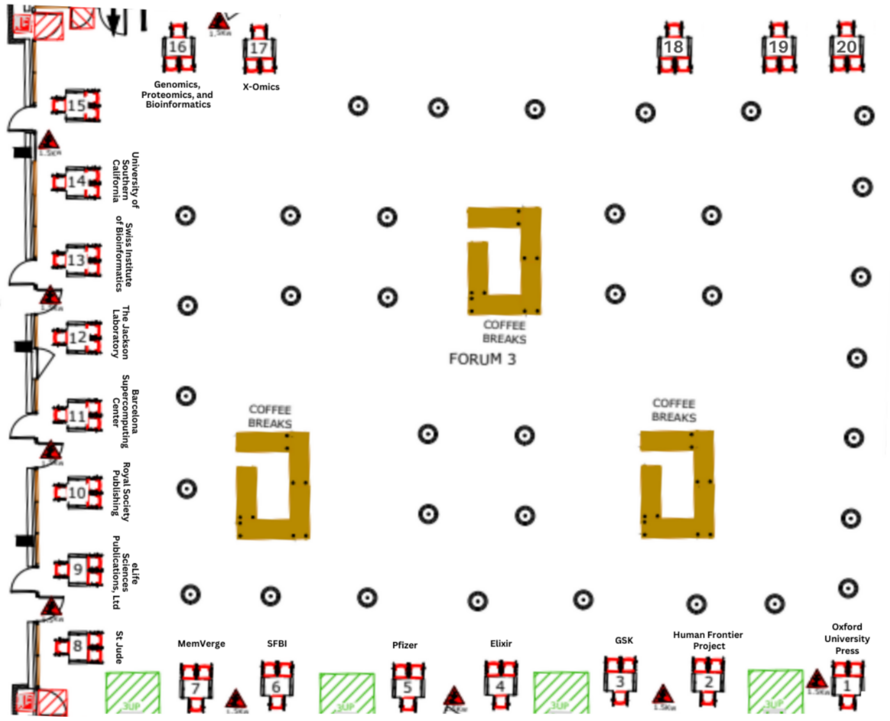
**Mark Gerstein**

Yale University

***A Gradual Evolution in Bioinformatics Research***

*Introduced by: Lim Soon Wong, Conference Co-chair National University of Singapore Singapore*

# ISMB/ECCB 2023 Exhibitors



## Exhibitors

1. Oxford University Press
2. Human Frontier Science Program
3. GSK
4. Elixir
5. Pfizer
6. SFBI
7. MemVerge
8. St. Jude Children's Research Hospital
9. eLife
10. The Royal Society
11. PerMedCoE
12. The Jackson Laboratory
13. Swiss Institute of Bioinformatics
14. UCS Leonard Davis
15. ECCB
16. Genomics, Proteomics, and Bioinformatics Journal
17. X-Omics
18. ISCB
19. ISCB-SC

# Schedule-at-a-glance
# Sunday, July 23

*All times in CEST*

| | |
|---|---|
| 9:00AM - 4:30PM | ISCB Board of Directors Meeting Room: Roseraie 3 (Level 3) |
| 9:00AM - 6:00PM | Student Council Symposium - Room: Pasteur Lounge (Level 1) |
| 9:00AM - 6:00PM | In-person Tutorial IP1, In-person Tutorial IP2, In-person Tutorial IP3, In-person Tutorial IP4 |
| 9:00AM - 1:00PM | In-person Tutorial IP5, In-person Tutorial IP6 |
| 2:00PM - 6:00PM | In-person Tutorial IP7 |
| 11:00AM - 6:00PM | Student Council Symposium: Posters Display Room: Place Haute (Level 1 adjacent Pasteur Lounge) |
| |  |
| 6:15PM - 6:30PM | ISMB/ECCB 2023 Welcome - Lumiére Auditorium |
| 6:30PM - 7:30PM |  **Distinguished Keynote:** Janet Kelso,<br>Max Planck Institute for Evolutionary Anthropology<br>Introduced by:<br>Anna-Sophie Fiston-Lavier, SFBI President,<br>French Society of Bioinformatics |
| 7:30PM - 9:00PM | Networking Reception - Forum (Level 3) |
| |  |

# REGISTRATION DESK
## IN HALL D'ACCUEIL TERREAUX
## HOURS

**Sunday, July 23: 8:00am - 10:00am**
**Morning and Full-day Tutorials Only, Student Council Symposium)**
**11:30am - 7:30pm**
**Monday, July 24: 7:30am - 6:30pm**
**Tuesday, July 25: 7:30am - 6:30pm**
**Wednesday, July 26: 7:30am - 6:30pm**
**Thursday, July 27: 7:30am - 12:00pm**

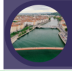
# Schedule-at-a-glance
# Monday, July 24

*All times in CEST*

8:30AM-8:45AM
Morning Welcome & Introduction of ISCB Distinguished Fellows 2023

8:45AM - 9:45AM

ISCB Innovator Award Keynote:
Dana Pe'er, BHoward Hughes Medical Institute
Introduced by:
Alessandra Carbone, Conference Co-chair, CNRS - Sorbonne Université France



9:45AM - 10:30AM
Caffeinate and Connect with exhibitors (Coffee Break) Forums: Level -2

10:30AM - 12:30PM
Sessions

- MLCSB (Room: Lumière Auditorium)
- 3Dsig(Room: Pasteur Auditorium)
- TransMed (Pasteur Lounge)
- NetBio (Room: Salle Saint Claire 3)
- Microbiome (Salle Roseraie 1/2)
- NIH-ELIXIR Track on the BioData Ecosystem (Salle Rhone 1)
- Technology Track Presentations (Salle Rhone 2)
- BOSC (Salle Rhone 3b)

12:30PM - 1:50PM
Lunch - Forums (Level -2)

12:45PM - 1:45PM
ISCB Town Hall
(Room: Auditorium Pasteur)

1:50PM - 3:30PM
Sessions Continue

- MLCSB (Room: Lumière Auditorium)
- 3Dsig(Room: Pasteur Auditorium)
- TransMed (Pasteur Lounge)
- NetBio (Room: Salle Saint Claire 3)
- Microbiome (Salle Roseraie 1/2)
- NIH-ELIXIR Track on the BioData Ecosystem (Salle Rhone 1)
- BioINFO Core (Salle Rhone 2)
- Bio-Ontologies (Salle Rhone 3b2
- BOSC (Salle Rhone 3b)

3:30PM - 4:00PM
Coffee Break (Caffeinate and Connect with exhibitors) Forums (Level -2)

4:00PM - 6:00PM
Sessions Continue

- MLCSB (Room: Lumière Auditorium)
- 3Dsig(Room: Pasteur Auditorium)
- TransMed (Pasteur Lounge)
- NetBio (Room: Salle Saint Claire 3)
- Microbiome (Salle Roseraie 1/2)
- NIH-ELIXIR Track on the BioData Ecosystem (Salle Rhone 1)
- Equity-focused research (4:00 - 5:00)
- Technology Track Presentations (5:00 - 6:00) (Salle Rhone 2)
- Bio-Ontologies (Salle Rhone 3a)
- BOSC (Salle Rhone 3b)

6:00PM - 7:00PM
Poster Happy Hour - Forums (Level -2)

# Schedule-at-a-glance
# Tuesday, July 25

*All times in CEST*

8:30AM-8:45AM Morning Welcome Room: Lumière Auditorium

8:45AM - 9:45AM

ISCB Overton Prize Keynote
Jingyi Jessica Li, Harvard University
Introduced by:
Martin Vingron, Chair, ISCB Awards Committee

9:45AM - 10:30AM Caffeinate and Connect with exhibitors (Coffee Break) Forums (Level -2)

10:30AM - 12:30PM Sessions

MLCSB (Room: Lumière Auditorium)

3Dsig(Room: Pasteur Auditorium)

Special Session: Large Language Models - Are these the next pocket calculators?
(Pasteur Lounge)

HiTSeq
(Salle Saint Claire 3)

Microbiome
(Salle Roseraie 1/2)

BioVis (Salle Rhone 1)

RegSys (Salle Rhone 2)

Bio-Ontologies (Salle Rhone 3a)

BOSC (Salle Rhone 3b)

12:30PM - 1:50PM Forums (Level -2)

12:45PM - 1:45PM Birds of a Feather Programming: Rooms 8 & 9

1:50PM - 3:30PM Sessions Continue

MLCSB (Room: Lumière Auditorium)

3Dsig(Room: Pasteur Auditorium)

Bioinformatics in France
(Pasteur Lounge)

HiTSeq
(Salle Saint Claire 3)

Microbiome
(Salle Roseraie 1/2)

BioVis (Salle Rhone 1)

RegSys (Salle Rhone 2)

Bio-Ontologies and BOSC Joint Program (Held in BOSC Room)
(Salle Rhone 3b)

Bio-Ontologies and BOSC Joint Program (Held in BOSC Room)
(Salle Rhone 3b)

3:30PM - 4:00PM Coffee Break (Caffeinate and Connect with exhibitors) Forums (Level -2)

4:00PM - 6:00PM Sessions Continue

MLCSB (Room: Lumière Auditorium)

3Dsig(Room: Pasteur Auditorium)

Bioinformatics in France
(Pasteur Lounge)

HiTSeq
(Salle Saint Claire 3)

Microbiome
(Salle Roseraie 1/2)

BioVis (Salle Rhone 1)

RegSys (Salle Rhone 2)

WEB
(Salle Rhone 3a)

BOSC (Salle Rhone 3b)

6:00PM - 7:00PM Poster Happy Hour - Forum (Level -2)

# Schedule-at-a-glance
# Wednesday, July 26

ISMB ECCB 2023
LYON FRANCE
July 23-27
ISCB

*All times in CEST*

8:30AM-8:45AM Morning Welcome

8:45AM - 9:45AM

**Distinguished Keynote:**
Hanah Margalit, The Hebrew University of Jerusalem
Introduced by:
Christine Orengo, ISCB President

9:45AM - 10:30AM Caffeinate and Connect with exhibitors (Coffee Break) Forums (Level -2)

10:30AM - 12:30PM Sessions

HiTSeq Lumière Auditorium)

EvolCompGen (Pasteur Auditorium)

iRNA (Pasteur Lounge)

Function (Salle Saint Claire 3)

CAMDA (Salle Roseraie 1/2)

Education (Salle Rhone 1)

RegSys (Salle Rhone 2)

Human Frontier Science Program (HFSP) (Salle Rhone 3a)

Technology Track Presentations (Salle Rhone 3b)

12:30PM - 1:50PM Lunch and Ideation Hall (Forums (Level -2)

1:50PM - 3:30PM Sessions Continue

HiTSeq Lumière Auditorium)

EvolCompGen (Pasteur Auditorium)

iRNA (Pasteur Lounge)

Function (Salle Saint Claire 3)

CAMDA (Salle Roseraie 1/2)

Education (Salle Rhone 1)

RegSys (Salle Rhone 2)

Human Frontier Science Program (HFSP) (Salle Rhone 3a)

Technology Track Presentations (Salle Rhone 3b)

3:30PM - 4:00PM Coffee Break (Caffeinate and Connect with exhibitors) Forums (Level -2)

4:00PM - 6:00PM Sessions Continue

HiTSeq Lumière Auditorium)

EvolCompGen (Pasteur Auditorium)

iRNA (Pasteur Lounge)

Function (Salle Saint Claire 3)

CAMDA (Salle Roseraie 1/2)

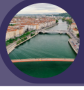
Education (Salle Rhone 1)

RegSys (Salle Rhone 2)

Human Frontier Science Program (HFSP) (Salle Rhone 3a)

Technology Track Presentations (Salle Rhone 3b)

6:00PM - 7:00PM Poster Happy Hour - Forum (Level -2)



# Schedule-at-a-glance
# Thursday, July 27

ISMB ECCB 2023 LYON FRANCE July 23-27 ISCB

*All times in CEST*

| | |
|---|---|
| 8:30AM - 9:30AM | Sessions |

| | | |
|---|---|---|
| General Computational Biology (Lumière Auditorium) | Function (Salle Saint Claire 3) | SysMod (Salle Rhone 2) |
| EvolCompGen (Pasteur Auditorium) | CAMDA (Salle Roseraie 1/2) | CompMS (Salle Rhone 3a) |
| iRNA (Pasteur Lounge) | VarI (Salle Rhone 1) | TextMining (Salle Rhone 3b) |

| | |
|---|---|
| 9:30AM - 10:00AM | Caffeinate and Connect with exhibitors (Coffee Break) Forums (Level -2) |
| 10:00AM - 12:00PM | Sessions |

| | | |
|---|---|---|
| General Computational Biology (Lumière Auditorium) | Function (Salle Saint Claire 3) | SysMod (Salle Rhone 2) |
| EvolCompGen (Pasteur Auditorium) | CAMDA (Salle Roseraie 1/2) | CompMS (Salle Rhone 3a) |
| iRNA (Pasteur Lounge) | VarI (Salle Rhone 1) | TextMining (Salle Rhone 3b) |

| | |
|---|---|
| 12:00PM - 1:20PM | Lunch Forums (Level -2) |
| 1:20PM - 3:00PM | Sessions Continue |

| | | |
|---|---|---|
| General Computational Biology (Lumière Auditorium) | Function (Salle Saint Claire 3) | SysMod (Salle Rhone 2) |
| EvolCompGen (Pasteur Auditorium) | CAMDA (Salle Roseraie 1/2) | CompMS (Salle Rhone 3a) |
| iRNA (Pasteur Lounge) | VarI (Salle Rhone 1) | TextMining (Salle Rhone 3b) |

| | |
|---|---|
| 3:00PM - 3:30PM | Coffee Break - Forums (Level -2) |
| 3:30PM - 4:30PM | Sessions Continue |

| | | |
|---|---|---|
| General Computational Biology (Lumière Auditorium) | Function (Salle Saint Claire 3) | SysMod (Salle Rhone 2) |
| EvolCompGen (Pasteur Auditorium) | CAMDA (Salle Roseraie 1/2) | CompMS (HFSP) (Salle Rhone 3a) |
| iRNA (Pasteur Lounge) | VarI (Salle Rhone 1) | TextMining (Salle Rhone 3b) |

4:30PM - 5:30PM

ISCB Accomplishments by a Senior Scientist Award Keynote
Mark Gerstein, Yale University
Introduced by: Lim Soon Wong, Conference Co-chair

5:30PM - 5:45PM

Awards Presentations & Conference Closing
Room: Lumière Auditorium

# Special Sessions

## TUESDAY, JULY 25TH

## SPECIAL SESSION: BIOINFORMATICS IN FRANCE

| | |
|---|---|
| 13:50-14:00 | **Guy Perrière**<br>*Opening Speech* |
| 14:00-14:30 | **Anna-Sophie Fiston-Lavier, SFBI, France**<br>*Invited Presentation: French Society of Bioinformatics (SFBI)* |
| 14:30-15:00 | **Anne-Francoise Adam-Blondon, INRAE, FRANCE**<br>*Invited Presentation: Institut Français de Bioinformatique, the french node of ELIXIR-FR* |
| 15:00-15:10 | **Sébastien Gradit**<br>*Statistical inference of repeated sequence contacts in Hi-C maps (Hi-C BERG)* |
| 15:10-15:20 | **Elijah Willie**<br>*The impact of similarity metrics on cell type clustering in highly multiplexed in situ imaging cytometry data* |
| 15:20-15:30 | **Lindsay Goulet, Université Paris-Saclay, France**<br>*Towards a machine learning approach for automated detection of well-to-well contamination in metagenomic data* |
| 16:00-16:10 | **Romane Junker**<br>*Integrating metagenetic datasets through microbial association networks to compare microbial communities from lacto-fermented vegetables* |
| 16:10-16:20 | **Yanis Asloudj, Laboratoire Bordelais de Recherche en Informatique (LaBRI), France**<br>*GORi: automated biological characterization of gene signatures under the scope of multiple controlled vocabularies* |
| 16:20-16:30 | **Vera Pancaldi**<br>*Tools for analysing spatial data in the context of immuno-oncology* |
| 16:30-17:15 | **Flora Jay, LISN, CNRS, University Paris-Saclay, France**<br>*Invited Presentation: Design and application of deep neural networks for population genetics* |
| 17:15-18:00 | **Yann Ponty**<br>*Invited Presentation: RNA bioinformatics: Still combinatorial in 2023?* |
| 18:00-19:00 | **Poster session** |
| 18:00-19:00 | **Social Event** |

# Special Sessions

## WEDNESDAY, JULY 26TH

## SPECIAL SESSION: HUMAN FRONTIER SCIENCE PROGRAM (HFSP) SYMPOSIUM

**10:30-10:50** **Guntram Bauer**
*Data science and the new HFSPO Strategy 2024-2032*

**10:50-11:50** **Minoru Kanehisa**
*Invited Presentation: Establishing a self-sustaining database for a sustainable society*

**11:50-12:10** **Johanna McEntyre**
*Invited Presentation: Open Access data resources - how to meet global challenges and community needs*

**12:10-12:30** **Amber Scholz, Leibniz Institute DSMZ, Germany**
*Invited Presentation: Who owns your data? Who should benefit from it? The effect of UN policy decisions on biological data management*

**13:50-14:20** **Josefina Campos**
*Invited Presentation: Interoperability, data structure and data sharing in the Argentina Genomics Network*

**14:20-14:50** **Halima Bensmail, Qatar computing research institute, Qatar**
*AI-driven drug repurposing and binding pose meta dynamics identifies novel targets for monkeypox virus*

**14:50-15:10** **Nicola Mulder, University of Cape Town, South Africa**
*Invited Presentation: The eLwazi open data science platform for biomedical research in Africa*

**15:10-15:30** **Martin Kelemen, University of Cambridge, United Kingdom**
*Investigating the effect of gene-country interactions on health and anthropometric traits in South Asian populations*

**16:00-16:50** **Philip Bourne**
*Invited Presentation: Biomedical Data Science: We Are Not Alone*

**16:50-17:10** **Guy Cochrane, Global Biodata Coalition, France**
*Invited Presentation: Towards a sustainable biodata infrastructure*

**17:10-17:30** **Christophe Godin, INRIA, France**
*Invited Presentation: TBC*

**17:30-18:00** **Philippe Sanseau**
*Invited Presentation: Data, computational biology and drug target discovery*

# Special Sessions

## TUESDAY, JULY 25TH

## SPECIAL SESSION: LARGE LANGUAGE MODELS - ARE THESE THE NEXT POCKET CALCULATORS?

| | |
|---|---|
| **10:30-11:00** | **Christian Dallago, NVIDIA**<br>*Invited Presentation: Large Language Models: Architectures, Training Strategies, and Applications* |
| **11:00-11:30** | **Alex Bateman**<br>*Invited Presentation: Plausible nonsense: An Editors worst nightmare* |
| **11:30-12:00** | **Patricia Palagi**<br>*Invited Presentation: LLMs for teaching – game changers* |
| **12:00-12:30** | **David Leslie**<br>*Invited Presentation: Scientific Discovery in the Age of Large Language Models* |

# Birds of a Feather Presentations

## TUESDAY, JULY 25TH

| | |
|---|---|
| **12:45-13:45** | **Sorin Draghici**<br>*NSF Funding opportunities for research in computational biology and bioinformatics*<br>**Patricia Carvajal-López**<br>*Bioinformatics core facility career progression* |

# Equity-focussed Research Presentations

## MONDAY, JULY 24TH

| | |
|---|---|
| **16:00-16:20** | ***Brett Beaulieu-Jones, University of Chicago, United States***<br>*Jointly Optimizing for Fairness Outperforms Post-hoc Bias Mitigation Strategies* |
| **16:20-16:40** | ***Will Thrift, Genentech, United States***<br>*Improved clinical trial equity for individualized cancer vaccines with deep machine learning* |
| **16:40-17:00** | ***Sara El-Gebali***<br>*Invited Presentation: Inclusion and Digital Equity from theory to practice* |

# Special Track: NIH ODSS/ELIXIR

## MONDAY, JULY 24TH

### Session: Core Resources at the Heart of Life Sciences

| | |
|---|---|
| 10:30-10:50 | **Juan Antonio Vizcaino, European Bioinformatics Institute (EMBL-EBI), United Kingdom**<br>*Invited Presentation: PRIDE & ProteomeXchange: Making proteomics data FAIR* |
| 10:50-11:10 | **Tom Pollard, Massachusetts Institute of Technology (MIT), United States**<br>*Invited Presentation: PhysioNet: A Quarter Century of Open Health Data* |
| 11:10-11:30 | **Ugis Sarkans, EMBL-EBI, UK**<br>*Invited Presentation: From ArrayExpress to BioStudies* |
| 11:30-11:40 | **Josephine Burgin, European Molecular Biology Laboratory, European Bioinformatics Institute, United Kingdom**<br>*Invited Presentation: The European Nucleotide Archive* |
| 11:40-11:50 | **Paul Sternberg**<br>*Invited Presentation: Alliance of Genomic Resources* |
| 11:50-12:00 | **Alex Bateman, EMBL-EBI, UK**<br>*Invited Presentation: InterPro: Bringing together protein families resources for sustainability* |
| 12:00-12:10 | **Nicola Bordin**<br>*Invited Presentation: CATH: Protein Structure Classification Database* |
| 12:10-12:20 | **Christian-Alexander Dudek, BRENDA (DSMZ), Germany**<br>*Invited Presentation: BRENDA: 35 Years of Empowering Enzymology and Beyond* |
| 12:20-12:30 | **Jan Gerken, Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures GmbH, Germany**<br>*Invited Presentation: SILVA - high quality ribosomal RNA datasets* |

### Session: The Federated/Distributed Landscape

| | |
|---|---|
| 13:50-14:10 | **Heidi Imker**<br>*Invited Presentation: A Landscape Analysis of Biodata Resources* |
| 14:10-14:30 | **Mallory Freeberg, EMBL European Bioinformatics Institute, United Kingdom**<br>*Invited Presentation: [Federated] EGA: Providing global discovery and access for sensitive human data* |
| 14:30-14:50 | **Ana Van Gulick**<br>*Invited Presentation: The Coopetition model of collaboration in the NIH Generalist Repository Ecosystem Initiative* |
| 14:50-15:10 | **Obi Griffith, Washington University, United States**<br>*CIViC: Accelerating the expert-crowdsourcing of cancer variant interpretation* |
| 15:10-15:30 | **Laura Hughes, Scripps Research, USA**<br>*Invited Presentation: NIAID Data Ecosystem Discovery Portal: creating a federated search engine to discover infectious and immune-mediated disease data* |

### Session: Knowledge & Impact from Data

| | |
|---|---|
| 16:00-16:20 | **Alan Bridge, SIB Swiss Institute of Bioinformatics, Switzerland**<br>*Invited Presentation: UniProtKB – a hub for protein knowledge* |
| 16:20-16:40 | **Melissa Haendel**<br>*Invited Presentation: National COVID Cohort Collaborative (N3C)* |
| 16:40-17:00 | **Jing Chen, University of California San Diego, USA**<br>*Invited Presentation: The Network Data Exchange (NDEx)* |
| 17:00-17:20 | **Henning Hermjakob, European Bioinformatics Institute, European Molecular Biology Laboratory (EMBL-EBI)**<br>*Invited Presentation: Connecting Molecules and Organisations - IMEx Molecular Interactions and Reactome Pathways* |
| 17:20-17:30 | **Ana Rath**<br>*Invited Presentation: Orphadata Science: a global core data resource for rare disease knowledge* |
| 17:30-17:40 | **Damian Szklarczyk**<br>*Invited Presentation: The STRING Database: A Comprehensive Functional Annotation of Non-Model Organism Proteomes* |
| 17:40-18:00 | **Melissa Harrison, EMBL-EBI, United Kingdom**<br>*Invited Presentation: Europe PMC - connecting the literature to data* |

# POSTERS

## MONDAY, JULY 24 • TUESDAY, JULY 25 • WEDNESDAY JULY 26

### Poster Session A

**Monday, July 24, between 18:00 CEST and 19:00 CEST**

*3D-SIG*
*Bio-Ontologies*
*BioInfo-Core*
*BOSC*
*Equity-focussed Research Presentations*
*MICROBIOME*
*MLCSB*
*NetBio*
*TransMed*

### Poster Session B:

**Tuesday, July 25, between 18:00 CEST and 19:00 CEST**

*3D-SIG*
*BioVis*
*HiTSeq*
*MICROBIOME*
*MLCSB*
*RegSys*
*Special Session: Bioinformatics in France*

### Poster Session C

**Wednesday, July 26, between 18:00 CEST and 19:00 CEST**

*CAMDA*
*CompMS*
*Education*
*EvolCompGen*
*Function*
*General Computational Biology*
*iRNA*
*SysMod*
*Text Mining*
*VarI*

# 3DSIG COSI

## COSI TRACK PRESENTATIONS

### MONDAY, JULY 24TH

**3D-SIG: Structural Bioinformatics and Computational Biophysics**

| | |
|---|---|
| **10:30-11:10** | **3DSIG Keynote**<br>**Burkhard Rost**<br>*Invited Presentation: Artificial Intelligence captures language of life written in proteins* |
| **11:10-11:30** | **Recep Adiyaman, University of Reading, United Kingdom**<br>*Improvement of protein tertiary and quaternary structure predictions using the ReFOLD refinement method and the AlphaFold2 recycling process* |
| **11:30-11:50** | **Brennan Abanades,** University of Oxford, United Kingdom<br>*ImmuneBuilder: Deep-Learning models for predicting the structures of immune proteins.* |
| **11:50-12:10** | **Shaun Kandathil, University College London, United Kingdom**<br>*Evaluating AlphaFold2 for Multi-domain Protein Structure Prediction* |
| **12:10-12:30** | **Castrense Savojardo,** University of Bologna, Italy<br>*CoCoNat: prediction of coiled-coil regions using protein language models* |
| **13:50-14:00** | **Rafael Najmanovich**<br>**Douglas Pires**<br>*Panel: 3DSIG: Past, Present and Future* |
| **14:00-14:20** | **Hyunbin Kim,** Seoul National University, South Korea<br>*Foldcomp: scalable solution for compressing huge protein structure database* |
| **14:20-14:40** | **Tim Kucera,** Max Planck Institute of Biochemistry, Germany<br>*ProteinShake: A Unified Framework for Deep Learning on Large Datasets of Protein Structures* |
| **14:40-15:00** | **Dmitry Ivankov,** Skolkovo Institute of Science and Technology, Russia<br>*Is the success of AlphaFold due to a better understanding of physics?* |
| **16:00-16:20** | **Eugene F. Baulin,** IIMCB in Warsaw, Poland<br>*CoRToise - Computational RNA Topoisomerase* |
| **16:20-16:40** | **Davyd Bohdan,** MIPT, Russia<br>*ARTEM tool for searching motifs in RNA 3D structures* |
| **16:40-17:00** | **Md Mahfuzur Rahaman,** University of Central Florida, United States<br>*Proceedings Presentation: RNAMotifComp: a comprehensive method to analyze and identify structurally similar RNA motif families* |
| **17:00-17:20** | **Marin Matic,** Scuola Normale Superiore, Italy<br>*Dissecting the sequence and structure determinants of GPCR - Gprotein selectivity via structural bioinformatics and machine learning* |
| **17:20-17:40** | **Francesca Vianello,** Exscientia, United Kingdom<br>*Automating Structure-Based Design: Integrating Fragment Hotspot Maps in Drug Discovery Pipelines at Scale* |
| **17:40-18:00** | **Jia-Ning Li,** School of Life Sciences, Northwestern Polytechnical University, China<br>*Proceedings Presentation: CProMG: Controllable Protein-Oriented Molecule Generation with Desired Binding Affinity and Drug-Like Properties* |

# 3DSIG COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

**3D-SIG: Structural Bioinformatics and Computational Biophysics**

| | |
|---|---|
| **10:30-11:10** | **3DSIG Keynote**<br>**Arne Elofson**<br>*Invited Presentation: Towards a Complete Structural Map of the Human Proteome Using AlphaFold* |
| **11:10-11:30** | **Neeladri Sen,** UCL, United Kingdom<br>*A structural database of chain-chain and domain-domain interfaces of proteins* |
| **11:30-11:50** | **Dingquan Yu,** EMBL, Germany<br>*AlphaPulldown, a python package for protein-protein interaction screens using AlphaFold-Multimer - and its latest updates* |
| **11:50-12:10** | **Fabrizio Pucci,** ULB, Belgium<br>*FNew computational insights on enzyme stability-activity trade-off* |
| **12:10-12:30** | **Natalia Fagundes Borges Teruel,** Université de Montréal, Canada<br>*Surfaces: A software for fast quantification and visualisation of biomolecular interactions* |
| **13:50-14:00** | **Rafael Najmanovich**<br>**Douglas Pires**<br>*3DSIG: Past, Present and Future (Part II)* |
| **14:00-14:20** | **Samuel Sledzieski,** Computer Science and Artificial Intelligence Laboratory, MIT, United States<br>*TT3D: Leveraging Pre-Computed Protein 3D Sequence Models to Predict Protein-Protein Interactions* |
| **14:20-14:40** | **Alex Morehead,** University of Missouri - Columbia, United States<br>*Proceedings Presentation: A Gated Graph Transformer for Protein Complex Structure Quality Assessment and its Performance in CASP15* |
| **14:40-15:00** | **Juami van Gils,** Vrije Universiteit Amsterdam, Netherlands<br>*Disordered flanks slow down the growth of amyloid fibrils in neurodegenerative disease, while hydrophobic surfaces accelerate growth* |
| **16:00-16:20** | **Yunzhuo Zhou,** University of Queensland, Australia<br>*DDMut: predicting effects of mutations on protein stability using deep learning* |
| **16:20-16:40** | **Joan Planas-Iglesias,** Loschmidt Labs., UEB, Masaryk University. International Clinical Research Center<br>*LoopGrafter: A Web Tool for Transplanting Dynamical Loops for Protein Engineering* |
| **16:40-17:00** | **Alessia David,** Centre for Integrative Systems Biology and Bioinformatics, Imperial College London, United Kingdom<br>*Missense3D-TM: a new algorithm to predict the effect of amino acid substitutions in transmembrane proteins* |
| **17:00-17:20** | **Piyumi Amarasinghe,** Monash University, Australia<br>*Proceedings Presentation: Getting 'φψχal' with proteins: Minimum Message Length Inference of joint distributions of backbone and sidechain dihedral angles* |
| **17:20-17:40** | **Carmen Al Masri,** Harmonic Discovery Inc., United States<br>*Unlocking the Conformational Landscape of Protein Kinases: A Custom MSA Approach with ColabFold for Active State Modeling* |
| **17:40-18:00** | **Roland Dunbrack,** Fox Chase Cancer Center, United States<br>*Combining rigorous structural bioinformatics and deep-learning-based protein structure prediction: AlphaFold2 models of all 438 catalytically competent human kinases in the active form* |

# BIOINFO-CORE

## COSI TRACK PRESENTATIONS

### MONDAY, JULY 24TH

| | |
|---|---|
| **13:50-<br>14:10** | **James McCafferty,** Wellcome Sanger Institute, United Kingdom<br>*Core Informatics at the Sanger Institute: Strategy and Futures* |
| **14:10-<br>14:15** | **Patricia Carvajal-López,** EMBL-EBI, United Kingdom<br>*Available tools to assess career progression in bioinformatics core facilities* |
| **14:15-<br>14:20** | **Kübra Narcı,** Deutsches Krebsforschungszentrum, Germany<br>*Standardizing and harmonizing NGS analysis workflows in the German Human Genome-Phenome Archive (GHGA) – A national secure infrastructure for omics data* |
| **14:20-<br>14:25** | **Jorge Boucas,** Max Planck Institute for Biology of Ageing, Germany<br>*Flaski - web Apps for life sciences* |
| **14:25-<br>14:30** | **Francisco Javier Lopez,** Genomics England, United Kingdom<br>*Learnings from Genomics England's experience developing WGS analysis pipelines to support a National-scale Genomic Medicine Service* |
| **14:30-<br>15:00** | **Hua Li**<br>**Meeta Mistry**<br>**Jenny Drnevich,** University of Illinois Urbana Champaign, United States of America<br>**Ellis Patrick**<br>**Ayushi Agrawal,** The J. David Gladstone Institutes, United States of America<br>*Panel: Spatial Data Panel: Challenges, Lessons, Best Practices* |
| **15:00-<br>15:20** | **Small discussions**<br>***Panel: Breakout Group Discussion*** |
| **15:20-<br>15:30** | **Small discussions**<br>***Panel:*** *Breakout Group Report* |

# Bio-Ontologies COSI

## COSI TRACK PRESENTATIONS

### MONDAY, JULY 24TH

**13:50-14:00** **Núria Queralt Rosinach**
***COSI Opening Remarks***

**14:00-15:00** **Ernesto Jimenez-Ruiz,** City, University of London, United Kingdom
***Invited Presentation:***
***Ontology Alignment for Life Sciences***

**15:00-15:30** **Ke Zhang,** ShanghaiTech University, China
*Proceedings Presentation: KR4SL: knowledge graph reasoning for explainable prediction of synthetic lethality*

**16:00-16:40** **Lynn Schriml,** University of Maryland School of Medicine, United States
*A 20-year journey developing the disease open science ecosystem*

**16:40-17:00** **Alice Rogier,** PhD, France
*ChemoOnto, an ontology to qualify the course of chemotherapies*

**17:00-17:20** **Jade Hotchkiss,** Division of Human Genetics, Department of Pathology, University of Cape Town, South Africa
*First Layperson Translation of the Sickle Cell Disease Ontology – Making SCD-Centred eHealth Platforms more Accessible*

**17:20-17:40** **Shuai Jiang,** Beijing Institute of Genomics Chinese Academy of Sciences (China National Center for Bioinformation), China
*Cell Taxonomy: a curated repository of cell types with multifaceted characterization*

**17:40-18:00** **Núria Queralt-Rosinach**
*Presenter Q&A*

# Bio-Ontologies COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

| | | |
|---|---|---|
| 10:30-11:30 | **Janna Hastings,** University of Zurich, Switzerland | ***Invited Presentation***: *Ontology-based Interpretability for Large Predictive Models* |
| 11:30-11:50 | **Kenneth Opap,** University of Cape Town, South Africa | *PRIOR: CANDIDATE GENE PRIORITIZATION BY ONTOLOGY INTEGRATION AND RANKING* |
| 11:50-12:10 | **Brian Schilder,** Imperial College London, United Kingdom | *Navigating the rare diseases landscape: a comprehensive approach to identify gene therapy targets based on cell type-phenotype associations* |
| 12:10-12:30 | **Núria Queralt-Rosinach** | *COSI Closing Remarks and Awards* |
| 13:50-14:10 | **Herve Menager,** Institut Pasteur, Université Paris Cité, France | *The Research Software Ecosystem: an open software metadata commons* |
| 14:10-14:30 | **Sierra Moxon,** LBNL, United States | *The Linked data Modeling Language (LinkML): a general-purpose data modeling framework* |
| 14:30-14:50 | **Justin Reese,** Lawrence Berkeley National Laboratory, United States | *KG-Hub: a framework to facilitate discovery using biological and biomedical knowledge graphs* |
| 14:50-14:55 | **Vasundra Touré,** Swiss Institute of Bioinformatics SIB, Switzerland | *The SPHN Semantic Interoperability Framework: From clinical routine data to FAIR research data* |
| 14:55-15:00 | **Matthew Crown,** Northumbria University, United Kingdom | *OMEinfo: global geographic metadata for -omics experiments* |
| 15:00-15:05 | **Bhavesh Patel,** FAIR Data Innovations Hub, California Medical Innovations Institute, United States | *FAIR-BioRS: Actionable guidelines for making biomedical research software FAIR* |
| 15:05-15:25 | **Jackson Callaghan,** Scripps Research, United States | *BioThings Explorer: a query engine for a federated knowledge graph of biomedical APIs* |
| 15:25-15:30 | **Nomi Harris** | *Open Time for Questions* |

# BIOVIS COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

BioVis:
Biological Data
Visualizations

biovis

| | |
|---|---|
| 10:30-11:30 | **Anna Vilanova**<br>***BioVis Keynote*** |
| 11:30-11:50 | **Test of Time Award** |
| 11:50-12:10 | **Trevor Manz,** Harvard Medical School, United States<br>*Effective Comparison of Single-Cell Embedding Visualizations* |
| 12:10-12:20 | **Christy Lee,** University of California, Los Angeles, United States<br>*scDEED: a statistical method for detecting dubious 2D single-cell embeddings* |
| 12:20-12:30 | **Shamim Ashrafiyan,** Goethe University Frankfurt, Germany<br>*GAZE-Shiny: comprehensive and interactive visualization of transcriptional regulation in single-cell resolution* |
| 13:50-14:10 | **Tatiana Galochkina,** Université Paris Cité and Université des Antilles and Université de la Réunion, France<br>*Poincaré maps for visualization of large protein families* |
| 14:10-14:20 | **Mo Rahman,** GeneDrop Inc., United States<br>*Seeing Beyond the Surface: The Continuous Development of Protein Design with Dalton* |
| 14:20-14:30 | **Zeeshan Ahmed,** Institute for Health, Health Care Policy and Aging Research. Rutgers, United States<br>*GVViZ: A physician-friendly bioinformatics application enabling interactive gene-disease data annotation, expression analysis, and visualization for translational research* |
| 14:30-14:50 | **Markus Joppich,** Ludwig Maximilian University of Munich, Germany<br>*Visualizing (differential) expression patterns with fuzzy concepts as FlowSets* |
| 14:50-15:00 | **Kyle Smith,** University of California, San Diego, United States<br>*RIVET: A visual interactive browser for tracking and curating SARS-CoV-2 recombinants* |
| 15:00-15:10 | **Zeynep Gümüş,** Mount Sinai School of Medicine, United States<br>*PhosNetVis: A Web-Based Platform for Kinase Enrichment Analysis and Visualizing Phosphoproteomics Networks* |
| 15:10-15:30 | **Kari Lavikka,** University of Helsinki, Finland<br>*Visualizing temporal and multi-regional evolution of tumor subclones with Jellyfish plots* |
| 16:00-16:10 | **Melina Malkani,** Bullis School, United States<br>*Best Practices for the Design of Health Dashboards* |
| 16:10-16:20 | **Giulia Cesaro,** University of Padua, Italy<br>*Interactive and effective visualization framework for interpreting and exploring cellular communication data* |
| 16:20-16:22 | **Shin Mi Hwa,** Department of Otorhinolaryngology, Yonsei University College of Medicine, South Korea<br>*Automated diagnosis of ear disease using ensemble deep learning with a big otoendoscopy image database* |
| 16:23-16:25 | **Justin Zhang,** Bergen County Academies, United States<br>*Topological Data Analysis and Persistence Theory Applications to Heart Arrhythmia* |
| 16:26-16:28 | **Fidel Ramirez,** Boehringer Ingelheim Pharma GmbH & Co. KG, Germany<br>*Single Cell Data Analysis Made Easy: scDisco an App for Non-Experts* |
| 16:29-16:31 | **Khaoula Elbedoui,** ENICarthage- LMTIC Tunisia, Tunisia<br>*Automated Acute Lymphoblastic Leukemia Detection and classification using Saliency Map* |
| 16:32-16:34 | **Haichao Wang,** Cancer Research UK Cambridge Institute, UK<br>*cfDNAPro: An R/Bioconductor package for robust and reproducible data analysis of cell-free DNA fragmentomic features* |
| 16:35-16:37 | **Luca Genz,** Leibniz Institut für Virologie, Universität Hamburg, Centre for Structural Systems Biology, Germany<br>*PICKLUSTER: A protein-interface clustering and analysis plug-in for UCSF ChimeraX* |
| 16:38-16:40 | **Aya Nakamura,** Graduate School of Medicine, Kyoto University, Japan<br>*Latent State Estimation of Cancer Patients Treated with Nivolumab Using Deep State Space Model* |

# BIOVIS COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH CONTINUED...

BioVis:
Biological Data
Visualizations

biovis

| | |
|---|---|
| 16:41-16:43 | **Astrid van den Brandt,** Eindhoven University of Technology, Netherlands<br>*Interactive Visualization of Gene Sets in Pangenomes* |
| 16:44-16:46 | **Banu Cetinkaya,** University of Tübingen, Germany<br>*Phylogenetic Context Using Phylogenetic Outlines* |
| 16:47-16:49 | **Sarah Ennis,** University of Galway, Ireland<br>*CCPlotR: An R package for the visualisation of cell-cell interactions* |
| 16:50-16:52 | **Indu Khatri,** Genmab B.V., Netherlands<br>*VIBE: An R package for the Visualization and Exploration of Bulk mRNA Expression data to prioritize cancer types for drug discovery* |
| 16:53-16:55 | **Gatis Melkus,** Institute of Mathematics and Computer Science, University of Latvia, Latvia<br>*Interactive visualisation for chromatin interaction networks* |
| 16:56-16:58 | **Pierre Grognet,** Institute for Integrative Biology of the Cell, Gif-sur-Yvette, France<br>*3D modeling of Hi-C contacts: seeing the spatial organization of fungal chromosomes* |
| 16:58-17:00 | **Xiaoyu Hou,** University of Queensland Diamantina Institute (UQDI) and University of Queensland Faculty of Medicine, Australia<br>*Understanding the contribution of immature myeloid cells to early melanoma establishment* |
| 17:00-18:00 | **Marc Baaden**<br>***Invited Presentation: Keynote Presentation:*** *Do we still need molecular graphics?* |

# BOSC COSI

## COSI TRACK PRESENTATIONS

### MONDAY, JULY 24TH

BOSC:
Bioinformatics
Open Source
Conference

| | |
|---|---|
| 10:30-10:35 | **Nomi Harris**<br>***BOSC opening remarks*** |
| 10:35-10:40 | ***Open Bioinformatics Foundation update*** |
| 10:40-10:45 | ***Platinum & Gold Sponsor videos*** |
| 10:45-10:50 | **Thomas Schlapp**<br>*CoFest summary* |
| 10:50-11:50 | **Sara EL-Gebali,** FAIRPoints & SciLifeLab-Data Centre, Sweden<br>*Invited Presentation: A New Odyssey: Pioneering the Future of Scientific Progress Through Open Collaboration* |
| 11:50-12:10 | **Prashant Uniyal,** Open Targets, Wellcome Genome Campus, United Kingdom<br>*Open Targets Platform and Open Targets Genetics: Supporting systematic open-source approach for drug-target identification and prioritisation* |
| 12:10-12:15 | **Michelle Audirac,** Harvard T.H. Chan School of Public Health, Harvard University, United States<br>*Systematic approach to preparing of medical claims data for biomedical research* |
| 12:15-12:20 | **Marina Pozhidaeva,** Deggendorf Institute of Technology, Germany<br>*Domain Specific Language and variables for systematic approach to genetic variant curation and interpretation* |
| 12:20-12:25 | **Ferdous Nasri,** Data Analytics & Computational Statistics, Germany<br>*Platform for global genomic surveillance of emerging diseases applied to Mpox* |
| 13:50-14:10 | **Renske de Wit,** Vrije Universiteit Amsterdam, Netherlands<br>*From 2023 to a FAIR Future; bridging the provenance metadata gap by centering the bioinformatics practitioner perspective* |
| 14:10-14:30 | **Todd Morse,** The Chan Zuckerberg Foundation, United States<br>*INTERPIN- a database for INtrinsic transcription TERminator hairPINs in bacteria* |
| 14:30-14:50 | **Priyanka Surana,** Wellcome Sanger Institute, United Kingdom<br>*Automated production engine to decode the tree of life* |
| 14:50-15:10 | **Tazro Ohta,** Institute for Advanced Academic Research, Chiba University, Japan<br>*Tonkaz: A workflow reproducibility scale for automatic validation of biological interpretation results* |
| 15:10-15:15 | **Cynthia Webster,** Ecology and Evolutionary Biology Department, United States<br>*EASEL (Efficient, Accurate, Scalable Eukaryotic modeLs), a tool for the improvement of eukaryotic structural and functional genome annotation* |
| 15:15-15:20 | **Brett Smith,** Curii Corporation, United States<br>*Realizing FAIR Principles For Data and Workflows with the Arvados Platform* |
| 16:00-16:05 | **Dimitri Perrin,** Queensland University of Technology, Australia<br>*Faster evaluation of CRISPR guide RNAs across entire genomes* |
| 16:05-16:10 | **Colin Diesh,** University of California, Berkeley, United States<br>*JBrowse 2: a modular genome browser with views of synteny and structural variation* |
| 16:10-16:15 | **Swapnil Sawant,** Phoenix Bioinformatics, United States<br>*PhyloGenes: A web-based tool for plant gene function inference using phylogenetics* |
| 16:20-16:25 | **Victoire Baillet,** Institut Pasteur, Université Paris Cité, France<br>*CCQTL: facilitating QTL mapping in the Collaborative Cross* |
| 16:25-16:30 | **Trevor Manz,** Harvard Medical School, United States<br>*higlass-python: A Programmable Genome Browser for Linked Interactive Visualization and Exploration of Genomic Data* |
| 16:30-16:35 | **Hiruna Samarakoon,** Genomics Pillar, Australia<br>*Accelerated nanopore basecalling with SLOW5 data format* |
| 17:00-17:20 | **Monica Munoz-Torres,** University of Colorado Anschutz Medical Campus, United States<br>*The GA4GH Phenopacket schema: A computable representation of clinical data for precision medicine* |

# BOSC COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

BOSC:
Bioinformatics
Open Source
Conference

| | |
|---|---|
| 10:30-11:30 | **Joseph M Yracheta,** Native Bio-Data Consortium, United States<br>*Invited Presentation: The Dissonance between Scientific Altruism & Capitalist Extraction: The Zero Trust and Federated Data Sovereignty Solution* |
| 11:30-11:50 | **Mitchell Shiell,** Ontario Institute of Cancer Research (OICR), Canada<br>*An Open Source Platform for Scalable Genomics Data Infrastructures* |
| 11:50-12:05 | **Chunlei Wu,** The Scripps Research Institute, United States<br>*BioThings SDK for building a knowledge base API ecosystem in the context of the Biomedical Translator Program* |
| 12:05-12:10 | **Sebastian Höpfl,** Institute for Stochastics and Applications (ISA), Germany<br>*Reproducible models in Systems Biology are higher cited* |
| 12:10-12:15 | **Bastian Greshake Tzovaras,** The Alan Turing Institute, United Kingdom<br>*AutSPACEs: a co-created and open source citizen science project to improve environments for sensory processing in autistic people* |
| 12:15-12:20 | **Bérénice Batut,** University of Freiburg & Open Life Science, Germany<br>*Open Life Science: A mentoring & training virtual program for Open Science ambassadors* |
| 12:20-12:25 | **Lisanna Paladin,** EMBL - European Molecular Biology Laboratory, Germany<br>*Building and Sustaining a Community of Computational Biologists at EMBL through Open-Source Tools and Four Pillars: Training, Community, Infrastructure, and Information* |
| 13:50-14:10 | **Session: Joint Session with Bio-Ontologies**<br>**Herve Menager,** Institut Pasteur, Université Paris Cité, France<br>*The Research Software Ecosystem: an open software metadata commons* |
| 14:10-14:30 | **Session: Joint Session with Bio-Ontologies**<br>**Sierra Moxon,** LBNL, United States<br>*The Linked data Modeling Language (LinkML): a general-purpose data modeling framework* |
| 14:30-14:50 | **Session: Joint Session with Bio-Ontologies**<br>**Justin Reese,** Lawrence Berkeley National Laboratory, United States<br>*KG-Hub: a framework to facilitate discovery using biological and biomedical knowledge graphs* |
| 14:50-14:55 | **Session: Joint Session with Bio-Ontologies**<br>**Vasundra Touré,** Swiss Institute of Bioinformatics SIB, Switzerland<br>*The SPHN Semantic Interoperability Framework: From clinical routine data to FAIR research data* |
| 14:55-15:00 | **Session: Joint Session with Bio-Ontologies**<br>**Matthew Crown,** Northumbria University, United Kingdom<br>*OMEinfo: global geographic metadata for -omics experiments* |
| 15:00-15:05 | **Bhavesh Patel,** FAIR Data Innovations Hub, California Medical Innovations Institute, United States<br>*FAIR-BioRS: Actionable guidelines for making biomedical research software FAIR* |
| 15:05-15:25 | **Session: Joint Session with Bio-Ontologies**<br>**Jackson Callaghan,** Scripps Research, United States<br>*BioThings Explorer: a query engine for a federated knowledge graph of biomedical APIs* |
| 15:25-15:30 | **Session: Joint Session with Bio-Ontologies**<br>**Nomi Harris**<br>*Presenter Q&A and Joint Session Closing* |
| 16:00-16:20 | **Tarcisio Mendes de Farias,** SIB Swiss Institute of Bioinformatics, Switzerland<br>*Ten lessons learned on improving the open data reusability of bioinformatics knowledge bases* |
| 16:20-16:25 | **Xiaofeng Liao,** RadboudUMC, Netherlands<br>*FAIR Data Cube, a FAIR data infrastructure for integrated multi-omics data analysis* |
| 16:25-16:30 | **Anja Adamov,** ETH Zurich, Switzerland<br>*Advancing FAIR meta-analyses of nucleotide sequence data with q2-fondue* |
| 16:30-16:35 | **Junda Huang,** Radboudumc, Netherlands<br>*Analysing multi-omics data through FAIR Data Points: a X-omics/TWOC demonstrator* |

# BOSC COSI

## COSI TRACK PRESENTATIONS

### TUESDAY, JULY 25TH CONTINUED

BOSC:
Bioinformatics
Open Source
Conference

16:40-
17:35

**Sara El-Gebali**
**Joseph Yracheta**
**Bastian Greshake-Tzovaras**
**Verana Ras**

*Panel: Panel on Open and Ethical Data Sharing*

17:35-
17:40

**Nomi Harris**

*BOSC Closing Remarks*

UNIVERSITY OF TURKU · MBC Medical Bioinformatics Centre · TURKU BIOSCIENCE · CSC · elixir · LUMI · TURKU · visitturku

eccb2024

16-20 September 2024
Turku, Finland

eccb2024

22nd European Conference on Computational Biology

Data and Algorithms
for health and science

www.eccb2024.fi

# CAMDA COSI

## COSI TRACK PRESENTATIONS

### WEDNESAY, JULY 26TH

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

| | |
|---|---|
| **10:30-10:40** | **David Kreil**<br>*Welcome* |
| **10:40-11:40** | **Edward Feil,** University of Bath, United Kingdom<br>***Invited Presentation:*** *How can large-scale genomics be used to manage antimicrobial resistance in non-clinical ('One-Health') settings?* |
| **11:40-12:00** | **Paweł Łabaj**<br>*The Anti-Microbial Resistance Prediction and Forensics Challenge - Introduction* |
| **12:00-12:20** | **Amay Ajaykumar Agrawal,** Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Germany<br>*Antimicrobial Resistance Prediction and Forensics* |
| **13:50-14:30** | **Dimitri Perrin,** Queensland University of Technology, Australia<br>*Geolocation of Antimicrobial Resistance Markers in Metagenomic Surveillance Data* |
| **14:30-14:50** | **Shoumi Sarkar,** University of Florida, United States<br>*Detecting Bacteriophages Associated with Antimicrobial Resistance in the Presence of Confounding Factors* |
| **14:50-15:30** | **Rodolfo Toscan,** Jagiellonian University - Małopolska Centre of Biotechnology, Poland<br>*Antimicrobial Resistance in Diverse Urban Microbiomes: Uncovering Patterns and Predictive Markers* |
| **16:00-16:30** | **Derry Mercer**<br>*Invited Presentation: Data diversity in Antimicrobial Resistance (AMR)* |
| **16:30-17:10** | **Mirna Vázquez Rosas Landa,** ICMyL, Mexico<br>*Antimicrobial Resistance Prediction and Forensics CAMDA 2023* |
| **17:10-17:20** | **Antonio Neme,** UNAM IIMAS, Mexico<br>*Exploratory analysis of antibiotic microbial resistance and its correlation with codon usage of microbes* |
| **17:20-17:30** | **Serghei Mangul,** University of Southern California, United States<br>*Evaluating the Robustness and Reproducibility of RNA-Seq Quantification Tools* |
| **17:30-17:40** | **Yu Ning Huang,** USC Alfred E. Mann School of Pharmacy and Pharmaceutical Sciences, United States<br>*A systematic assessment of the completeness of TCR databases across Mus musculus strains.* |
| **17:40-17:50** | **Elodine Coquelet,** CEA, France<br>*Data Lakehouse to support the developpement of AI models for predicting patient clinical response to targeted and immuno-therapies* |
| **17:50-18:00** | **Wenzhong Xiao**<br>*Day 1 closing remarks* |

# CAMDA COSI

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA

| | |
|---|---|
| 10:00-<br>10:10 | **Paweł Łabaj**<br>***Opening*** |
| 10:10-<br>11:10 | **Karsten Borgwardt,** Max Planck Institute of Biochemistry , Germany<br>*Invited Presentation: Predicting medical complications in intensive care units using machine learning* |
| 11:10-<br>11:30 | **Joaquin Dopazo**<br>*The Synthetic Clinical Health Records Challenge - Introduction* |
| 11:30-<br>11:50 | **Carlos Loucera,** Andalusian Platform for Computational Medicine, Spain<br>*Invited Presentation: Synthetic Clinical Health Records Challenge - the background analysis* |
| 13:20-<br>14:00 | **Malik Yousef,** Zefat Academic College, Israel<br>*CAMDA 2023 Challenge: Predictions of Pathology before Diagnosis from Electronic Health Record Visits* |
| 14:00-<br>14:10 | **Wenzhong Xiao**<br>*Future of Synthetic Clinical Health Records challenges* |
| 14:10-<br>14:20 | **Paweł Łabaj**<br>*Future of Anti-Microbial Resistance Prediction based challenges* |
| 14:20-<br>15:00 | **Michal Linial,** The Hebrew University of Jerusalem, Israel<br>*Hypothyroidism Genetics: Functional Insights from Gene-Based Association Studies in Large Populations* |
| 15:30-<br>15:50 | **David Kreil**<br>*CAMDA Trophy ceremony* |
| 15:50-<br>16:10 | **Serdar Bozdag, University of North Texas, United States**<br>*Proceedings Presentation: PPAD: A deep learning architecture to predict progression of Alzheimer's disease* |
| 16:10-<br>16:20 | **David Kreil**<br>*Closing remarks* |

# COMPMS COSI

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

CompMS: Computational Mass Spectrometry

| | |
|---|---|
| 8:30-<br>9:30 | **Laura Goracci**<br>***Invited Presentation: Lipostar 2: tools and workflows for LC-MS based untargeted lipidomics and epilipidomics*** |
| 10:00-<br>10:20 | **Azat Tagirdzhanov,** Helmholtz Institute for Pharmaceutical Research Saarland (HIPS), Germany<br>*VarMet: high-throughput annotation of small molecule mass spectra via the modification-tolerant search of chemical databases* |
| 10:20-<br>10:40 | **Johanna Galvis, University of Bordeaux,France**<br>*DIMet : An open-source tool for Differential analysis of Isotope-labeled Metabolomics data* |
| 10:40-<br>11:00 | **Tim Daniel Rose,** Structural and Computational Biology Unit, European Molecular Biology Laboratory, Germany<br>*Metabolic Networks approach improves molecular Annotation for Imaging Mass Spectrometry* |
| 11:00-<br>11:20 | **Ali Rahnavard,** The George Washington University, United States<br>*massSight: Metabolomics meta-analysis through multi-study data scaling, integration, and harmonization* |
| 11:20-<br>11:40 | **Oliver Crook,** University of CambridgeOxford, United Kingdom<br>*Residue resolved hydrogen deterium exchange using ResHDX* |
| 11:40-<br>12:00 | **Kyowon Jeong,** University of Tübingen, Germany<br>*Precursor deconvolution error estimation: the missing puzzle piece in false discovery rate in top-down proteomics* |
| 13:20-<br>14:20 | **Bernhard Renard**<br>***Invited Presentation: Learning and Understanding Spectra*** |
| 14:20-<br>14:40 | **Daniela Ferretti,** Max Planck Institute of Biochemistry, Germany<br>*MaxQuantAtlas creates large-scale, accurate cellular protein concentration maps from heterogeneous proteomics data* |
| 14:40-<br>15:00 | **Cecile Le Sueur,** EMBL Heidelberg, Germany, Germany<br>*Hierarchical Gaussian Process models uncover the dark meltome of Thermal Proteome Profiling experiments* |
| 15:30-<br>15:50 | **Kumar Saurabh Singh,** Wageningen University and Research, Netherlands<br>*Integrative omics for the discovery of biosynthetic pathways using MEANtools (MEtabolite ANticipation tools)* |
| 15:50-<br>16:30 | **Tomáš Pluskal,** IOCB Prague, Czech Republic<br>*Invited Presentation: Streamlining mass spectrometry data processing and spectral library generation in MZmine 3* |

# EDUCATION COSI

## COSI TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

Education: Computational Biology and Bioinformatics Education and Training

10:30-11:10

**Eija Korpelainen,** CSC - IT Center for Science, Finland

***Invited Presentation: Managing rapidly evolving training needs in the single-cell and spatial era***

11:10-11:30

**Marta Lloret-Llinares,** EMBL's European Bioinformatics Institue, United Kingdom

*The PerMedCoE training programme: building capacity in personalised medicine*

11:30-11:50

**Sofia Fertuzinhos,** Yale University, United States

*Bridging the Knowledge Gap: The Evolving Role of the Bioinformatics Support Hub in Facilitating Access to -Omics Data Analysis*

11:50-12:10

**Constance Jeffery,** University of Illinois at Chicago, United States

*MSFP: Undergraduate “Collaborate from Home” Research in Macromolecular Structure and Function*

12:10-12:30

**Frédéric Lemoine,** Institut Pasteur, France

*Proceedings Presentation: Reprohackathons: Promoting reproducibility in bioinformatics through training*

13:50-14:10

**Michelle D. Brazas,** Ontario Institute for Cancer Research, Canada

*Bioschemas Training Profiles: Development and implementation of a set of specifications for standardizing training information*

14:10-14:30

**Verena Ras,** Computational Biology Division, University of Cape Town, South Africa

*Making H3ABioNet Training FAIR and Impactful*

14:30-14:50

**Geert van Geest,** SIB Swiss Institute of Bioinformatics, Switzerland

*Glittr.org encourages re-use and co-development of FAIR training materials*

14:50-15:20

**Sarah Morgan**

*Invited Presentation: Bioinformatics Education Summit 2023 - outcomes and insights*

16:00-16:20

**Stephen Piccolo,** Brigham Young University, United States

*Evaluating ChatGPT's ability to solve basic- and moderate-level programming exercises used in an introductory bioinformatics course for undergraduates*

16:20-17:00

**Mohammad Asif Khan,** University of Doha for Science and Technology, Qatar

*Invited Presentation: Grand Challenges in Bioinformatics Education and Training*

17:00-18:00

**Asif Khan**
**Eija Korpelainen**
**Michelle Brazas**
**Russell Schwartz**
**Jason Williams**

*Panel: Panel discussion: Grand Challenges in Bioinformatics Education and Training*

# EVOLCOMPGEN COSI

## COSI TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

| | |
|---|---|
| 10:30-<br>10:50 | **Brice Letcher,** LBMC, ENS Lyon & CNRS, France<br>*Deciphering developmentally programmed DNA elimination in Mesorhabditis nematodes* |
| 10:50-<br>11:10 | **Mattéo Delabre,** University of Montreal, Canada<br>*An extended super-reconciliation model with synteny cuts and transfers through unsampled or extinct lineages* |
| 11:10-<br>11:30 | **Edward Braun,** University of Florida, United States<br>*Genome-scale compression-based phylogeny estimation: An improved approach that uses the physicochemical properties of amino acids.* |
| 11:30-<br>11:50 | **Ricardo C. Rodriguez de la Vega,** AgroParisTech, France<br>*Tempo and mode of degeneration in independently evolved non-recombining regions* |
| 11:50-<br>12:00 | **Giulia Sassi,** University of Parma, Italy<br>*Fast and performant pipeline for coevolutionary analysis of eukaryotic genes* |
| 12:00-<br>12:10 | **Vahiniaina Andriamanga,** Institute for Integrative Biology of the Cell, France<br>*Exploring the evolution of metabolic networks in fungi* |
| 12:10-<br>12:20 | **Laura Natalia González García,** Universidad de los Andes, Colombia<br>*Efficient homology-based annotation of transposable elements using minimizers* |
| 12:20-<br>12:30 | **Abigail Djossou,** University of Sherbrooke, Canada<br>*A Splice Aware Approach to Predict Genes in Eukaryotes.* |
| 13:50-<br>14:10 | **Tom Lesluyes,** The Francis Crick Institute, United Kingdom<br>*Robust and platform-independent CNA calling with ASCAT v3* |
| 14:10-<br>14:20 | **Gwanghoon Jung,** Pusan National University, South Korea<br>*Improving genome variation calls from non-human sequencing data using machine learning* |
| 14:20-<br>14:30 | **Yury Bukhman,** Morgridge Institute for Research, United States<br>*Deciphering mammalian genomes* |
| 14:30-<br>14:40 | **Menaka Thambiraja,** SASTRA DEEMED TO BE UNIVERSITY, India<br>*Comparative Genomics study of Bos Genome* |
| 14:40-<br>14:50 | **Sarah Farhat,** Institut Systématique Evolution Biodiversité (ISYEB), France<br>*Whole genome duplication and gene evolution in the hyperdiverse venomous gastropods* |
| 14:50-<br>15:00 | **Sean Chun-Chang Chen,** Taipei Medical University, Taiwan<br>*Comparative Genomics of the Arthropoda* |
| 15:00-<br>15:20 | **Yuval Tabach,** The Hebrew University-Hadassah Medical School, Israel<br>*Predicting Cancer-Protective Variants using comparative genomics* |
| 15:20-<br>15:30 | **Salvatore Cosentino,** The University of Tokyo, Japan<br>*SonicParanoid2: fast, accurate and comprehensive orthology inference with machine learning and language models* |
| 16:00-<br>16:20 | **Hanqing Zhao,** University of Twente, Netherlands<br>*Proceedings Presentation: Genome-wide Scans for Selective Sweeps using Convolutional Neural Networks* |
| 16:20-<br>16:30 | **Milana Frenkel-Morgenstern,** Bar-Ilan University, Israel<br>*EvoProDom: evolutionary modeling of protein families by assessing translocations of protein domains* |
| 16:30-<br>16:50 | **Xiaoyue Cui,** Carnegie Mellon University, United States<br>*Probing domain architecture design using language models* |
| 16:50-<br>17:00 | **Blessy Antony,** Virginia Polytechnic Institute and State University, United States<br>*Zoonosis Prediction Using Language Models* |

# EVOLCOMPGEN COSI

## COSI TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

**17:00-17:10** **Dongwook Kim,** Seoul National University, South Korea

*UFCG: database of universal fungal core genes and pipeline for genome-wide phylogenetic analysis of fungi*

**17:10-17:20** **Pavitra Selvakumar,** The Institute of Mathematical Sciences, (HBNI), India

*Clade Identification and Understanding Evolutionary Trajectory of Candida auris through Genome Rearrangements*

**17:20-17:40** **Yoann Anselmetti,** University of Sherbrooke, Canada

*Multiple RNA tree Robinson-Foulds Phylogeny*

**17:40-18:00** **Yasamin Tabatabaee,** University of Illinois at Urbana-Champaign, United States

*Proceedings Presentation: Phylogenomic branch length estimation using quartets*

# EVOLCOMPGEN COSI

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

EvolCompGen: Evolution & Comparative Genomics

8:30-
8:40

**Svetlana Shabalina, National Center for Biotechnology Information, United States**

*Nucleotide content differences in high and low pathogenic human coronaviruses affect RNA structural features, selective constraints, and compensatory evolution*

8:40-
8:50

**Rajeev Azad,** University of North Texas, United States

*Reconstructing horizontal gene flow network to understand prokaryotic evolution*

8:50-
9:10

**Hannes Neubauer,** Twincore/Hannover Medical School (MHH), Germany

*Improved interpretability of bacterial genome-wide associations using gene cluster centric k-mers*

9:10-
9:30

**Wataru Iwasaki,** The University of Tokyo, Japan

*Machine learning enables prediction of metabolic system evolution in bacteria*

10:00-
10:20

**Alexey Markin,** USDA-ARS, United States

*Proceedings Presentation: Phylogenetic Diversity Statistics for All Clades in a Phylogeny*

10:20-
10:30

**Felix L. Wascher,** Institute of Computational Biology, Department of Biotechnology, Austria

*Back to the roots: Phylogeny of wild and cultivated beets*

10:30-
10:50

**Maria Chikina,** University of Pittsburgh, United States

*AFconverge: alignment-free phylogenetic method for predicting convergent evolution of regulatory elements*

10:50-
11:00

**Zehra Köksal,** University of Copenhagen, Denmark

*SNPtotree – a software for sorting haploid variants into phylogenetic trees*

11:00-
11:20

**Kirti Biharie,** Delft University of Technology, Netherlands

*Proceedings Presentation: Cell type matching across species using protein embeddings and transfer learning*

11:20-
11:40

**Axel Fehrenbach,** University of Tübingen, Germany

*Uncovering the Dynamics of CRISPR Array Evolution with a New Maximum Likelihood Approach*

11:40-
11:50

**Andrea Tanzer, Medical University of Vienna, Austria**

*Evolutionary conservation of RNA editing - a case study in Filamin genes*

11:50-
12:00

**Abhishek Sharma,** National Centre for Biological Science, India

*Bioinformatics Analysis of Mutations Sheds Light on the Evolution of Dengue NS1 Protein With Implications in the Identification of Potential Functional and Druggable Sites*

13:20-
13:40

**Ziyun Guang,** Carleton College, United States

*Proceedings Presentation: A weighted distance-based approach for deriving consensus tumor evolutionary trees*

13:40-
14:00

**Etienne Sollier,** DKFZ, Germany

*Joint copy number and mutation phylogeny reconstruction from single-cell amplicon sequencing data*

14:00-
14:20

**Emilia Hurtado,** The University of British Columbia, Canada

*PhyClone: Accurate Bayesian reconstruction of cancer phylogenies from bulk sequencing*

14:20-
14:40

**Toby Baker,** The Francis Crick Institute, London, United Kingdom

*GRITIC sheds light on the evolution of copy number gains in genome doubled tumors*

14:40-
14:50

**Sarah Sandmann,** Institute of Medical Informatics, Germany

*Visualizing Clonal Evolution with clevRvis*

14:50-
15:00

**Ziqi Deng,** Centro de Biotecnología y Genómica de Plantas, Spain

*Enhancing Phylogenetic Data Interpretation with TreeProfiler, PhyloCloud, and ETE Toolkit*

# EVOLCOMPGEN COSI

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH, CONTINUED

EvolCompGen: Evolution & Comparative Genomics

EvolCompGen

| | | |
|---|---|---|
| 15:30-15:40 | **Sina Majidian,** University of Lausanne, Switzerland | *Orthology inference at scale with FastOMA* |
| 15:40-16:00 | **Viktor Senderov,** Ecole normale supérieure, France | *A Probabilistic Programming Approach to Investigate the Coevolution of Genes and Phenotypes in Birds* |
| 16:00-16:10 | **Chun Wu,** Rowan University, United States | *L-shaped distribution of the relative substitution rate (c/μ) observed for SARS-COV-2's genome, inconsistent with the selectionist theory, the neutral theory and the nearly neutral theory but a near-neutral balanced selection theory* |
| 16:10-16:30 | **Nadia Mabrouk**<br>**Dannie Durand** | *Panel: Panel discussion* |

## iSCB Green Pledge

**When attending conferences, I pledge to:**

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

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

# FUNCTION COSI

## COSI TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

## Function: Gene and Protein Function Annotation

| | |
|---|---|
| 10:30-11:10 | **Yana Bromberg**<br>*Invited Presentation: Learning from unpopular activities: can unknown functions guide exploration of microbiome environmental preferences?* |
| 11:10-11:30 | **Marcin Joachimiak,** Lawrence Berkeley National Laboratory, United States<br>*Understanding Earth’s Ecosystems with Machine Learning* |
| 11:30-11:50 | **Hong Su,** Max Planck Institute for Multidisciplinary Sciences, Germany<br>*A universal operon predictor for prokaryotic (meta-)genomics data using self-training* |
| 11:50-12:10 | **Anicet Ebou,** Laboratoire de Bioinformatique et Biostatistiques, Cote d'Ivoire<br>*hkgfinder: find and classify prokaryotic housekeeping genes for multilocus sequence analysis* |
| 12:10-12:30 | **Jérôme Arnoux,** Paris Saclay University, France<br>*PANORAMA: comparative pangenomics tools to explore interspecies diversity of microbial genomes* |
| 13:50-14:10 | **Olivier Lichtarge,** Baylor College of Medicine, United States<br>*Functional Variants Identify Sex-specific Genes and Pathways in Alzheimer’s Disease* |
| 14:10-14:30 | **Stephan Breimann,** Department of Bioinformatics, Technical University of Munich, Germany<br>*CHARTING γ-SECRETASE SUBSTRATES BY EXPLAINABLE AI* |
| 14:30-14:50 | **Pawel Szczerbiak,** Jagiellonian University, Poland<br>*Leveraging massive protein structure datasets for function prediction on a metagenomic scale* |
| 14:50-15:10 | **Joana Pereira,** Biozentrum and SIB Swiss Institute of Bioinformatics, University of Basel, Switzerland<br>*AlphaFold meets large-networks: deep-learning assisted protein family discovery at an unprecedented scale* |
| 15:10-15:30 | **Antoniya Aleksandrova,** National Institutes of Health, United States<br>*Systematic Analysis of Symmetry in Membrane Protein Function and Evolution* |
| 16:00-16:20 | **Tunca Dogan,** Hacettepe University, Turkey<br>*Holistic Protein Representation (HOPER): Few-Shot Protein Function Prediction with Multimodal Representation Learning* |
| 16:20-16:40 | **Patricia Medina,** CABD-CSIC, Spain<br>*Functional annotation of the regeneration process of a non-model organism using Language Models.* |
| 16:40-17:00 | **Flavio Pazos Obregón,** Institut Pasteur Montevideo, Uruguay<br>*Gene function prediction in five model eukaryotes exclusively based on gene relative location through machine learning* |
| 17:00-17:10 | **Kevin Muret,** Université Paris-Saclay, France<br>*Co-transcriptional cis-R-loop forming lncRNAs: a new lncRNA subclass?* |
| 17:10-17:20 | **Deborah Giordano,** Istituto di Scienze dell’Alimentazione, Italy<br>*Applications of bioinformatics methodologies in the study of lipoxygenases from diatoms* |
| 17:20-17:30 | **Aysun Urhan,** Delft University of Technology, Netherlands<br>*SAP: Synteny-aware gene function prediction for bacteria using protein embeddings* |
| 17:30-17:40 | **Miguel Fernández Martín,** Barcelona Supercomputing Center - Life Sciences, Spain<br>*Prediction of bacterial interactomes based on genome-wide coevolutionary networks: an updated implementation of the ContextMirror approach* |
| 17:40-17:50 | **Zachary Flamholz,** Albert Einstein College of Medicine, United States<br>*Large language models improve annotation of viral proteins* |
| 17:50-18:00 | **Dukka Kc,** Michigan Technological University, United States<br>*Predicting S-nitrosylation Sites in Proteins using a Transformer-based Protein language model* |

# FUNCTION COSI

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

## Function: Gene and Protein Function Annotation

| | |
|---|---|
| 8:30-<br>8:50 | **Aditi Shenoy,** Stockholm University, Sweden<br>*M-Ionic: Prediction of metal ion binding sites from sequence using residue embeddings* |
| 8:50-<br>9:10 | **Carlo De Rito,** University of Parma, Italy<br>*Machine-learning analysis of neofunctionalization following gene tandem duplication in vertebrate evolution* |
| 9:10-<br>9:30 | **Takeshi Obayashi,** Tohoku University, Japan<br>*Subagging of Principal Components for Sample Balancing: Building a Condition-Independent Gene Coexpression Resource from Public Transcriptome Data* |
| 10:00-<br>10:40 | **Walter Reade,** Kaggle / Google, USA<br>*Invited Presentation: Crowdsourcing (Data) Science on Kaggle* |
| 10:40-<br>11:00 | **M. Clara De Paolis Kaluza,** Khoury College of Computer Sciences, United States<br>*Kaggle-hosted Critical Assessment of protein Function Annotation algorithms (CAFA)* |
| 11:00-<br>11:20 | **Damiano Piovesan,** University of Padova, Italy<br>*CAFA-evaluator: A Python Tool for Benchmarking Ontological Classification Methods* |
| 11:20-<br>11:40 | **Shaojun Wang,** Fudan Unicersity, China<br>*NetGO 3.0: Protein Language Model Improves Large-scale Functional Annotations* |
| 11:40-<br>12:00 | **Erva Ulusoy,** Hacettepe University, Turkey<br>*Mutual Annotation-Based Prediction of Protein Domain Functions with Domain2GO* |
| 13:20-<br>13:40 | **Vishal Joshi,** EMBL-EBI, United Kingdom<br>*Predicting function in UniProt : rule-based and natural language models* |
| 13:40-<br>14:00 | **Jianlin Cheng,** University of Missouri - Columbia, United States<br>*Proceedings Presentation: Combining protein sequences and structures with transformers and equivariant graph neural networks to predict protein function* |
| 14:00-<br>14:20 | **Thanh Binh Nguyen,** The University of Queensland, Australia<br>*LEGO-CSM: a tool for functional characterisation of proteins* |
| 14:20-<br>14:40 | **David Medina,** Universidad de Magallanes, Chile<br>*Exploring machine learning algorithms and protein language model strategies to develop functional enzyme classification systems* |
| 14:40-<br>15:00 | **Function COSI Track Chairs**<br>*Function COSI Discussion- what do you think and what would you like to see in the future* |
| 15:30-<br>15:50 | **Andreas Grigorjew,** University of Helsinki, Finland<br>*Sensitive inference of alignment-safe intervals from biodiverse protein sequence clusters using EMERALD* |
| 15:50-<br>16:10 | **Mark Wass,** University of Kent, United Kingdom<br>*Identifying how evolution has tuned myosin function as species have got larger* |
| 16:10-<br>16:30 | **Alexandru Dumitrescu,** Aalto University, Finland<br>*Proceedings Presentation: TSignal: A transformer model for signal peptide prediction* |

# GENERAL COMP BIO

## COSI TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

| | |
|---|---|
| 8:30-8:50 | **Nico Pfeifer,** University of Tübingen, Germany<br>*Proceedings Presentation: PlasmoFAB: A Benchmark to Foster Machine Learning for Plasmodium falciparum Protein Antigen Candidate Prediction* |
| 8:50-9:10 | **Xuegong Zhang,** Tsinghua University, China<br>*hECA: Human Ensemble Cell Atlas as a Virtual Body for "In Data" Cellular Experiments* |
| 9:10-9:30 | **Gerda Cristal Villalba Silva,** Baylor College of Medicine, Brazil<br>*Cell reference atlas for transcriptional alterations of Mouse Trigeminal Ganglion Neurons revealed by Single-Cell Analysis* |
| 10:00-10:20 | **Erik Wright,** University of Pittsburgh, United States<br>*Accurately clustering enormous numbers of sequences with Clusterize* |
| 10:20-10:40 | **Florian Schmidt,** ImmunoScape Pte Ltd, Singapore<br>*Machine learning guides identification of virus antigen specificity based on deep T cell phenotypic profiles* |
| 10:40-11:00 | **Leonard Dervishi,** Case Western Reserve University, United States<br>*Proceedings Presentation: Privacy Preserving Population Stratification for Collaborative Genomic Research* |
| 11:00-11:20 | **Muyu Yang,** Carnegie Mellon University, United States<br>*Proceedings Presentation: UNADON: Transformer-based model to predict genome-wide chromosome spatial position* |
| 11:20-11:40 | **Vincent Wagner,** University of Stuttgart, Germany<br>*Proceedings Presentation: The impossible challenge of estimating non-existent moments of the Chemical Master Equation* |
| 11:40-12:00 | **Julian Stamp,** Brown University, United States<br>*Leveraging the Genetic Correlation between Traits Improves the Detection of Epistasis in Genome-wide Association Studies* |
| 12:00-12:20 | **Yunpei Xu,** Central South University, China<br>*Proceedings Presentation: CellBRF: a feature selection method for single-cell clustering using cell balance and random forest* |
| 13:20-13:40 | **Roei Zucker,** hebrew university of jerusalem, Israel<br>*Inferring Sex-Specific Genetic Signal in Hypertension by Gene-Based Association Methods on UK-Biobank Data* |
| 13:40-14:00 | **Aleix Bayona-Feliu,** Institute for Research in Biomedicine (IRB BARCELONA), Spain<br>*Genetic interactions between translesion DNA synthesis enzymes in cancer* |
| 14:00-14:20 | **Tony Hauptmann,** Johannes Gutenberg University of Mainz, Germany<br>*A Fair Experimental Comparison of Neural Network Architectures for Latent Representations of Multi-Omics for Drug Response Prediction* |
| 14:20-14:40 | **Yojana Gadiya,** University of Bonn, Germany<br>*Pharmaceutical patent landscaping: A novel approach to understand patents from the drug discovery perspective* |
| 14:40-15:00 | **Ashwin Adrian Kallor,** University of Gdansk, Poland<br>*CARMEN: a pan-HLA and pan-cancer proteogenomic database on antigen presentation to support cancer immunotherapy* |
| 15:30-15:50 | **Chuling Hu,** Sun Yat-sen University, China<br>*Integrative Multi-Omics Analysis Reveals Novel Immune Subtypes of Colorectal Cancer* |
| 15:50-16:10 | **Fuyi Li,** Northwest A&F University, China<br>*ProsperousPlus: An integrated platform for protease-specific substrate cleavage prediction and machine learning model construction of more than 100 proteases* |
| 16:10-16:30 | **Hakime Öztürk,** DKFZ, Germany<br>*Variant impact based patient similarity networks for cancer subtype analysis* |

# HITSeq COSI

## TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

**HiTSeq: High Throughput Sequencing Algorithms & Applications**

| | |
|---|---|
| 10:35-11:30 | **Irene Papatheodorou**<br>*Invited Presentation: Using single cell data to understand disease and cell type differences across species* |
| 11:30-11:50 | **Alister D'Costa,** University of Toronto, Canada<br>*Detecting Chromosomal Translocations using Augmented Genome Sequence Graphs* |
| 11:50-12:10 | **Alexander Schoenhuth,** Bielefeld University, Germany<br>*VeChat: Correcting errors in long reads using variation graphs* |
| 12:10-12:30 | **Can Firtina,** ETH Zurich, Switzerland<br>*Proceedings Presentation: RawHash: Enabling Fast and Accurate Real-Time Analysis of Raw Nanopore Signals for Large Genomes* |
| 13:40-14:10 | **Antonio Collesei,** Venetian Oncology Institute (IOV-IRCSS), Italy<br>*ALLSTAR: Inference of ReliAble CausaL RuLes between Somatic MuTAtions and CanceR Phenotypes* |
| 14:10-14:30 | **Arnab Chakrabarti,** RWTH Aachen University, Germany<br>*Estimate mutational signature exposure from sparse clinical sequencing data.* |
| 14:30-14:50 | **Yeremia Gunawan Adhisantoso,** Leibniz University Hannover, Germany<br>*PEKORA: High-Performance 3D Genome Reconstruction Using K-th Order Spearman's Rank Correlation Approximation* |
| 14:50-15:10 | **Laura Martens,** Technical University Munich, Germany<br>*Modeling fragment counts improves single-cell ATAC-seq analysis* |
| 15:10-15:30 | **Derek Aguiar,** University of Connecticut, United States<br>*Proceedings Presentation: Deep statistical modelling of nanopore sequencing translocation times reveals latent non-B DNA structures* |
| 16:00-16:20 | **Timothé Rouzé,** CNRS, Univ Lille, France<br>*SuperSampler: efficient scaled sketches for metagenomics and extensive genomics compositional analysis* |
| 16:20-16:40 | **Giulio Ermanno Pibiri,** Ca' Foscari University of Venice, Italy<br>*Proceedings Presentation: Locality-Preserving Minimal Perfect Hashing of K-Mers* |
| 16:40-17:00 | **Marco Oliva,** University of Florida, United States<br>*Building a Pangenome Alignment Index via Recursive Prefix-Free Parsing* |
| 17:00-17:20 | **Hartmut Häntze,** National Cheng Kung University, Taiwan<br>*Proceedings Presentation: Effects of Spaced k-mers on Alignment-Free Genotyping* |
| 17:20-17:40 | **Mingfu Shao,** The Pennsylvania State University, United States<br>*Proceedings Presentation: Seeding with Minimized Subsequence* |
| 17:40-18:00 | **Antoine Limasset,** CNRS, France<br>*Proceedings Presentation: Scalable sequence database search using Partitioned Aggregated Bloom Comb-Trees* |

# HITSeq COSI

## TRACK PRESENTATIONS

**HiTSeq: High Throughput Sequencing Algorithms & Applications**

### WEDNESDAY, JULY 26TH

| | |
|---|---|
| **10:35-11:30** | **Jan Korbel**<br>*Invited Presentation: Deciphering genomic disease mechanisms via single-cell & single-molecule sequencin* |
| **11:30-11:50** | **Andrew Mikalsen,** University at Buffalo, United States<br>*Proceedings Presentation: Coriolis: Enabling metagenomic classification on lightweight mobile devices* |
| **11:50-12:10** | **Jaebeom Kim,** Seoul National University, South Korea<br>*Metabuli: sensitive and specific metagenomic classification through a novel joint analysis of amino-acid and DNA sequences.* |
| **12:10-12:30** | **Dehan Cai,** City University of Hong Kong, Hong Kong<br>*HaploDMF: viral haplotype reconstruction from long reads via deep matrix factorization* |
| **13:50-14:10** | **Sandra Romain,** INRIA, France<br>*Proceedings Presentation: SVJedi-graph: improving the genotyping of close and overlapping Structural Variants with long reads using a variation graph* |
| **14:10-14:30** | **Jens-Uwe Ulrich,** Hasso Plattner Institute, Germany<br>*Taxor: Fast and space-efficient taxonomic classification of long reads* |
| **14:30-14:50** | **Gryte Satas,** Memorial Sloan Kettering Cancer Center, United States<br>*Leveraging Evolutionary Constraints to Refine Somatic Variant Calls from Single-Cell Sequencing Data* |
| **14:50-15:10** | **Jarno Alanko,** University of Helsinki, Finland<br>*Proceedings Presentation: Themisto: a scalable colored k-mer index for sensitive pseudoalignment against hundreds of thousands of bacterial genomes* |
| **15:10-15:30** | **Timofey Prodanov,** Heinrich Heine University, Germany<br>*Proceedings Presentation: A multi-locus approach for accurate variant calling in low-copy repeats using whole-genome sequencing* |
| **16:00-16:20** | **Koichiro Majima,** Nagoya University Graduate School of Medicine, Japan<br>*Variational Inference for Single-Cell Transcriptome with DNA Barcoding Reconstructs Unobserved Cell States and Differentiation Trajectories* |
| **16:20-16:40** | **Alice Lacan,** University Paris-Saclay (Univ. Evry), France<br>*Proceedings Presentation: GAN-based Data Augmentation for Transcriptomics: Survey and Comparative Assessment* |
| **16:40-17:00** | **Mikaela Koutrouli,** Novo Nordisk Foundation Center of Protein Research, Denmark<br>*Visualizing Spatial Transcriptomics with U-CIE Color Encoding* |
| **17:00-17:20** | **Corentin Thuilliez,** Gustave Roussy Cancer Campus, France<br>*CellFromSpace: A versatile tool for spatial transcriptomic data analysis through reference-free deconvolution and guided cell type/activity annotation* |
| **17:20-17:40** | **Michael P Lynch,** University of Limerick, Ireland<br>*demuxSNP: supervised demultiplexing of scRNAseq data using cell hashing and SNPs* |
| **17:40-18:00** | **Asia Mendelevich,** Altius Institute for Biomedical Sciences, United States<br>*Proceedings Presentation: Foreign RNA spike-ins enable accurate allele-specific expression analysis at scale* |

# iRNA COSI

## TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

iRNA:
Integrative
RNA Biology

IRB
Integrative RNA Biology
group

| | | |
|---|---|---|
| 10:30-10:40 | **Michelle Scott** | ***Introduction to iRNA COSI session*** |
| 10:40-11:20 | **Irmtraud Meyer** | *Invited Presentation: Methods for investigating the dancing transcriptome* |
| 11:20-11:40 | **Liang Huang,** Oregon State University, United States | *LinearDesign: Algorithm for Optimized mRNA Design Improves Stability and Immunogenicity (Nature paper)* |
| 11:40-12:00 | **Marc Horlacher,** Helmholtz Center Munich, Germany | *Towards In-Silico CLIP-seq: Predicting Protein-RNA Interaction via Sequence-to-Signal Learning* |
| 12:00-12:20 | **Timothy Warwick,** Goethe University Frankfurt, Germany | *Probabilistic models of RNA•DNA:DNA triplex formation accurately predict genome-wide RNA-DNA interactions* |
| 12:20-12:30 | **Coline Gianfrotta,** Univ. Paris-Saclay, France, France | *On the predictibility of A-minor motifs from their local contexts* |
| 13:50-14:10 | **Tianshuo Zhou,** Oregon State University, United States | *Proceedings Presentation: RNA Design via Structure-Aware Multi-Frontier Ensemble Optimization* |
| 14:10-14:20 | **Lambert Moyon,** Helmholtz Center Munich, Germany | *A systematic benchmark of machine learning methods for protein-RNA interaction prediction* |
| 14:20-14:40 | **Ranjan Kumar Maji,** Goethe University and Uniklinikum Frankfurt, Germany | *miRarmature: a time series analysis framework for paired miRNA and RNA-seq data reveals new regulatory dynamics* |
| 14:40-15:00 | **Karina Jouravleva,** University of Massachusetts Medical School, United States | *High-throughput analysis of microRNA-binding thermodynamics and kinetics by RNA Bind-n-Seq (RBNS)* |
| 15:00-15:20 | **Stéphane Labialle,** Université de Lorraine, France | *Molecular function of the non-coding RNAs snord116 involved in Prader Willi syndrome* |
| 15:20-15:30 | **Multiple Multiple** | *Poster flash talks* |
| 16:00-16:40 | **Julien Gagneur** | *Invited Presentation: Calling and predicting aberrant splicing* |
| 16:40-17:00 | **Ruiyan Hou,** The University of Hong Kong, Hong Kong | *CamoTSS: analysis of alternative transcription start sites for cellular phenotypes and regulatory patterns from 5' scRNA-seq data* |
| 17:00-17:10 | **Mathias Witte Paz,** University of Tübingen, Germany | *TSS-Captur - A Transcription Starting Site-based Characterization Pipeline for Transcribed but Unclassified Prokaryotic RNA transcripts* |
| 17:10-17:30 | | *Poster flash talks* |
| 17:30-18:00 | | *Extra time for poster viewing* |

# iRNA COSI

## TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

iRNA: Integrative RNA Biology

IRB Integrative RNA Biology group

| | |
|---|---|
| **8:30-8:50** | **Clarence Mah,** University of California San Diego, United States<br>***Machine learning methods for decoding subcellular RNA organization from spatial transcriptomics data*** |
| **8:50-9:10** | **Jan Gorodkin,** University of Copenhagen, Denmark<br>*CRISPRon-ABE: Enhanced CRISPR adenine base editing design from data generation and deep learning* |
| **9:10-9:30** | **Ezequiel Calvo-Roitberg,** UMass Chan Medical School, United States<br>*Kinetic barcoding: A novel tool to estimate multi-temporal RNA biogenesis kinetics* |
| **10:00-10:20** | **Teresa Rummel,** Julius-Maximilians-Universität, Würzburg, Germany<br>*grandR: a comprehensive package for nucleotide conversion RNA-seq data analysis* |
| **10:20-11:00** | **Maayan Salton,** Hebrew University, Israel<br>*Invited Presentation: Decoding the Masters of Gene Expression: Unraveling the Influence of Promoters and Enhancers on Alternative Splicing* |
| **11:00-11:20** | **Mathieu Quesnel-Vallières,** University of Pennsylvania, United States<br>*Discovery of new immunotherapy targets in cancer from transcriptomic data* |
| **11:20-11:40** | **Klemens Hertel,** University of California, Irvine, United States<br>*Nutritional Control of Splicing Fidelity Contributes to Methionine Dependence of Cancer* |
| **11:40-12:00** | **Rubén Chazarra-Gil,** Barcelona Supercomputing Center, Spain<br>*Analyzing human population differences in alternative splicing at single-cell resolution* |
| **13:20-13:30** | **Sylvain Mareschal,** Hospices Civils de Lyon, Bron, France<br>*Detecting aberrant splicing events in isolated patient samples using short read RNA-seq with SAMI* |
| **13:30-13:40** | **San Jewell,** University of Pennsylvania, United States<br>*A Unified MAJIQ-L View of Transcriptome Complexity from Short and Long RNA-seq Reads* |
| **13:40-14:00** | **Asa Ben-Hur,** Colorado State University, United States<br>*Evidence for the role of transcription factors in the co-transcriptional regulation of intron retention* |
| **14:00-14:20** | **Karine Choquet,** Harvard Medical School, United States<br>*Pre-mRNA splicing order across long multi-intronic transcripts* |
| **14:20-14:40** | **Hoang Thu Trang Do,** Universität des Saarlandes, Germany<br>*Deregulation of Epigenetic Marks is Associated with Differential Exon Usage of Developmental Genes* |
| **14:40-15:00** | **Maria Vlasenok,** Skolkovo Institute of Science and Technology, Russia<br>*Transcriptome sequencing suggests that pre-mRNA splicing counteracts widespread intronic cleavage and polyadenylation* |
| **15:30-15:50** | **Alexander Jürgen Petri,** Stockholm University, Sweden<br>*Proceedings Presentation: isONform: reference-free transcriptome reconstruction from Oxford Nanopore data* |
| **15:50-16:20** | **Hagen Tilgner**<br>*Invited Presentation: Technologies for RNA isoform investigations across mouse brain development and brain regions as well as human brain structures* |
| **16:20-16:30** | **Klemens Hertel**<br>*Poster prize and closing remarks* |

# MICROBIOME COSI

## TRACK PRESENTATIONS

### MONDAY, JULY 24TH

MICROBIOME

| | |
|---|---|
| 10:30-11:15 | **Nicola Segata**<br>*Invited Presentation: Computational metagenomics to mine the hidden diversity of the human microbiome* |
| 11:15-11:45 | **Wei Wei,** the Pennsylvania State University, United States<br>*Proceedings Presentation: Finding phylogeny-aware and biologically meaningful averages of metagenomic samples: L2UniFrac* |
| 11:45-12:00 | **David Koslicki,** Penn State University, United States<br>*YACHT: an ANI-based statistical test to detect microbial presence/absence in a metagenomic sample* |
| 12:00-12:15 | **Pande Putu Erawijantari,** University of Turku, Finland<br>*Predicting Incident Heart Failure from the Microbiome: The FINRISK DREAM challenge* |
| 12:15-12:30 | **George Bouras,** The University of Adelaide, Australia<br>*Multiomic Integration Reveals Low Intra-tumoural Bacterial Load is Associated with Mesenchymal Phenotype and Increased Patient Mortality in Human Papilloma Virus Negative Head and Neck Squamous Cell Carcinomas* |
| 13:50-14:20 | **Todd Treangen,** Rice University, United States<br>*Proceedings Presentation: Bakdrive: Identifying a Minimum Set of Bacterial Species Driving Interactions across Multiple Microbial Communities* |
| 14:20-14:35 | **Xiangnan Xu,** Humboldt-Universität zu Berlin, Germany<br>*Unraveling Diet-Related Heterogeneous Microbial Interactions with NEGMoE: A Nutrition-Aware Graphical Mixture of Experts Model* |
| 14:35-14:50 | **Feargal Ryan,** South Australian Health and Medical Research Institute & Flinders University, Australia<br>*A systems immunology study to assess the impact of early-life antibiotic exposure and the gut microbiota on infant vaccine immune responses.* |
| 14:50-15:05 | **Hannah-Marie Martiny,** Technical University of Denmark, Denmark<br>*A curated data resource of 214K metagenomes for characterization of the global antimicrobial resistome* |
| 15:05-15:20 | **Martin Larralde,** European Molecular Biology Laboratory, Germany<br>*Deciphering the secondary metabolism of the human gut microbiome* |
| 15:20-15:30 | **Zhong Wang,** Lawrence Berkeley National Lab, United States<br>*Axolotl: A Scalable Apache Spark-based Library for High-troughput Genomic Data Analysis* |
| 16:00-16:30 | **Mihir Mongia,** Carnegie Mellon, United States<br>*Proceedings Presentation: AdenPredictor: Accurate prediction of the adenylation domain specificity of nonribosomal peptide Biosynthetic Gene Clusters in Microbial Genomes* |
| 16:30-16:45 | **Ruoshi Zhang, Max Planck Institute for Multidsciplinary Sciences, Germany**<br>*Spacedust: de novo discovery of conserved gene clusters in microbial genomes* |
| 16:45-17:00 | **Caner Bagci,** University of Tuebingen, Germany<br>*BGC Atlas: A Web Resource for Exploring the Diversity of Biosynthetic Gene Clusters in Metagenomes* |
| 17:00-17:15 | **Xinpeng Zhang,** University of Nebraska-Lincoln, United States<br>*dbCAN-seq update: CAZyme gene clusters and substrates in microbiomes* |
| 17:15-17:30 | **Luise Rauer,** University of Augsburg, Germany<br>*Meta-analysis of bacterial mock communities reveals status of FAIR principles and impact of protocol biases on microbiome sequencing results* |
| 17:30-17:45 | **Mary Maranga,** Jagiellonian University, Poland<br>*Functional annotation of metagenomes and microbial genomes using a deep learning-based method* |
| 17:45-18:00 | **Anatoly Sorokin, Okinawa Institute of Science and Technology, Japan**<br>*Analysis of the Functional Characteristics of Microbial Communities with FBA-PRCC* |

# MICROBIOME COSI

## TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

| | |
|---|---|
| 10:30-<br>11:15 | **Karoline Faust**<br>***Invited Presentation: From hairballs to hypotheses: network analysis applied to microbiome data*** |
| 11:15-<br>11:45 | **Jiayu Shang, City University of Hong Kong, Hong Kong**<br>*Proceedings Presentation: PhaVIP: Phage VIrion Protein classification based on chaos game representation and Vision Transformer* |
| 11:45-<br>12:00 | **Romane Junker, Université Paris-Saclay, France**<br>*Integrating metagenetic datasets through microbial association networks to compare microbial communities from lacto-fermented vegetables* |
| 12:00-<br>12:15 | **Seungjun Ahn,** University of Florida, United States<br>*Differential Co-Abundance Network Analyses for Microbiome Data Adjusted for Clinical Covariates Using Jackknife Pseudo-Values* |
| 12:15-<br>12:30 | **Giacomo Baruzzo,** University of Padova, Italy<br>*Comprehensive benchmarking of differential abundance methods in microbiome data* |
| 13:50-<br>14:20 | **Luis Pedro Coelho,** Fudan University, China<br>*Proceedings Presentation: SemiBin2: self-supervised contrastive learning leads to better MAGs for short- and long-read sequencing* |
| 14:20-<br>14:35 | **Hansheng Xue,** Australian National University, Australia<br>*Metagenomic Binning using Graph Neural Networks* |
| 14:35-<br>14:50 | **Xubo Tang,** City University of Hong Kong, Hong Kong<br>*Identifying plasmid contigs from metagenomic data using Transformer* |
| 14:50-<br>15:05<br>\ | **Ataberk Donmez,National Cancer Institute, National Institutes of Health, United States**<br>*stRainy: assembly-based metagenomic strain phasing using long reads* |
| 15:05-<br>15:20 | **Roland Faure,** Univ. Rennes, France<br>*HairSplitter: separating similar strains in metagenome assemblies* |
| 15:20-<br>15:30 | **Chandrima Bhattacharya,** Weill Cornell Medicine, United States<br>*Genomic Drivers for Prioritizing Candidates during Genome Mining* |
| 16:00-<br>16:30 | **Aniket Mane,** Simon Fraser University, Canada<br>*Proceedings Presentation: PlasBin-flow: A flow-based MILP algorithm for plasmid contigs binning* |
| 16:30-<br>16:45 | **Yazhini Arangasamy,** Max Planck Institute for Multidisciplinary Sciences, Germany<br>*McDevol: probabilistic metagenome binning using Bayesian statistics* |
| 16:45-<br>17:00 | **Beatriz García-Jiménez,** Biome Makers Inc., United States<br>*AI-Powered Latent Prediction of Soil Microbiome from Environmental Data* |
| 17:00-<br>17:15 | **Jim Shaw,** University of Toronto, Canada<br>*Fast and robust metagenomic sequence comparison through sparse chaining with skani* |
| 17:15-<br>17:30 | **Milot Mirdita,** Seoul National University, South Korea<br>*Petasearch: Efficient and Sensitive Sequence Comparison at Scale* |
| 17:30-<br>17:45 | **Anupam Gautam,** University of Tübingen/Max Planck Institute for Biology Tübingen, Germany<br>*Using AnnoTree to Get More Assignments, Faster, in DIAMOND+MEGAN Microbiome Analysis* |
| 17:45-<br>18:00 | **Sara Fumagalli,** University of Milano-Bicocca, Italy<br>*MADAME, an easy-to-use tool for retrieving data and metadata in microbiome analysis* |

# MLCSB COSI

## TRACK PRESENTATIONS

MLCSB: Machine Learning in Computational and Systems Biology

### MONDAY, JULY 24TH

**10:30-11:30** **Anshul Kundaje,** Stanford University, USA

*Invited Presentation: Deciphering multiple facets of the cis-regulatory code with deep learning models of regulatory DNA*

**11:30-11:40** **Lucas Ferreira Silva,** Harvard/ MGH, United States

*DNA-Diffusion: Generative diffusion models for enhancing gene expression control through synthetic regulatory elements*

**11:40-11:50** **Surag Nair,** Stanford University, United States

*Contemporary multi-task deep learning models of regulatory DNA exhibit widespread sensitivity to spurious sequence features*

**11:50-12:00** **Pyaree Mohan Dash,** Berlin Institute of Health at Charité - Universitätsmedizin, Germany

*Massively parallel characterization of transcriptional regulatory elements in three diverse human cell types*

**12:00-12:10** **Anupama Jha,** University of Washington, United States

*Chrome-Zoo: cross-species chromatin profile prediction using DNA Zoo data*

**12:10-12:20** **Kelly Cochran,** Stanford University, United States

*ProCapNet: Dissecting the cis-regulatory syntax of transcription initiation with deep learning*

**12:20-12:30** **Alex Hawkins-Hooker,** University College London, United Kingdom

*Getting Personal with Epigenetics: Towards Individual-specific Epigenomic Imputation with Machine Learning*

**14:30-15:30** **Bo Wang**
**Dana Pe'er**
**Mo Lotfollahi**

*Panel: MLCSB Panel: Biological Foundation Models*

**16:00-17:00** **Smita Krishnaswamy**

*Invited Presentation: Deep Geometric Methods for Learning Dynamics and Interactions from Cellular Data*

**17:00-17:20** **Aurélien Beaude,** Université Paris Saclay, France

*Proceedings Presentation: AttOmics: Attention-based architecture for diagnosis and prognosis from Omics data*

**17:20-17:40** **Yueqi Sheng,** Harvard University, United States

*Proceedings Presentation: Robust reconstruction of single cell RNA-seq data with iterative gene weight updates*

**17:40-17:50** **Geert-Jan Huizing,** Institut Pasteur, Université Paris Cité, France

*Paired single-cell multi-omics data integration with Mowgli*

**17:50-18:00** **Richard H. Scheuermann,** J. Craig Venter Institute, United States

*Machine learning-based informative feature selection for single cell RNA sequencing cell type characterization*

# MLCSB COSI

## TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

## MLCSB: Machine Learning in Computational and Systems Biology

**10:30-11:30**
**Jennifer Listgarten**

***Invited Presentation: Some Thoughts on Machine Learning-based Protein Engineering***

**11:30-11:50**
**Haoting Zhang,** University of Cambridge, United Kingdom

*Proceedings Presentation: SynBa: Improved estimation of drug combination synergies with uncertainty quantification*

**11:50-12:10**
**Eric Lee,** Department of Molecular Oncology, BC Cancer Agency, Canada

*Proceedings Presentation: SpatialSort: A Bayesian Model for Clustering and Cell Population Annotation of Spatial Proteomics Data*

**12:10-12:20**
**Eloise Berson,** Stanford University, United States

*Whole Genome Deconvolution Unveils Alzheimer's Resilient Epigenetic Signature*

**12:20-12:30**
**Will Thrift,** Genentech, United States

*Graph-pMHC: Graph Neural Network Approach to MHC Class II Peptide Presentation and Antibody Immunogenicity*

**14:10-14:30**
**Alperen Dalkiran,** Middle East Technical University, Turkey

*Proceedings Presentation: Transfer Learning for Drug-Target Interaction Prediction*

**14:30-14:50**
**Zhijian Huang,** Central South University, China

*Proceedings Presentation: DeepCoVDR: Deep transfer learning with graph transformer and cross-attention for predicting COVID-19 drug response*

**14:50-15:10**
**Mogan Gim,** Korea University, South Korea

*Proceedings Presentation: ArkDTA: Attention Regularization guided by non-Covalent Interactions for Explainable Drug-Target Binding Affinity Prediction*

**15:10-15:20**
**Erva Ulusoy,** Hacettepe University, Turkey

*SELFormer: Molecular Representation Learning via SELFIES Language Models*

**15:20-15:30**
**Atabey Ünlü,** Hacettepe University, Turkey

*Target Specific De Novo Design of Drug Candidate Molecules with Graph Transformer-based Generative Adversarial Networks*

**16:00-17:00**
**Jean-Phillipe Vert,** Owkin, France

*Invited Presentation: Deep learning for biological sequences*

**17:00-17:20**
**Jonas Christian Ditz,** University of Tübingen, Germany

*Proceedings Presentation: COmic: Convolutional Kernel Networks for Interpretable End-to-End Learning on (Multi-)Omics Data*

**17:20-17:30**
**Pranam Chatterjee,** Duke University, United States

*Structure-Independent Peptide Binder Design via Generative Language Models*

**17:30-17:40**
**Nikolaus Fortelny,** University of Salzburg, Austria

*Reliable interpretability of deep learning on biological networks*

**17:40-17:50**
**Judith Bernett,** Technical University of Munich, Germany

*Cracking the black box of deep sequence-based protein-protein interaction prediction*

**17:50-18:00**
**Yaron Orenstein,** Bar-Ilan University, Israel

*G4mismatch: Deep neural networks to predict G-quadruplex propensity based on G4-seq data*

# NETBIO COSI

## TRACK PRESENTATIONS

NetBio:
Network Biology

### MONDAY, JULY 24TH

| | |
|---|---|
| 10:30-11:10 | **Natasa Przulj**<br>*Invited Presentation: Omics Data Fusion for Understanding Molecular Complexity Enabling Precision Medicine* |
| 11:10-11:30 | **Paolo Pellizzoni,** ETH Zurich, Switzerland<br>*Proceedings Presentation: Higher-order genetic interaction discovery with network-based biological priors* |
| 11:30-11:50 | **Sergio Doria-Belenguer,** Barcelona Supercomputing Centre, Spain<br>*The axes of biology: a novel axes-based network embedding approach to decipher the fundamental mechanisms of the cell* |
| 11:50-12:10 | **Benoît Aliaga,** Centre de Recherches en Cancérologie de Toulouse, France<br>*Exploring the relation between evolutionary gene age, gene expression and chromatin 3D structure in cancer* |
| 12:10-12:30 | **Mireya Diaz, Western Michigan University, United States**<br>*Cytokine Module Dynamics during Respiratory Challenges among Pre-diabetic Individuals* |
| 13:50-14:10 | **Enio Gjerga,** University Hospital Heidelberg, Germany<br>*Proceedings Presentation: Characterising Alternative Splicing Effects on Protein Interaction Networks with LINDA* |
| 14:10-14:30 | **Giacomo Baruzzo,** University of Padova, Italy<br>*scSeqComm: a statistical and network-based framework to infer inter- and intra-cellular communication from single-cell RNA sequencing data* |
| 14:30-14:50 | **Florian Klimm,** Novo Nordisk Research Centre Oxford, United Kingdom<br>*Identifying and refining regulatory pathways through full-genome loss-of-function correlation networks* |
| 14:50-15:10 | **Océane Cassan,** LIRMM, Univ Montpellier, France<br>*Gene-specific optimization of binding sites integration to expression data improves regression-based Gene Regulatory Network inference in Arabidopsis thaliana* |
| 15:10-15:30 | **Addie Woicik,** University of Washington, United States<br>*Proceedings Presentation: Gemini: Memory-efficient integration of hundreds of gene networks with high-order pooling* |
| 16:00-16:20 | **Kerr Ding,** Georgia Institute of Technology, United States<br>*Supervised biological network alignment with graph neural networks* |
| 16:20-16:40 | **Joseph Szymborski,** McGill University, Canada<br>*Accurate Cross-Species, Out-of-Distribution Predictions of Protein-Protein Interactions using Deep Learning* |
| 16:40-17:00 | **Samuel Pastva,** Institute of Science and Technology Austria, Austria<br>*Proceedings Presentation: Trap spaces of multi-valued networks: Definition, computation, and applications* |
| 17:00-17:20 | **Sara Mohammad-Taheri,** Northeastern Univerusity, United States<br>*Proceedings Presentation: Optimal adjustment sets for causal query estimation in partially observed biomolecular networks* |
| 17:20-18:00 | **Desmond Higham**<br>*Invited Presentation: Triadic Closure and Bistability in Evolving Networks* |

# REGSYS COSI

## TRACK PRESENTATIONS

### TUESDAY, JULY 25TH

RegSys:
Regulatory &
Systems
Genomics

**10:30-11:10** **Julien Gagneur**

*Invited Presentation: Exploring in-silico representations of the regulatory code*

**11:10-11:30** **Mathys Grapotte,** CNRS - Sanofi, France

*Impact of transcription initiation at microsatellites on gene expression*

**11:30-11:50** **Shaun Mahony,** The Pennsylvania State University, United States

*Joint sequence and chromatin neural networks characterize the differential abilities of Forkhead transcription factors to engage inaccessible chromatin*

**11:50-12:10** **Christopher Hill,** NIH, United States

*Proceedings Presentation: ChromDL: A Next-Generation Regulatory DNA Classifier*

**12:10-12:30** **Maria Chikina,** University of Pittsburgh, United States

*Proceedings Presentation: An intrinsically interpretable neural network architecture for sequence to function learning*

**13:50-14:30** **Caroline Uhler**

*Invited Presentation: Causal Representation Learning in the Context of Gene Regulation*

**14:30-14:50** **Ishika Luthra,** University of British Columbia, Canada

*Biochemical activity is the default DNA state in eukaryotes*

**14:50-15:10** **Luca Pinello,** Massachusetts General Hospital, Boston

*CRISPR-CLEAR - In-Situ Investigation of Genotype-to-Phenotype Relationship with Nucleotide Level Resolution CRISPR saturation mutagenesis screens*

**15:10-15:30** **Jessica Zhou,** University of California San Diego, United States

*Genome-wide analysis of CRISPR perturbations indicates that enhancers act multiplicatively, but provides no evidence for epistatic-like enhancer interactions*

**16:00-16:40** **Nir Yosef**

*Invited Presentation: Analysis for single cell genomics in multi-donor settings*

**16:40-17:00** **Xiuwei Zhang,** Georgia Institute of Technology, United States

*scDisInFact: disentangled learning for integration and prediction of multi-batch multi-condition single cell RNA-sequencing data*

**17:00-17:20** **Amin Emad,** McGill University, Canada

*Simulating scRNA-seq using causal generative adversarial networks*

**17:20-17:40** **Jingyi Jessica Li,** University of California, Los Angeles, United States

*scDesign3 generates realistic in silico data for multimodal single-cell and spatial omics*

**17:40-18:00** **Jacob Schreiber**, Stanford University, United States

*DragoNNFruit: Learning cis- and trans-regulatory factors of chromatin accessibility profiles at single base and single cell resolution*

# REGSYS COSI

## TRACK PRESENTATIONS

### WEDNESDAY, JULY 26TH

RegSys:
Regulatory &
Systems
Genomics

| | |
|---|---|
| **10:30-<br>11:10** | **Mikhail Spivakov**<br>***Invited Presentation: Probing the relationship between enhancer activity, connectivity, and gene expression*** |
| **11:10-<br>11:30** | **Vipin Kumar,** NCMM, University of Oslo, Norway<br>*BootTHiC: Integrating HiC and transcriptomics to detect transcriptional hubs* |
| **11:30-<br>11:50** | **Aayush Grover,** Department of Computer Science, ETH Zürich, Switzerland<br>*UniversalEPI: An Attention-based Method to Predict Chromatin Interactions in Unseen and Rare Cell Types* |
| **11:50-<br>12:10** | **Ferhat Ay,** La Jolla Institute for Immunology, United States<br>*Identifying genetic variants associated with chromatin looping and genome organization* |
| **12:10-<br>12:30** | **Yanlin Zhang,** McGill University, Canada<br>*Proceedings Presentation: Reference panel guided super-resolution inference of Hi-C data* |
| **13:50-<br>14:30** | **Laura Cantini,** CNRS and Institut Pasteur, France<br>*Invited Presentation: Multi-modal learning for single-cell multi-omics data integration* |
| **14:30-<br>14:50** | **Aryan Kamal,** EMBL, Germany<br>*Active repression of alternative cell fates safeguards hepatocyte identity and prevents liver tumorigenesis* |
| **14:50-<br>15:10** | **Pierre De Langen,** Aix Marseille Univ, France<br>*Normal and cancer tissues are accurately characterised by intergenic transcription at RNA polymerase 2 binding sites* |
| **15:10-<br>15:30** | **Mihir Bafna,** Georgia Institute of Technology, United States<br>*Proceedings Presentation: CLARIFY: Cell-cell interaction and gene regulatory network refinement from spatially resolved transcriptomics* |
| **16:00-<br>16:40** | **Ana Conesa**<br>*Invited Presentation: Third-generation sequencing technologies to investigate the complexity of transcriptomes* |
| **16:40-<br>17:00** | **Hatice Osmanbeyoglu,** University of Pittsburgh, United States<br>*STAN, a computational framework for inferring spatially informed transcription factor activity networks* |
| **17:00-<br>17:20** | **Cassandra Burdziak,** Memorial Sloan Kettering Cancer Center, United States<br>*Proceedings Presentation: scKINETICS: inference of regulatory velocity with single-cell transcriptomics data* |
| **17:20-<br>17:40** | **Ibrahim Ihsan Taskiran,** VIB-KU Leuven Center for Brain & Disease Research, Belgium<br>*Cell type directed design of synthetic enhancers* |
| **17:40-<br>18:00** | **Marta Mele,** Barcelona Supercomputing Center, Spain<br>*A robust statistical framework for genewise single cell differential expression metaanalysis in the context of population based single cell studies.* |

# SYSMOD COSI

## TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

**SysMod: Computational Modeling of Biological Systems**

SYSMOD

| | |
|---|---|
| 8:30-8:40 | **Matteo Barberis**<br>*Introduction to SysMod 2023* |
| 8:40-9:20 | **Ina Koch,** Goethe University Frankfurt, Germany<br>***Invited Presentation: Petri net formalism in biology at the molecular and cellular leve*** |
| 9:20-9:30 | **Eberhard Voit,** Georgia Institute of Technology, United States<br>*Biological Multiscale Systems Analysis with Template-and-Anchor Models* |
| 10:00-10:20 | **Mathieu Bolteau,** Nantes Université, France<br>*Boolean networks as a framework to model human preimplantation development* |
| 10:20-10:40 | **Maulik Nariya,** Institut de Génétique et de Biologie Moléculaire et Cellulaire, France<br>*Modeling oscillatory gene regulation dynamics during the cell cycle in embryonic stem cells* |
| 10:40-11:00 | **Louison Fresnais,** Université de Toulouse, France<br>*Condition-specific modelling and network topological analysis to improve the understanding of chemical's metabolic Mechanisms of Action* |
| 11:00-11:20 | **Yulan van Oppen,** University of Groningen, Netherlands<br>*Fast parameter estimation for ODE-based models of heterogeneous cell populations* |
| 11:20-11:40 | **Domagoj Doresic,** IRU Mathematics and Life Sciences, University of Bonn, Croatia<br>*Efficient integration of censored, ordinal, and nonlinear-monotone data in parameter estimation for ODE models* |
| 11:40-12:00 | **Srijith Sasikumar,** IIT Madras, India<br>*Exploring metabolic plasticity of quantitative trait nucleotides and their combinations using systems biology approaches* |
| 13:20-13:40 | **Sandra Timme,** Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, Germany<br>*Unraveling the Complex Interplay between Acinetobacter baumannii and Staphylococcus aureus in Co-infections: A Mathematical Modeling Approach* |
| 13:40-14:00 | **Krishna Rani Kalari,** Mayo Clinic, United States<br>*Systems biology modeling of signaling networks using kinetic parameters and multi-omics data* |
| 14:00-14:20 | **Fabian Fröhlich,** Francis Crick Institute, United Kingdom<br>*Untangling the role of allostery and transcriptional adaption in resistance to MAPK inhibitors* |
| 14:20-14:40 | **Adam Streck,** Max Delbrück Center for Molecular Medicine in the Helmholtz Association (MDC), Germany<br>*SMITH–Stochastic Model of Intra-Tumor Heterogeneity* |
| 14:40-15:00 | **Mikele Milia,** University of Padova, Italy<br>*Modeling the tumor microenvironment with a hybrid Multi-Agent Spatio-Temporal model fed with sequencing data* |
| 15:30-15:40 | **Garhima Arora,** Translational Health Science and Technology Institute,India<br>*Emergent metabolic landscape in the transitory ovarian cancer cell niche revealed through genome-scale metabolic modeling* |
| 15:40-16:20 | **Thomas Höfer**<br>*Invited Presentation: Inferring and engineering tumor evolution* |
| 16:20-16:30 | **Chiara Damiani**<br>*Closing remarks* |

# Text Mining COSI

## TRACK PRESENTATIONS

### THURSDAY, JULY 27TH

Text Mining for Healthcare and Biology

| | |
|---|---|
| 8:30-9:10 | **Martin Krallinger**<br>*Invited Presentation: Implementing text mining resources for clinical variables applied to literature and medical texts: applications in biomaterial research, cardiology, occupational health and phenotypes* |
| 9:10-9:30 | **Esmaeil Nourani,** University of Copenhagen, Denmark<br>*Text mining for disease-lifestyle relations based on a novel lifestyle factors ontology* |
| 10:00-10:20 | **Katerina Nastou,** University of Copenhagen, Denmark<br>*IS1000: a better corpus for evaluating species named entity recognition methods* |
| 10:20-10:40 | **Robert Leaman,** NCBI/NLM/NIH, United States<br>*AIONER: An all-in-one scheme for biomedical named entity recognition using deep learning* |
| 10:40-10:50 | **Brett Beaulieu-Jones,** University of Chicago, United States<br>*Instruction fine-tuning large language models with context-derived weak supervision improves clinical information extraction* |
| 10:50-11:00 | **Sylwia Szymanska,** Silesian University of Technology, Poland<br>***Word embeddings capture functions of low complexity regions: scientific literature analysis using a transformer-based language model*** |
| 11:00-11:20 | **Xiangru Tang,** Yale University, United States<br>*Integrating 3D and 2D Molecular Representations with Biomedical Text via a Unified Pre-trained Language Model* |
| 11:20-11:40 | *Poster lightning presentations* |
| 13:20-14:00 | **Aurélie Névéol**<br>*Invited Presentation: Reproducibility in biomedical natural language processing and applications to bioinformatics workflows* |
| 14:00-15:00 | **Larry Hunter**<br>**Harry Caufield**<br>*Panel: Applications of ChatGPT and large language models in biology and medicine* |

# TRANSMED COSI

## TRACK PRESENTATIONS

### MONDAY, JULY 24TH

TransMed: Translational Medicine Informatics & Applications

| | |
|---|---|
| 10:30-10:40 | **Reinhard Schneider**<br>***Introduction*** |
| 10:40-11:20 | **Maggie Cheang**<br>*Invited Presentation: Integrative analysis of multi-scale multi-omics data in clinical trials to predict treatment response* |
| 11:20-11:40 | **Monica Dayao,** Carnegie Mellon University, United States<br>*Proceedings Presentation: Deriving spatial features from in situ proteomics imaging to enhance cancer survival analysis* |
| 11:40-11:50 | **Soufyan Lakbir,** Vrije Universiteit Amsterdam, Netherlands<br>*CIBRA identifies genomic alterations with a system-wide impact* |
| 11:50-12:00 | **Rachel Melamed,** UMass Lowell Department of Biological Science, United States<br>*Integrating disease genetics and drug bioassays to discover drug impacts on the human phenome* |
| 12:00-12:10 | **Pourya Naderi Yeganeh,** Beth Israel Deaconess Medical Center/ Harvard Medical School, United States<br>*iQPA: A functional phenotyping platform that mitigates risk of clinical failure in drug discovery by matching the underlying biological mechanism in laboratory models to human diseases* |
| 12:10-12:20 | **Jon Sánchez,** Barcelona Supercomputing Center, Spain<br>*Analysis of electronic health records from three distinct and large populations reveals high prevalence and biases in the co-administration of drugs known to interact* |
| 12:20-12:30 | **Annalise Schweickart,** Harmonic Discovery, Inc., United States<br>*Delineating Drug Class and Target-Specific Adverse Events of Kinase Inhibitors* |
| 13:50-14:10 | **David Froelicher,** MIT and Broad Institute of MIT and Harvard, United States<br>*Enabling collaborative analysis of genomic data silos with privacy* |
| 14:10-14:30 | **Harry Robertson,** University of Sydney, Australia<br>*Transferable Omics Prediction (TOP) Reveals Common Mechanisms of Allograft Rejection across Distinct Organs* |
| 14:30-14:50 | **Florian Massip,** PSL-Research University, France<br>*Smoking-dependent expression alterations in nasal epithelium reveal immune impairment linked to germline variation and lung cancer risk* |
| 14:50-15:10 | **Michelle Li,** Harvard Medical School, United States<br>*Deep learning for diagnosing patients with rare genetic diseases* |
| 15:10-15:30 | **Panagiotis Nikolaos Lalagkas,** UMass Lowell, United States<br>*Leveraging disease comorbidity for drug repurposing: insights from Mendelian and Complex diseases* |
| 16:00-16:10 | **Philippos Tsourkas,** University of Wisconsin Madison, United States<br>*Identifying predictive biomarkers of patient response to neoadjuvant chemo-hormonal therapy and prostatectomy in multifocal prostate cancer with radiology and clinical data* |
| 16:10-16:20 | **Zhuoxuan Li,** HKU, Hong Kong<br>*SpatialDM: Rapid identification of co-expressed ligand-receptor reveals cell-cell communication patterns in spatial transcriptomics* |
| 16:20-16:30 | **Stephen Ramsey,** Oregon State University, United States<br>*ARAX: a graph-based modular reasoning tool for translational biomedicine* |
| 16:30-16:40 | **Dea Gogishvili,** Vrije Universiteit Amsterdam, Netherlands<br>*Discovery of novel CSF biomarkers to predict progression in dementia using machine learning* |
| 16:40-16:50 | **Cristina Baciu,** University Health Network, Canada<br>*A Machine Learning Tool Integrating Circulating Cell-Free DNA Methylation and Clinical Variables for Non-Invasive Diagnosis of Liver Graft Pathology* |
| 16:50-17:00 | **Alexis Nolin-Lapalme,** Institut de cardiologie de Montréal, Canada<br>*Predicting genetic ancestry using 12-lead ECG: underlying a potential danger for fairness* |
| 17:00-17:10 | **Heba Sailem, King's College London, United Kingdom**<br>*Computationally effective weakly supervised model for histopathological image classification* |
| 17:10-17:50 | **Alfonso Valencia**<br>*Invited Presentation: TBD* |
| 17:50-18:00 | **Venkata Satagoapm**<br>*Closing* |

# VarI COSI

## TRACK PRESENTATIONS

### THURDAY, JULY 27TH

**VarI: Variant Interpretation**

| | |
|---|---|
| 8:30-<br>8:40 | **Julien Gagneur**<br>**Antonio Rausell**<br>*Opening Remarks* |
| 8:40-<br>8:50 | **Yazdan Asgari,** Paris-Saclay University, France<br>*Developing a new pipeline for exploring pleiotropy of GWAS data at gene-level* |
| 8:50-<br>9:30 | **Matthieu Foll,** International Agency for Research on Cancer, France<br>*Invited Presentation: Multi-omics characterization of rare heterogeneous tumors* |
| 10:00-<br>10:10 | **Vaishali Waman, University College London, United Kingdom**<br>*Predicting human and viral protein variants affecting COVID-19 susceptibility* |
| 10:10-<br>10:30 | **Kivilcim Ozturk,** UC San Diego, United States<br>*Interface-guided phenotyping of coding variants* |
| 10:30-<br>10:40 | **Swatantra Pradhan,** Tata Consultancy Services, India<br>*An augmented transformer model trained on family specific variant data leads to improved prediction of variants of uncertain significance* |
| 10:40-<br>10:50 | **Nigreisy Montalvo, Université Paris Cité, France**<br>*Pathogenicity scoring of genetic variants through federated learning across independent institutions reaches comparable or superior performance than the centralized-data model counterparts.* |
| 10:50-<br>11:00 | **Julian Gough,** MRC Laboratory of Molecular Biology, United Kingdom<br>*Hypothesis-free phenotype prediction within a genetics-first framework* |
| 11:00-<br>11:20 | **Alexander Schoenhuth,** Bielefeld University, Germany<br>*Predicting the prevalence of complex genetic diseases from individual genotype profiles using capsule networks* |
| 11:20-<br>12:00 | **Jörg Menche**<br>*Invited Presentation: Network Medicine – From protein-protein to human-machine interactions* |
| 13:20-<br>13:40 | **Rongting Huang,** The University of Hong Kong, Hong Kong<br>*XClone: detection of allele-specific subclonal copy number variations from single-cell transcriptomic data* |
| 13:40-<br>14:00 | **David Wang,** University of Pennsylvania, United States<br>*Comprehensive Identification and Characterization of Splicing Associated Variants with Coverage Aware Statistical Models* |
| 14:00-<br>14:10 | **Nina Baumgarten,** Goethe University, Germany<br>*A statistical approach to identify regulatory DNA variations combined with epigenomics data reveals novel non-coding disease genes* |
| 14:10-<br>14:20 | **Eleni Giannoulatou,** Victor Chang Cardiac Research Institute, Australia<br>*SpliceSM: machine learning discovery of splice-altering variants using susceptibility maps* |
| 14:20-<br>15:00 | **Nicky Whiffin**<br>*Invited Presentation: Strategies to annotate and interpret non-coding variants in rare disease* |
| 15:30-<br>15:50 | **Yasser Mohseni Behbahani,** Sorbonne Université, France<br>*Proceedings Presentation: Deep Local Analysis deconstructs protein - protein interfaces and accurately estimates binding affinity changes upon mutation* |
| 15:50-<br>16:10 | **Jayoung Ryu,** Harvard Medical School, United States<br>*Modeling endogenous editing outcome of base editor reporter screens with CRISPR-Bean discovers causal variants for cellular LDL uptake* |
| 16:10-<br>16:20 | **Daniele Raimondi,** KU Leuven, Belgium<br>*From genotype to phenotype in Arabidopsis thaliana: in-silico genome interpretation predicts 288 phenotypes from sequencing data* |
| 16:20-<br>16:30 | **Julien Gagneur**<br>**Antonio Rausell**<br>*Closing Remarks* |

# TECHNOLOGY TALK

## PRESENTATIONS

### MONDAY, JULY 24TH

**10:30-10:50** **Denis Bienroth,** Murdoch Children's Research Institute, Australia

*VR-Omics: Exploration of spatial transcriptomes in 3D and in Virtual Reality*

**10:50-11:10** **David Yuan**

*European Nucleotide Archive: one of the largest and long-standing public databases for genomics*

**11:10-11:30** **Howard Baek,** Fred Hutchinson Cancer Center

*Enhancing Access to Genomics Tools*

**11:30-11:50** **Howard Baek**

*Resources and Tools for Ethical Data Handling*

**11:50-12:10** **Qian Liu**

*R/Bioconductor Tools For Reusable and Reproducible Genomic Data Management and Analysis*

**17:00-17:40** **Jessica Miller**

*Introduction to Open Science*

# TECHNOLOGY TALK

## PRESENTATIONS

### WEDNESDAY, JULY 26TH

10:30-10:50
**Jon Jiang,** MemVerge Inc., United States
*WaveRider: A Dynamic Rightsizing Framework for Cost-Effective and Robust Bioinformatics Workloads on the Cloud*

10:50-11:10
**Mitchell Shiell,** Ontario Institute of Cancer Research (OICR), Canada
*Creating FAIR Data Repositories with Overture Microservices*

11:10-11:30
**Filippo Utro,** IBM, United States
*Accelerating Disease and Drug Discovery in molecular biology*

11:30-11:50
**Nicola Bordin**
*Scaling up Protein Classification: CATH-AlphaFlow and ChainSaw*

11:50-12:10
**Philippe Youkharibache,** NCI/NIH, USA
*iCn3D: an open source structural bioinformatics platform for collaborative research, scientific education and 3D publishing*

12:10-12:30
**Frederic Cazals**
*The Structural Bioinformatics Library: ∗ a software instrument for the road ahead*

13:50-14:30
**Nikolina Nakic**
*Advancing drug discovery through genetics and genomics*

14:30-14:50
**Judith Zaugg**
*Systems epigenetics to study cellular processes and disease mechanisms*

14:50-15:10
**Francisco Azuaje,** Genomics England, UK
*Integrating and accelerating research through AI for bringing benefits to patients*

15:10-15:30
**Julio Saez-Rodriguez**
*Knowledge-based machine learning to extract disease mechanisms from multi-omics data*

16:00-16:40
**Joe Salens,** Pfizer, USA
*Careers in Computational Biology and Machine Learning at Pfizer, Project Examples*

16:40-17:00
**Janet Piñero**
*DISGENET Plus: unlocking the potential of genomics for precision medicine and drug development*

17:00-17:20
**José Carbonell-Caballero**
*PerMedCoE: A roadmap to scalability in Personalized Medicine*

17:20-18:00
**Manali Ghosh,** St. Jude Children's Research Hospital, United States
*What to look for when searching for a postdoc position; a perspective from St. Jude Children’s Research Hospital*

# ISCB Appreciates the Support of the Following Sponsors

ISMB
ECCB
2023
LYON
FRANCE
July 23-27
iSCB

NIH National Institutes of Health
Office of Data Science Strategy

HFSP
International
Human Frontier
Science Program
Organization

GSK

elixir

sfbi
société française de bioinformatique

MÉTROPOLE
GRAND LYON

GL events
LYON
EVENTS

Pfizer

MemVerge

St. Jude Children's Research Hospital®
Finding cures. Saving children.
ALSAC • DANNY THOMAS, FOUNDER

BioTuring™

# ISMB 2024

## SAVE THE DATE

JULY 12-16, 2024

WWW.ISCB.ORG/ISMB2024

# MEET YOUR
# ISCB BOARD OF DIRECTORS

## ISCB EXECUTIVE OFFICERS & DIRECTORS

**Christine Orengo, Ph.D.**
*President, ISCB*
Professor
University College London
UNITED KINGDOM

**Predrag Radivojac, Ph.D.**
*President-elect, ISCB*
*Professor*
Northeastern University
USA

**Alex Bateman, Ph.D.**
*Vice President, ISCB*
Head of Protein Sequence Resources
EMBL- EBI
UNITED KINGDOM

**Nicola Mulder, Ph.D.**
Vice President, ISCB
Professor
University of Cape Town
SOUTH AFRICA

**Russell Schwartz, Ph.D.**
*Vice President, ISCB*
*Professor*
Carnegie Mellon University
USA

**Janet Kelso, Ph.D.**
Group Leader
MPI for Evolutionary Anthropology
GERMANY

**Michelle Brazas, Ph.D.**
*Secretary, ISCB*
Senior Program Manager
Ontario Institute for Cancer Research
CANADA

## ISCB BOARD OF DIRECTORS

**Bonnie Berger, Ph.D.**
Professor
Applied Mathematics and Computer Science
MIT
USA

**Yana Bromberg, Ph.D.**
Professor
Emory University
USA

**Ana Conesa, MD PhD**
*COSI Representative to the Board, ISCB*
Research Professor
Spanish National Research Council
SPAIN

**Francisco De La Vega, Ph.D.**
*VP of Hereditary Disease*
Tempus Labs Inc.
USA

**Terry Gaasterland, Ph.D.**
*Professor*
University of California San Diego
USA

**Christophe Dessimoz, Ph.D.**
Prof.
University of Lausanne
SWITZERLAND

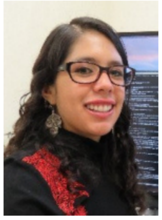
**Bruno Gaeta, Ph.D.**
Senior Lecturer and Bioinformatics Program Director
University of New South Wales
AUSTRALIA

# MEET YOUR
# ISCB BOARD OF DIRECTORS

**Nomi Harris, MSc**
Program Manager
Lawrence Berkeley National Laboratory
USA

**Wataru Iwasaki, Ph.D.**
Associate Professor
The University of Tokyo
JAPAN

**Thomas Lengauer, Ph.D.**
*Prof. Dr.*
Max Planck Institute for Informatics
GERMANY



**Alejandra Medina Rivera, Ph.D.**
Associate Resaercher
Laboratorio Internacional de Investigación sobre el Genoma Humano, UNAM
MEXICO

**Tijana Milenkovic, Ph.D.**
*ISCB COSI Representative to the Board,*
Frank M. Freimann Collegiate Associate Professor of Engineering
University of Notre Dame
USA

**Laxmi Parida, Ph.D.**
*IBM Fellow*
IBM T J Watson Research Center
USA

**R. Gonzalo Parra, Ph.D.**
*Student Council Representative, ISCB*
Postdoc
Barcelona Supercomputing Center
SPAIN

**Lucia Peixoto, Ph.D.**
*Assistant Professor*
Washington State University, Spokane
USA

***Christian Schönbach, Ph.D.**
*Affiliates Group Representative, ISCB*
Professor
Nazarbayev University
KAZAKHSTAN

**Alfonso Valencia, Ph.D.**
PROFESSOR
Barcelona Supercomputing Center - Centro Nacional de Supercomputacion (BSC)
SPAIN

**Mark Wass, Ph.D.**
COSI Representative to the Board, ISCB
Reader in Computational Biology
University of Kent
UNITED KINGDOM

**Xuegong Zhang, Ph.D.**
Professor
Tsinghua University
CHINA

## UPCOMING
## ISCB ACADEMY SERIES

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

### Upcoming Webinars

**August 29, 2023 at 11:00 AM EDT**
*Systems Biomedicine and Pharmaceutics: Multiscale Modeling of Tissue Remodeling and Damage*
by Ashlee N Ford Versypt, University of Buffalo
Hosted by SysMod

### Upcoming Practical Training and Tutorials

*Note: Space in tutorials is limited and you must register before you can attend. Tutorial registration closes 48 hours before the start of the tutorial.*

**September 28, 2023 at 10:00 AM UTC**
*Using the Ensembl genome browser and REST API to retrieve genome annotation data Part 1*
by Benjamin Moore -
Hosted by ISCB

**September 29, 2023 at 10:00 AM UTC**
*Using the Ensembl genome browser and REST API to retrieve genome annotation data Part 2*
by Benjamin Moore -
Hosted by ISCB

*https://www.iscb.org/iscbacademy-webinars*

**WWW.ISCB.ORG**

***CONNECTING, TRAINING, EMPOWERING, WORLDWIDE***