ISCBNEWSLETTER

QUARTERLY UPDATE FROM THE SOCIETY

Strong Line-up Taking Shape at ISMB/ECCB 2021

Through the years, the ISMB/ECCB conference has quickly become synonymous with collaboration, dialogue, and innumerable learning opportunities. These core characteristics exist regardless of where the conference is held. This year sees the conference being moved to a fully virtual planform to ensure attendee safety. This environment will not only allow for the expected characteristics of the conference but enable broader reach and increased opportunities for collaboration and networking, dialogue with colleagues and mentees, and above all learning opportunities across the breadth of the field of bioinformatics and computational biology.

Capitalizing on the successes from last year and improving our platform in response to your suggestions, ISMB/ECCB 2021 will bridge time zones, enabling our global community to gather, share, network, and learn all from the comfort of your choosing.
 ISMB/ECCB 2021 will bring together the perfect recipe of cutting-edge science, knowledge building, tutorials, community based and online networking opportunities, student-focused symposium, and so much more to create the most profound computational biology enriched online experience.

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MARK YOUR CALENDARS

iSCB

INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

This years conference will feature many of the expected proceedings talks and abstract presentations that include highlights (previously published research) and late- breaking research. In addition, Each day of the conference will highlight new research, highlights from the COVID-19 track, Special Sessions and surprising opportunities for virtual social events and networking, the characteristics that make this conference so successful.

The 2021 COSI tracks areas are: • 3DSIG • Bio-Ontologies • BIOINFO-CORE • BioVis • BOSC: Bioinformatics Open Source Conference • CAMDA • CompMS • Education • Evolution and Comparative Genomics • Function • HitSeq • iRNA • MLCSB • MICROBIOME • NetBio • RegSys • SysMod • Text Mining• TransMed • VarI • General Computational Biology

The bulk of the ISMB/ECCB program will be determined by abstract and proceedings sub-missions. Abstract submissions are still being accepted. Submit your work today to be a part of this ground breaking event, bringing you the science you expect directly to your computer or virtual landscape. The Abstract submission deadline is **May 06, 2021**. ISCB is making every effort to create a virtual experience that mirrors an in-person experience with less sore feet at the end of the day. We look forward to "seeing" you in July for ISMB/ECCB 2021, the premier virtual event of the year!

Don't forget to submit your research! Spread the knowledge at ISMB/ECCB 2021. Submit your research today at https://www.iscb.org/ismbeccb2021-submit

CALL FOR SUBMISSIONS

ABSTRACT SUBMISSIONS	MAY 6, 2021
ABSTRACTS SARS-COV-2/COVID-19	MAY 6, 2021
TECHNOLOGY TRACK SUBMISSIONS	MAY 13, 2021

HTTPS://WWW.ISCB.ORG/ISMBECCB2021-SUBMIT

ISCB CONGRATULATES THE 2021 CLASS OF FELLOWS

The ISCB Fellows program was created to honor members who have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. Begun in 2009, 2021 marks the 12th anniversary of the program. In early December of each year, ISCB has sought Fellow's nominations from our members, with eligibility restrictions based on selection criteria focused most heavily on the significance of scientific contributions.

We were pleased to receive many outstanding nominations this year, and the Fellows Selection Committee members carefully considered each one. Ultimately, thirteen nominees were elected as this year's newest Fellows.

Atul Butte, University of California

At the University of California in San Francisco Atul Butte is at the forefront of translational medicine informatics, including public data mining, integrative genomics and drug repurposing.
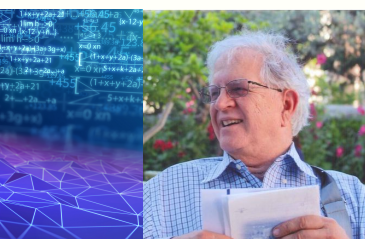
A. Keith Dunker, Indiana University School of Medicine

A pioneer of the development and application of statistical and computational methods to understand the prevalence, the patterns of evolution, and the functional repertoire of intrinsically disordered proteins across all domains of life.

### Eran Halperin, University of California, Los Angeles

Transformative work in the field of computational genomics through novel algorithms and theory that has enabled large-scale studies of genetic variation data.

Wolfgang Huber, European Molecular Biology Lab (EMBL)

Co-founder of Bioconductor, which provides robust software that ensures use and fosters collaboration, and outstanding research in the meticulous modelling of stochastic and systematic sources of variation in a data generating technology and state-of-the-art statistical methods to infer parameters from data,
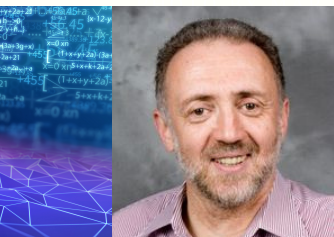
Sorin Istrail, Brown University

Foundational contributions to computational biology, including physical mapping, protein folding, sequencing the human genome, haplotype phasing and assembly, and regulatory genomics, as well as launching the RECOMB conference and JCB.

Christina Leslie, Memorial Sloan Kettering

Recognized as bringing rigorous statistical machine learning techniques to computational biology, including basic science and clinical settings, as well as major contributions to conferences and consortia.
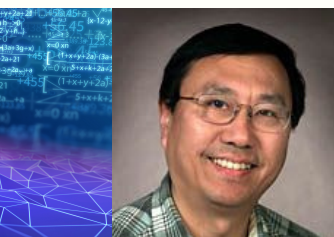
Ming Li, University of Waterloo

Fundamental, impactful contributions to computational biology and bioinformatics including linear approximation and optimized spaced seeds, and introducing deep learning to proteomics, significantly improving neoantigen de novo sequencing for cancer immunotherapy.

Nuria Lopez Bigas, Institute for Research in Biomedicine Barcelona

Leading innovator in computational cancer biology who has been instrumental in understanding the effects of chemotherapeutics on cancer and optimizing treatments to support translational interpretation for clinical applications.
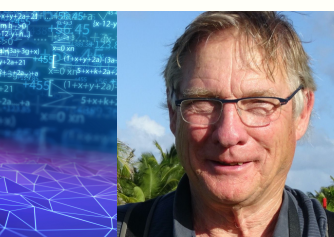
John Moult, University of Maryland

Major contributions to protein fold prediction and impact of sequence variation on protein structure and function, as well as his organization of Critical Assessments, most notably CASP and also CAGI, to tackle grand challenges in biology.

Dana Pe'er, Memorial Sloan Kettering

Extraordinary record of scientific accomplishments through combining rigorous foundational machine learning with a deep understanding of biology, including contributions that have revolutionized the space of molecular interaction inference and single cell analysis, with applications to cancer and other diseases.

Teresa Przytycka, National Center for Biotechnology Information, National Institute of Health

Recognized for her fundamental algorithmic contributions to a wide range of problems in computational systems biology, especially in network analysis, network-based approaches to uncover disease genes, network reconstruction, regulatory roles of DNA conformation dynamics and RNA aptamer analysis.

Eytan Ruppin, National Cancer Institute, National Institutes of Health

Numerous contributions to neuroscience (neural modeling of brain disorders), neural computing (reinforcement learning dynamics and language learning), computational systems biology and computational study of cancer metabolism, including his work on synthetic lethality (SL), leading to the discovery of the first metabolic SL drug target to treat cancer.

Gustavo Stolovitzky, IBM Research

Pioneer in the use of crowdsourcing in computational biology, providing a unique service to the community and creating resources and benchmarks that led to breakthroughs in network biology, cancer genomics and translational biomedicine; founder of the DREAM Challenges; and instrumental involvement in the growth of the Computational Biology Center at IBM, establishing the Systems Biology program, and creating the Nanobiotechnology program that leveraged the vast IBM resources in microelectronics for genomics research.

ISCB will be honoring the 2021 Class of Fellows at the ISCB Town Hall during the Virtual ISMB/ECCB 2021, July 25 at 10:00 AM
Congratulations, 2021 Class of ISCB Fellows!

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.

Anna Tramontano
Computational Biologist
1957 – 2017

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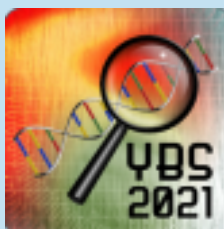
https://www.iscb.org/support-iscb

MARK YOUR CALENDARS FOR THESE UPCOMING EVENTS

GLBIO 2021

May 10 - 13, 2021

Virtual Event

YBS 2021

May 23, 2021

Virtual Event

ISCB-Africa ASBCB 2021

June 7 - 10, 2021

Virtual Event

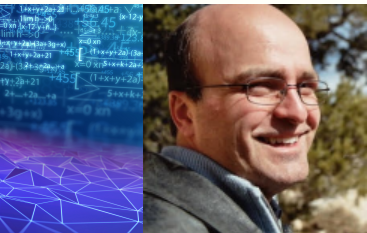**ISMB/ECCB 2021**

June 25 - 30, 2021

Virtual Event

Rocky 2021

December 02 - 04, 2021

Colorado

https://www.iscb.org/iscb-conference-events

ISMB/ECCB 2021 DISTINGUISHED KEYNOTES

Eduardo Rocha

Genomes and Genetics

Institut Pasteur

Eduardo Rocha studied Chemical Engineering and Applied Maths, did a PhD in Bioinformatics and a Habilitation in Biology. He is the director of the Genome & Genetics department at Pasteur Institute, where he heads the Microbial Evolutionary Genomics lab since 2008. He is a Specialist in comparative genomics, in particular in the use of bioinformatics and biostatistics to study microbial evolution. His research aims at understanding how and why genomes are organized, and how such organizational features evolve in respect to genome dynamics and bacterial adaptation. In the last decade, his work has focused on the role of mobile genetic elements in shaping gene repertoires and driving functional innovation.

Rodrigo A. Gutierrez

FONDAP Center for Genome Regulation

Millennium Institute for Integrative Biology

Universidad Catolica de Chile

Dr. Gutiérrez is Full Professor and past Chair at the Department of Molecular Genetics and Microbiology, P. Universidad Católica de Chile. Deputy Director of the Millennium Institute for Integrative Biology and Principal Investigator at the FONDAP Center for Genome Regulation. He has received several awards and honors during his career, including the Howard Hughes Medical Institute International Early Career Scientist award, John A. Boezi Memorial Alumnus Award from Michigan State University and the Friedrich Wilhelm Bessel Research Award of the Alexander von Humboldt Foundation. He is one of the founders of the Chilean Society of Plant Biologists and was the first elected president.

Kate Jones

Genetics, Evolution & Environment

University College London

Kate Jones is Professor of Ecology and Biodiversity in the Centre for Biodiversity and Environmental Research (CBER), within the Research Department of Genetics, Evolution and Environment (GEE) at University College London. Kate has held appointments at the University of Cambridge, Columbia University, Imperial College London, and is an honorary fellow at the Zoological Society of London. Kate is one of the academic leads for UCL's new EAST campus in the Queen Elizabeth Olympic Park London opening in 2022, directing a new applied ecology group - the Nature-Smart Research Centre. Kate is one of the academic leads for UCL's new EAST campus in the Queen Elizabeth Olympic Park London opening in 2022, directing a new applied ecology group - the Nature-Smart Research Centre. Kate has written over 100 articles and book chapters in prestigious journals such as Nature and Science and is a scientific advisor for a number of international biodiversity charities and chaired The Bat Conservation Trust for 5 years, and won the Leverhulme Prize for outstanding contributions to Zoology in 2008. Kate regularly appears in the national and international media, including the Life Scientific on BBC Radio 4 in 2015. Allegedly*, Charles Darwin is her 8th cousin (6 times removed)

ISCB AWARD & ISMB/ECCB 2021 DISTINGUISHED KEYNOTES

ISCB Accomplishments by a Senior Scientist Award Keynote

Peer Bork

EMBL Heidelberg

The Accomplishments by a Senior Scientist Award recognizes a member of the computational biology community who is more than two decades post-degree and has made major contributions to the field of computational biology. Peer Bork is being honored as the 2021 recipient of this award.

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Peer Bork has been at EMBL since 1991, head of Units since 2001; the current strategic head of Bioinformatics at EMBL Heidelberg since 2011 and an ERC Advanced Investigator. Bork received his PhD in biochemistry in 1990 and his habilitation in theoretical biophysics in 1995.

His group, the Bork group, focus on gaining insights into the functioning of biological systems and their evolution by comparative analysis and integration of complex molecular data. Together with other groups at EMBL, they hope to establish interaction maps between chemical compounds and microbes, individually and in communities using advanced multi-omics approaches, with application for human (e.g. individualized diet) or planetary health (e.g. pesticide response biomarkers).

Peer Bork has made tremendous contributions to bioinformatics on a plethora of fronts within the field. This includes his early work on protein domains (leading to the SMART database), genome analysis of higher eukaryotes (leading to authorships on the human, mouse, and rat genome papers), work on one of the most used methods for analysis of mutation data (PolyPhen), large-scale phylogeny (leading to iToL), inventing several of the method for inferring gene/protein networks (leading to the STRING database), analysis of drugs and adverse reactions (leading to STITCH and SIDER) and most recently pioneering microbiome research.

In addition to the research as evidenced in his impressive list of over 590 publications, he has had immense impact also as a mentor. The majority of his many postdocs over the years have moved on to become successful group leaders themselves.

ISCB Innovator Award Keynote

Ben Raphael

Lewis-Sigler Institute, Princeton University

The year 2016 marked the launch of the ISCB Innovator Award, which is given to a leading scientist who is within two decades of receiving the PhD degree, has consistently made outstanding contributions to the field, and continues to forge new directions. Ben Raphael is the 2021 recipient of the ISCB Innovator Award.

Ben Raphael received an S.B. in Mathematics from MIT, a Ph.D. in Mathematics from the University of California, San Diego (UCSD), and completed postdoctoral training in Bioinformatics and Computer Science at UCSD.

Ben Raphael is a Professor of Computer Science at Princeton University. His research focuses on the design of combinatorial and statistical algorithms for the interpretation of biological data. Recent areas of emphasis include cancer evolution, network/pathway analysis of genetic variants, and structural variation in human and cancer genomes. His group's algorithms have been used in multiple projects from The Cancer Genome Atlas (TCGA) and the International Cancer Genome Consortium (ICGC). He co-led the TCGA Pancreatic Adenocarcinoma project and the network analysis in the ICGC Pan-Cancer Analysis of Whole Genomes (PCAWG).

Ben is considered by many to be the leader in algorithmic computational cancer biology. He is the recipient of the Alfred P. Sloan Research Fellowship, the NSF CAREER award, and a Career Award at the Scientific Interface from the Burroughs Wellcome Fund. His papers cover a range of topics in computational cancer biology. These include the problems of separating genomic mixtures of cancer cells according to the mutations present in their genomes; analyzing temporal progression of mutations in cancer; identifying recurrent copy number aberrations; and discovering important sets of mutations across cohorts of cancer patients according to a statistical signal of anti-correlation, or mutual exclusivity, between mutations in the set. Several of Ben's algorithms -- including his THetA and AncesTree algorithms for analyzing mixtures of cancer cells, his Dendrix and Multi-Dendrix algorithms for analyzing mutually exclusive mutations, and his HotNet algorithm (RECOMB 2010, Nature Genetics 2015) for network analysis of cancer mutations -- have become standards by which other research groups benchmark their algorithms. Ben's computational approach to discover important cancer mutations using mutual exclusivity has inspired many other groups to work on this problem.

ISCB Overton Prize Keynote

### Barbara Engelhardt

Princeton University

The Overton Prize recognizes the research, education, and service accomplishments of early to mid-career scientists who are emerging leaders in computational biology and bioinformatics. The Overton Prize was instituted in 2001 to honor the untimely loss of G. Christian Overton, a leading bioinformatics researcher and a founding member of the ISCB Board of Directors. Barbara Engelhardt is being recognized as the 2021 recipient of the Overton Prize. Barbara Engelhardt joined the Princeton Computer Science Department in 2014 from Duke University, where she had been an assistant professor in Biostatistics and Bioinformatics and Statistical Sciences. She graduated from Stanford University and received her Ph.D. from the University of California, Berkeley

Barbara Engelhardt's research is in developing statistical models and machine learning methods for the analysis of biomedical data, with a focus on studying complex associations, time-series, sequential decision-making, and predicting the effects of perturbations in human cohorts, single cell data, and hospital patient data. In the field of single cell genomics, dimension reduction is a pressing problem and she has contributed a scalable and robust approach to dimension reduction using a Gaussian process latent variable model (GPLVM) with t-distributed residuals. Her group also developed approaches to determine the specific set of genes that differentiate particular types of cellular pathology images using machine learning methods like convolutional autoencoders and sparse canonical correlation analysis. Her research group has a reputation for producing rigorous and creative statistical approaches for the analysis of complex biomedical data.

As part of the Genotype-Tissue Expression (GTEx) Consortium, Dr. Engelhardt performed key analyses to identify regulatory DNA variation that is linked to distal gene expression changes ("trans-eQTLs"). In the context of this large scale experimental effort, she determined trans-eQTLs across 49 human tissues and 838 individuals. Notable results include a confirmation of the greater tissue specificity of trans-eQTL versus mutations that are nearby the gene they regulate. Based on her expertise and creativity she has contributed numerous novel machine learning and statistics methods to important projects from genomics, population genetics, and human genetics.

Barbara Engelhardt has been an outspoken advocate for women and under-represented groups in the sciences. She has used her voice to advocate on behalf of these groups both through traditional means and on social media. Notably, Dr. Engelhardt's research group, housed in a computer science department, currently includes five women graduate students and postdocs and she has served as a mentor, both formally and informally for many women and individuals from under-represented groups, proving Dr. Engelhardt's status as a leader in the field of computational biology and bioinformatics
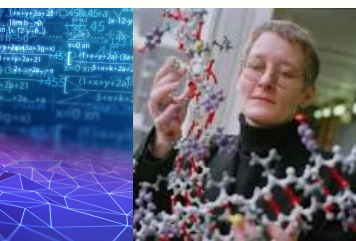
ISCB Outstanding Contributions Award

Teresa Attwood

the University of Manchester

The Outstanding Contributions to ISCB Award recognizes an ISCB member for outstanding service contributions toward the betterment of ISCB through exemplary leadership, education, and service.

The 2021 recipient of the Outstanding Contributions to ISCB Award is Teresa Attwood. Teresa Attwood is a Professor of Bioinformatics in the Department of Computer Science and School of Biological Sciences at the University of Manchester and a visiting fellow at the European Bioinformatics Institute (EMBL-EBI).

A visionary within the field, she saw early on the power of bioinformatics education from the beginning. Teresa Attwood coauthored (with Paul Higgs) one of the first books in bioinformatics, which became a reference in Universities worldwide. Teresa was quick to recognize that ISCB was ideally situated to lead the global promotion for a strong bioinformatics education.

Teresa Attwood has been a champion of the bioinformatics education community where she has been instrumental in putting in place ISCB platforms that allow the education community to highlight their work and which raise the awareness of ISCB as a leader in bioinformatics education globally.

A longstanding and involved ISCB member, Teresa Attwood continued to further bioinformatics education on behalf of the global bioinformatics community and ISCB through many years of service. In 2001 she joined Phil Bourne's ISCB Education Working Group to define the topic areas in a complete bioinformatics curriculum and identify the available learning resources. This group was the precursor of the creation of the ISCB Education Committee (2002).

Attwood was instrumental in launching the Global Organization for Bioinformatics Learning, Education and Training (GOBLET, 2012) as a network of global training organizations and individuals. Understanding the need to link GOBLET with ISCB, Terri worked with Fran Lewitter on the ISCB Education Committee Leadership Task Force (Summer 2016) to align the missions of GOBLET with those of ISCB and the emerging Education COSI, thereby ensuring the two organizations work in harmony towards their respective goals.

Teresa Attwood is being recognized for her many years of significant contributions to both ISCB and the broad bioinformatics and bio-curation communities.
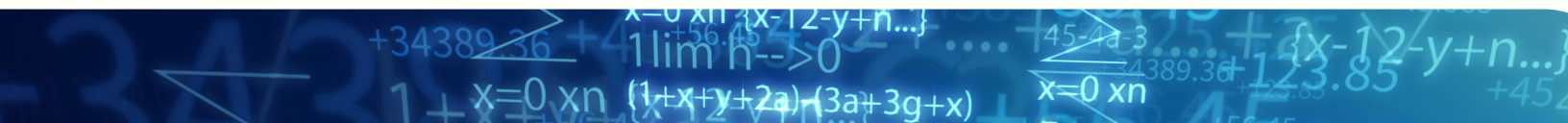
REGISTER TODAY TO ATTEND
DEADLINE: MAY 3RD

REGISTER TODAY

GLBIO

YOUTH BIOINFORMATICS SYMPOSIUM 2021

The International Society for Computational Biology (ISCB) will host the Youth Bioinformatics Symposium (YBS) 2021, exploring computational biology as a virtual live event on Sunday, May 23, 2021.

YBS is a one-day event that provides an opportunity for students to come together and introduces students to the amazing world of computational biology. Our virtual symposium will allow them to engage with and learn about three popular tools used in research in our online workshops, inform them of the many career areas that bioinformatics is now appearing in, and ask questions.

We hope you join us to make YBS 2021 a success!

YBS 2021 COLLEGE FAIR

SHOWCASE YOUR SCHOOL!

- On Demand access for students to learn about your school and its degree programs
- The ability to submit videos, brochures and infographics for up to 4 different degrees/programs
- Virtual table during the symposium to speak to students and their families

MORE INFORMATION:
WWW.ISCB.ORG/YBS2021-PROGSCHED/YBS2021-COLLEGE-FAIR

Registration is $300

https://iscb.swoogo.com/collegefair-YBS2021

VIRTUAL ISMB/ECCB 2021 SPECIAL SESSIONS

SST01: Representation learning in biology

Organizers:

Christian Dallago, Technical University of Munich, Germany

Ananthan Nambiar, University of Illinois at Urbana-Champaign, United States

Ali Madani, Salesforce Research, United States

Peter Koo, Cold Spring Harbor Laboratory, United States

Biological data needs to be transformed in a meaningful representation to fully take advantage of computational techniques. Human curation of computable representations has long been preferred for analytical and predictive tasks on biological data. However, the hand-crafted expert approach poses challenges for the encoding of vast biological datasets of yet-uncharacterized biological processes. In recent years, advanced statistical approaches, such as deep learning, have shown great promise in delivering tools to learn computable representations of data. These approaches learn representations even in the absence of supervised understanding, and thus could be transformational in biology. Over the last few years, many representation learning approaches have been used to gain insights into biological processes using protein or genome sequences, chemical sequences, transcriptomics and proteomics data, and biomedical imaging.

In this special session we would like to give an overview of how representation learning has reached various disciplines in biology, and how it adds to the toolkit available to bio-researchers today. Additionally, we want to give a platform for machine learning experts to discuss the fundamental statistical tools necessary to learn useful representations. For this purpose, we invited prominent speakers who played a role in the advancement of representation learning in biology. The focus of the talks will cover the broad concept of representation learning in biology with particular use cases in areas like learning embeddings for protein sequences or transcriptomics. The target audience for this program are machine learning scientists interested in moving into the biological domain and biologists interested in understanding cutting-edge concepts in machine learning. Finally, we open the floor to emerging researchers by promoting submissions via lightning talks and a poster session. Find up to date details at https://representation.learning.bio

SST02: Computational Biology going Green

Organizers:

Geoff Barton, University of Dundee, United Kingdom

Alex Bateman, EMBL-EBI, United Kingdom

Michael Inouye, University of Cambridge and Baker Institute, United Kingdom

We are living at a time of unprecedented human driven environmental change that threatens catastrophic changes for society and the environment. Our science has great potential to contribute to environmental science and biodiversity research outcomes. Globally, IT is thought to account for up to 7% of carbon dioxide emissions and this is likely to grow. Therefore, computationally biology is directly contributing to the climate crisis. In this special session we will draw in experts from across Computational Biology and High Performance Computing (HPC) to present on the challenges for making computation sustainable.

This will cover computational efficiency, life cycle, local data centres, cloud and costs.

The following topics and questions would be considered within the scope of this special session:

- How to design a green data centre
- How do I know if my cloud provider is green?
- Discussion of the size of required computation to solve a problem. Do you really need to compute across all the data?
- Impact of GPU vs conventional computer hardware.
- Short and high intensity (e.g. 10,000 cpus for 1 hour) computing vs longer lowintensity (laptop or few cores for days/weeks).
- How green is your desktop?
- What happens to hardware at the end of its life?
- How often should I refresh my computer hardware?
- How to influence your institution to consider the environmental impact of computing in data centre planning.

SST03: New developments in AI for Integrating imaging and genomic data

Organizers:

Olivier Gevaert, Stanford University, United States

William Hsu, UCLA, United States

Arvind Rao, University of Michigan, United States

Vast amounts of biomedical data are now routinely available for patients, ranging from radiographic images to clinical and genomic data, spanning multiple biological scales. AI and machine learning are increasingly used to enable pattern discovery to link such data for improvements in patient diagnosis, prognosis and tailoring treatment response. Yet, few studies focus on how to link different types of imaging and molecular data in synergistic ways, and to develop data fusion approaches for clinical decision support. This tutorial will describe considerations, approaches, software toolkits, and open challenges related to multi-omics, multi-modal and multi-scale data fusion of imaging and molecular data.

This special session will focus on emerging AI applications on spatial transcriptomics data, and the use of multi-modal data for clinical oncology. Bioinformaticists and computational biologists will get an in-depth overview of the different types of imaging data that exist, how to model them, and how they can be linked to genomic data.

SST04: Emerging gain-of-function mutations and their characterization by multi-omics network biology

Organizers:

Zeynep Coban-Akdemir, The University of Texas Health Science Center at Houston, United States

Stephen Yi, The University of Texas at Austin, United States

Traditionally, disease causal mutations were thought to disrupt gene function. However, it becomes more clear that many deleterious mutations could exhibit a 'gain-of-function' (GOF) behavior1. Systematic investigation of such mutations has been lacking and largely overlooked. Advances in next-generation sequencing have identified thousands of genomic variants that perturb the normal functions of proteins, further contributing to diverse phenotypic consequences in disease2. Elucidating the functional pathways rewired by GOF mutations will be crucial for prioritizing disease-causing variants and their resultant therapeutic liabilities3. In distinct cell types (with varying genotypes), precise signal transduction controls cell decision, including gene regulation and phenotypic output4. When signal transduction goes awry due to GOF mutations, it would give rise to various disease types. Quantitative and molecular technologies are in demand to understand cellular networks and their perturbations by GOF mutations, bridging genotype and phenotype in health and disease5. This may provide explanations for 'missing heritability' in previous genome-wide association studies. We envision that it will be instrumental to push current paradigm towards a thorough functional and quantitative modeling of all GOF mutations and their mechanistic molecular events involved in disease development and progression. Many fundamental questions pertaining to genotype-phenotype relationships remain unresolved. For example, what are common types of genomic aberrations leading to GOF? how do interaction networks undergo rewiring upon GOF mutations? Which GOF mutations are key for gene regulation and cellular decisions? What are the GOF mechanisms at the RNA and protein regulation levels? Is it possible to leverage GOF mutations to reprogram signal transduction in cells, aiming to cure disease? To begin to address these questions, in this special session, we will cover a wide range of topics regarding GOF disease mutations and their characterization by multi-omic networks. We highlight the fundamental function of GOF mutations and discuss the potential mechanistic effects in the context of signaling networks 6,7. We also discuss advances in bioinformatic and computational resources, which will dramatically help with studies on the functional and phenotypic consequences of GOF mutations.

Together, this special session leads to an emerging area in computational biology, and is becoming an important area of research in the future. The session is innovative because it will provide unique insights in prioritizing driver functional GOF disease mutations, and uncovering individualized molecular mechanisms. Furthermore, it is significant because it will greatly facilitate the functional annotation of a large number of GOF mutations, providing a fundamental link between genotype and phenotype in human disease.
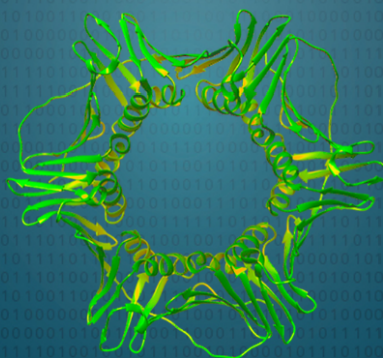
Bioinformatics Advances is a fully open access, peer-reviewed journal published jointly by Oxford University Press and by the International Society for Computational Biology.

For more information, please visit:

https://academic.oup.com/bioinformaticsadvances

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https://www.iscb.org/sponsorship

SST05: Single Cell and Spatial Data Analysis

Organizers:

Malte Luecken, Helmholtz Center Munich, Germany

Shyam Prabhakar, Genome Institute of Singapore

Florian Schmidt, Genome Institute of Singapore

Fabian Theis, Helmholtz Center Munich, Germany

Barbara Treutlein, ETH Zürich, Switzerland

Since its first usage in 2009, single cell technology (SCT) has revolutionized our understanding of molecular biology. We obtained unprecedented resolution on cellular identity, diversity, development, and function. The rapid advancement of SCT in the past decade renders SCT to be the default approach to profile transcriptomes, proteomes and more recently also genomes as well as epigenomes. With the emergence of multimodal assays to profile various "omics" within a single cell, SCTs have crossed the next frontier in enabling new biological discoveries not only in basic science but also with respect to clinical applications. The latter will tremendously benefit from single cell perturbation experiments. They provide unique insights on cell-cell signaling and interaction, which are critical for translational applications. Spatial methods such as single-cell in situ sequencing and imaging-based methods add a new dimension to the study of single cells in diverse tissues, which will open new opportunities, for instance in cancer biology and neuroscience. Ultimately, it is increasingly clear that SCTs will be key to bringing personalized and precision medicine into the clinic.

However, to leverage the unique advantages of single cell data, it must be analysed in a scalable, yet robust and interpretable way. Due to the diversity, technical biases and high level of noise in single cell data, software and algorithm development are challenging. For instance, the best clustering strategy for a specific transcriptomics data type might prove to be not at all usable for single cell chromatin accessibility data. Even within a single data modality, the experimental strategy greatly influences data analysis. Methods that integrate datasets to build reference atlases that overcome limitations of individual experiments again pose new questions on what is meaningful variation versus unwanted noise between datasets. Recently, high throughput assays for multi-modal and/or spatial characterization of single cells have added yet another layer of complexity. The development of integrative data analysis methods is thus essential to obtaining biological insights that can be translated into a product for diagnostic or personalized / precision medicine strategy.

Time	Title	Authors
11:00 - 11:30	Keynote Speaker	**Joseph Powell**, Garvan-Weizmann Center for Cellular Genomics, Australia
11:30 - 12:00	Keynote Speaker	**Zemin Zhang**, Integrated Science Research Center, Peking University and Principal Investigator, BIOPIC and Beijing Advanced Innovation Center for Genomics, China
12:00 - 12:20	Contributed Talks	
12:40 - 14:00	Contributed Talks	
14:20 - 14:50	Keynote Speaker	**Sarah A. Theichmann**, Cellular Genetics Programme Head, Wellcome Sanger Institute Director of Research, Cavendish Laboratory, University of Cambridge, United Kingdom
14:50 - 15:20	Keynote Speaker	**Samantha A Morris**, Assistant Professor of Developmental Biology and Genetics, Allen Distinguished Investigator, New York Stem Cell Foundation Robertson Investigator, Washington University School of Medicine, United States

ISMB/ECCB 2021 Communities of Special Interest (COSIs) Tracks

The organized community sessions (COSI tracks) includes area specific keynote presentations, a selection of talks, which are featured in OUP Bioinformatics in the ISMB/ECCB 2021 Proceedings supplement, as well as highlight and late- breaking research talks. The 2021 COSI Tracks feature the following communities of special interest:

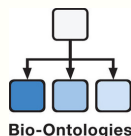## 3DSIG: Structural Bioinformatics and Computational Biophysics

Track Chairs:

Iris Antes, Technical University of Munich, Germany
Douglas Pires, The University of Melbourne, Australia
Rafael Najmanovich, Université de Montreal, Canada

It is impossible to fully understand biological systems without understanding the 3D structure of their constituting parts and their interactions. As such the topics relevant for 3DSIG are wide and include, but are not restricted to Structure-based drug discovery including polypharmacology and network pharmacology; Structure representation, classification and prediction;

BIOINFO-CORE

Track Chairs:

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

Bioinfo-core is a worldwide body of people that manage or staff bioinformatics cores within organizations of all types including academia, academic medical centers, medical schools, biotechs and pharmas.

Bio-Ontologies

Track Chairs:

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

Bio-Ontologies Community of Special Interest Group (COSI) covers the latest and most innovative research in the application of ontologies, the organization and dissemination of knowledge, and the development and application of knowledge-based methods in biomedicine and life sciences.

BOSC: Bioinformatics Open Source Conference

Track Chairs:

Nomi L. Harris, Lawrence Berkeley National Laboratory, United States
Karsten Hokamp, Trinity College Dublin, Ireland

BOSC covers all aspects of open science / open source bioinformatics, including standards and ontologies; approaches that promote open science and sharing of data, results and software; bioinformatics tools and libraries; and ways to grow open source communities while promoting diversity within them.

BioVis: Biological Data Visualization

Track Chairs:

Danielle Albers Szafir, University of Colorado at Boulder, United States

Jan Byška, Masaryk University, Czech Republic

Helena Jambor, TU Dresden, Germany

The BioVis track aims to educate, inspire, and engage bioinformatics and biology researchers in state-of-the-art visualization research and visualization researchers in problems in biological data visualization.

CAMDA: Critical Assessment of Massive Data Analysis

*Extended Abstracts Deadline: May 31, 2021

Track Chairs:

David Kreil, Boku University Vienna, Austria

Joaquin Dopazo, Fundación Progreso y Salud, Spain

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

Wenzhong Xiao, Harvard Medical School, United States

The large, complex data sets for the Critical Assessment of Massive Data Analysis (CAMDA) contest include built-in truths for calibration. In an open-ended competition, however, both seasoned researchers and cunning students push the boundaries of our field, with unexpected questions or angles of approach often bringing the most impressive advances.

Education: Computational Biology Education

Track Chair:

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

Education-COSI focuses on bioinformatics and computational biology education and training across the life sciences.

CompMS: Computational Mass Spectrometry

Track Chairs:

Wout Bittremieux, University of California San Diego, United States

Isabell Bludau, Max Planck Institute of Biochemistry, Germany

Lindsay Pino, University of Pennsylvania, United States

Timo Sachsenberg, University of Tübingen, Germany

COSI CompMS promotes the efficient, high-quality analysis of mass spectrometry data through dissemination and training in existing approaches and coordination of new, innovative approaches.

Evolution and Comparative Genomics
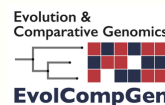
Track Chairs:

Edward L. Braun, University of Florida, United States

Janani Ravi, Michigan State University, United States

Giltae Song, Pusan National University, Korea

Evolution and comparative genomics are deeply intertwined with computational biology. Computational evolutionary methods, such as phylogenetic inference methods or multiple sequence alignment are widely used, yet remain far from "solved" and are indeed intense areas of research.

Function: Gene and Protein Function Annotation

Track Chairs:

Iddo Friedberg, Iowa State University, United States

Kim Reynolds, University of Texas Southwestern Medical Center, United States

Mark Wass, University of Kent, United Kingdom

The mission of the Function Community of Special Interest (Function-COSI) is to bring together computational biologists, experimental biologists, biocurators, and others who are dealing with the important problem of gene and gene product function prediction, to share ideas and create collaborations.

HitSeq: High-throughput Sequencing

Track Chairs:
Can Alkan, Bilkent University, Turkey
Ana Conesa, University of Florida, United States
Francisco M. De La Vega, Stanford University, United States
Dirk Evers, Dr. Dirk Evers Consulting, Germany
Kjong Lehmann, ETH-Zürich, Switzerland

HiTSeq is a community of special interest devoted to the latest advances in computational techniques for the analysis of high-throughput sequencing (HTS) data. Sessions will be devoted to discussing the latest advances in computational techniques for the analysis of high-throughput sequencing (HTS) datasets and will provide a forum for in-depth presentations of the methods and discussions among the academic and industry scientists working in this field.

iRNA: Integrative RNA Biology

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

iRNA track covers the full range of research topics in the field of RNA Biology, from computational and high-throughput experimental methods development to their application in different aspects of RNA processing, structure, and function.

MLCSB: Machine Learning in Computational and Systems Biology

Track Chairs:
Anshul Kundaje, Stanford University, United States
Gabriele Schweikert, Dundee University, Scotland

Systems Biology and Machine Learning meet in the MLCSB COSI. The community is the place for researchers of these areas to exchange ideas, interact and collaborate.

MICROBIOME

Track Chairs:
Thea Van Rossum, EMBL Heidelberg, Germany
Zhong Wang, Joint Genome Institute, United States

The MICROBIOME Community of Special Interest aims at the advancement and evaluation of computational methods in microbiome research, especially metaomic approaches. Based on the Critical Assessment of Metagenome Interpretation (CAMI), the COSI supplies users and developers with exhaustive quantitative data about the performance of methods in relevant scenarios.

NetBio: Network Biology

Track Chair:
Martina Kutmon, Maastricht University, Netherlands

As large scale, systems-level data are becoming increasingly available, modeling and analyzing them as networks is widespread. Network Biology Community serves to introduce novel methods and tools, identify best practices and highlight the latest research in the growing and interdisciplinary field of network biology.

RegSys: Regulatory and Systems Genomics

Track Chairs:

Shaun Mahony, Penn State University, United States

Anthony Mathelier, University of Oslo, Norway

Judith Zaugg, EMBL, Germany

Regulatory genomics involves the study of the genomic control system, which determines how, when and where to activate the blueprint encoded in the genome. Regulatory genomics is the topic of much research activity worldwide. Since computational methods are important in the study of gene regulation, the RegSys COSI meeting focuses on bioinformatics for regulatory genomics.

SysMod: Computational Modeling of Biological Systems

Track Chairs:

Laurence Calzone, Institut Curie, France

Claudine Chaouiya, Aix-Marseille Université, France

Andreas Dräger, University of Tübingen, Germany

María Rodríguez Matínez, IBM Research Europe, Switzerland

Juilee Thakar, University of Rochester Medical Center, United States

The Computational Modeling of Biological Systems (SysMod) aims to create a forum for systems modelers and bioinformaticians to discuss common research questions and methods. The session will focus on the conjoint use of mathematical modeling and bioinformatics to understand biological systems functions and dysfunctions.

Text Mining: Text Mining in Bioinformatics

Track Chairs:

Cecilia Arighi, University of Delaware, United States

Robert Leaman, NCBI/NLM/NIH, United States

This session brings together researchers that create text mining tools with researchers who currently use or are interested in using text mining tools to make new discoveries. The primary goal is to link at least two distinct audiences: those who are not text mining specialists, but who could use the results in their work (e.g., bioinformaticians and computational biologists),

VarI: Variant Interpretation

Track Chair:

Emidio Capriotti, University of Bologna, Italy

Hannah Carter, University of California, San Diego, United States

Antonio Rausell, Imagine Institute for Genetic Diseases, France

The VarI COSI meeting is dedicated to the recent advances in the analysis and interpretation of the genetic variants.

TransMed: Translational Medical Informatics

Track Chairs:

Irina Balaur, University of Luxembourg

Wei Gu, University of Luxembourg

Venkata Satagopam, University of Luxembourg

Mansoor Saqi, Kings College London, United Kingdom

Maria Secrier, University College London, United Kingdom

TransMed covers the current developments in the field of clinical and translational medicine informatics. Analysis of large amounts of multi-omics, imaging (medical and molecular), mobile sensor, clinical and health records data is paving the way for precision medicine. In the TransMed track, we will explore the current status of computational biology and advance machine learning approaches within the field of clinical and translational medicine.

General Computational Biology

Track Chairs:
Xin Gao, King Abdullah University of Science and Technology, Saudi Arabia
Xuegong Zhang, Tsinghua University, China

Novel techniques in emerging areas of computational biology, including intersections with other fields.

https://www.iscb.org/ismbeccb2021-submit/submit-abstracts

NIH/ODSS Special Track

NIH National Institutes of Health
Office of Data Science Strategy

The Office of Data Science Strategy (ODSS) leads implementation of the NIH Strategic Plan for Data Science through scientific, technical, and operational collaboration with the institutes, centers, and offices that comprise NIH. The office was formed in 2018 within the Division of Program Coordination, Planning, and Strategic Initiatives, which plans and coordinates trans-NIH initiatives and research supported by the NIH Common Fund. This 4th edition of the NIH ODSS sponsored track at ISMB/ECCB 2021 will feature updates on the research being conducted by NIH ODSS and its partners as well as funding updates.

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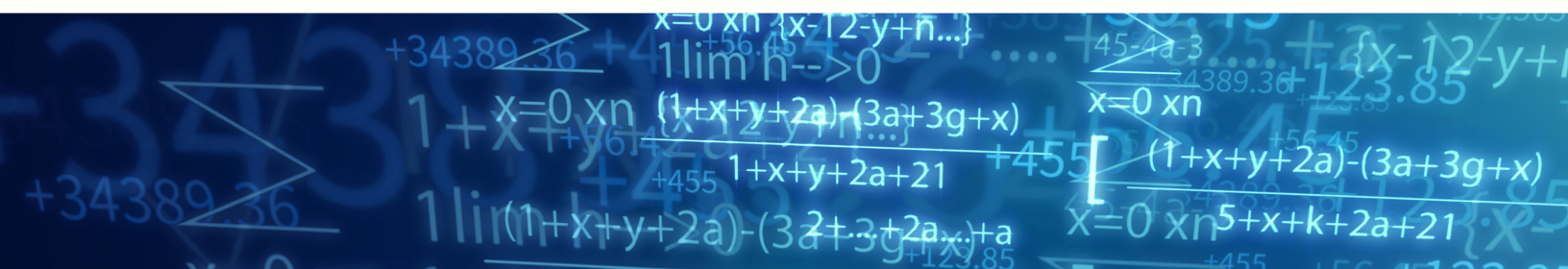
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ISMB/ECCB 2021 Virtual Tutorial Program

Tutorial 1: tidytranscriptomics : introduction to tidy analysis of single-cell and bulk RNA sequencing data

Thursday, July 22, 11:00 - 15:00 UTC

Presenters:

Maria Doyle, Peter MacCallum Cancer Centre, Australia

Stefano Mangiola, The Walter and Eliza Hall Institute of Medical Research, Australia

This tutorial will present how to perform analysis of single-cell and bulk RNA sequencing data following the tidy data paradigm (Wickham and others 2014). The tidy data paradigm provides a standard way to organise data values within a dataset, where each variable is a column, each observation is a row, and data is manipulated using an easy-to-understand vocabulary. Most importantly, the data structure remains consistent across manipulation and analysis functions.

This can be achieved with the integration of packages present in the R CRAN and Bioconductor ecosysten, including tidyseurat, tidySingleCellExperiment, tidybulk, tidyHeatmap (Mangiola and Papenfuss 2020) and tidyverse (Wickham et al. 2019). These packages are part of the tidytranscriptomics suite that introduces a tidy approach to RNA sequencing data representation and analysis.

Tutorial 2: Comprehensive analysis of immunogenomics sequencing data in the cloud to facilitate reproducibility and rigor of immunogenomics research

Thursday, July 22, 15:00 - 19:00 UTC

Presenters:

Serghei Mangul, University of Southern California, United States

Kerui Peng, University of Southern California, United States

Mikhail Shugay, Pirogov Russian National Research Medical University, Russia

Victor Greiff, University of Oslo, Norway

Steven H. Kleinstein, Yale University, United States

Kenneth B. Hoehn, Yale University, United States

Immunogenomics is a field in which genetic information at different levels of biological organization (epigenetics, transcriptomics, metabolomics, cells, tissues, and clinical data) has been characterized and utilized to understand the immune system and immune responses. Immunogenomics studies have offered new opportunities for deepening our understanding of adaptive immune receptors (B-cell receptors, antibodies, T-cell receptors) in the context of a variety of human diseases, such as infectious diseases, cancer, autoimmune conditions, and neurodegenerative disease. Given the importance of adaptive immune receptor research for drug and vaccine discovery, the field is growing at an exponential pace, as exemplified by the user statistics of several immune receptor sequence analysis software suites and databases (Immcantation: >52,000 downloads, >14,000 unique visitors in 2019. VDJTools: >10,000 visitors per year, VDJdb: > 19,000 visitors in 2019 and >40,000 views in 2019). With the number of users exploding, there is a need for software tutorials that lay focus on both rigorous analysis methods as well as reproducibility and interoperability.

We will cover the current stage of immunogenomics methods by providing hybrid lectures and hands-on training sessions. The audience will be equipped with knowledge in this field and the essential skills to conduct adaptive immune receptor analysis independently.

Tutorial 3: Meta-learning for Bridging Labeled and Unlabeled Data in Biomedicine

Friday, July 23, 15:00 - 19:00 UTC

Presenters:

Maria Brbic, Stanford University, United States

Chelsea Finn, Stanford University, United States

Jure Leskovec, Stanford University, United States

In biomedical domains labeled datasets are often very difficult and time-consuming to obtain, requiring a lot of costly manual effort and expert knowledge to hand-label classes before machine learning methods can even be used. This results in many scarcely labeled or completely unlabeled datasets. For instance, in protein function prediction a large number of functional labels have only a few labeled genes, or in single-cell transcriptomics novel and rare cell types appear across large, heterogeneous single-cell datasets.

While machine learning methods excel on tasks with a large number of labeled datasets that can support learning of highly parameterized models, to solve central problems in biomedicine we need methods that can generalize to unseen domains and datasets given only a few labeled training examples, or in the extreme case to completely unlabeled datasets. Meta-learning methods solve this challenge by acquiring prior knowledge over previously labeled tasks in order to learn to generalize to a new task with insufficient labeled data.

This tutorial will cover principles and recent advancements of meta-learning with the case studies designed based on their high relevance for advancing new biomedical discoveries. We will present representation learning methods that bridge labeled and unlabeled data by learning to generalize across datasets given only a few labeled examples or extremely without any labeled data with an emphasis on interpretability. The tutorial will equip participants with the ability to understand fundamentals and state-of-the-art meta-learning methods and to utilize the learned concepts and methods in their own research.

Tutorial 4: A practical introduction to multi-omics integration and network analysis

Thursday, July 22, 11:00 – 15:00 UTC
Friday, July 23, 11:00 – 15:00 UTC

Presenters:
Ashfaq Ali, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Lund University
Rui Benfeitas, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Stockholm University
Nikolay Oskolkov, National Bioinformatics Infrastructure Sweden, Science for Life Laboratory, Lund University

Advances in next generation sequencing (NGS) and mass spectrometry have recently allowed us to probe deeper and systematically into different layers of biological information flow. We can now capture snapshots of cellular states at single-cell or tissue levels on genomic, transcriptomic, metabolomic, and proteomic levels, to examine relationships between thousands of features in each of these omics and a given phenotype or disease. However, characterization beyond individual omic levels to understand how multi-omic relationships jointly relate with a given phenotype remains a challenge. How may identify the features with the largest phenotypic impact, and how can we identify patterns among the different layers?

In this tutorial we will introduce several different approaches for integration of multi-omics data including supervised and unsupervised learning and network analyses. We will highlight some of the key issues in dealing with the high multidimensionality that characterizes multi-omic data and techniques to address them. We will also discuss some of the most successful methods for multi-omic data abstraction, and how machine learning approaches can be used in unraveling biological relationships. We will show how biological network analyses can be used to identify patterns within and between omics, and how communities of features may be related with phenotypic data and biologic functions. Finally, we will discuss how meta-analyses and network meta-analyses can be used in analyzing studies from independent experiments.

Tutorial 5: Inside the 'Black Box': Explainable Deep Learning Models For Image and Sequence Classification

Thursday, July 22, 11:00 - 15:00 UTC
Friday, July 23, 11:00 - 15:00 UTC

Presenters:
Panagiotis Alexiou, Central European Institute of Technology, Masaryk University, Czech Republic
Petr Simecek, Central European Institute of Technology, Masaryk University, Czech Republic

Computational Biologists have been using Machine Learning techniques based on Artificial Neural Networks for decades. New developments in the Machine Learning field over the past years have revolutionized the efficiency of Neural Networks and bring us to the era of Deep Learning. In the news, you can read about Deep Learning beating experts in Go, Chess and StarCraft, translating texts and speech between languages, turning the steering wheels of self-driving cars and even to tag kittens, Not-Hotdogs, and tumours in images. In our field, we have witnessed such systems reaching competitive accuracy with experienced radiologists, predicting folding of proteins and calling single nucleotide polymorphisms in genomic data better than any other method.

In this tutorial we utilize three powerful components that are freely available for use: TensorFlow is an open source library for deep learning and machine learning in general. Thanks to the second one, Google Collaboratory, computational resources needed to train TensorFlow models are available without cost. And finally, TensorFlow.js, will enable us to deploy the trained model as a static web page that can be easily hosted, e.g. on GitHub Pages. We will demonstrate Google Collaboratory + TensorFlow + TensorFlow.js on two examples: classification of images (cells & tissues) and classification of genomic sequences.

The key part of the tutorial will be evaluation and interpretation of the trained model. What could go wrong and how to diagnose it? We will start with simple techniques, like measuring the impact of simple perturbation, and end with an Integrated Gradient method to identify part of input mostly contribution to the decision, introduced in a paper "Axiomatic Attribution for Deep Networks".

Tutorial 6: Nextflow and nf-core: Scalable and FAIR Biomedical Analysis Workflows

Thursday, July 22, 15:00 - 19:00 UTC
Friday, July 23, 15:00 - 19:00 UTC

Presenters:
Phil Ewels, nf-core creator; Bioinformatics Team Leader, SciLifeLab, Sweden
Evan Floden, Nextflow co-creator; Seqera Labs, Spain
Paolo Di Tommaso, Nextflow co-creator; Seqera Labs, Spain

Nextflow is an open-source workflow management system that prioritizes portability and reproducibility. It enables users to develop and seamlessly scale genomics workflows locally, on HPC clusters, or in major cloud providers' infrastructures. Developed since 2014 and backed by a fast-growing community, the Nextflow ecosystem is made up of users and developers across academia, government and industry. It counts over 1M downloads and over 10K users worldwide.

nf-core is a framework for the development of collaborative, peer-reviewed, best-practice analysis pipelines. All nf-core pipelines are written in Nextflow and benefit from the ability to be executed on most computational infrastructures, as well as having native support for container technologies such as Docker and Singularity. The nf-core community has developed a suite of tools that automate pipeline creation, testing, deployment and synchronization. The goal is to provide a framework for high-quality bioinformatics pipelines that can be used across all institutions and research facilities.

This intensive tutorial is targeted at bioinformaticians and will cover everything to get users started with Nextflow and nf-core.

Tutorial 7: The state-of-the-art in microbial community bioinformatics

Thursday, July 22, 15:00 - 19:00 UTC
Friday, July 23, 15:00 - 19:00 UTC

Organizers & Presenters:
Curtis Huttenhower, Harvard T.H. Chan School of Public Health, United States
Melanie Schirmer, Technical University of Munich, Germany
Nicola Segata, University of Trento, Italy

Presenters:
Eric Franzosa, Harvard T.H. Chan School of Public Health, United States
Philipp Muench, Helmholtz Centre for Infection Research, Germany
Kelsey Thompson, Harvard T.H. Chan School of Public Health, United States
Aaron Walsh, Broad Institute of MIT and Harvard, United States

This tutorial will introduce attendees to the current state-of-the-art in computational and quantitative methods for microbial community analyses. These will focus on integrating modern culture-independent sequencing (shotgun metagenomics and metatranscriptomics) with other molecular data (metabolomics, metaproteomics) and applying appropriate, accurate upstream bioinformatics and downstream biostatistics. This will include both human microbiome epidemiology and environmental microbial ecological, phylogenetic, and toxicology applications.

Attendees are assumed to be familiar with basic microbial community concepts and with command line environments, ideally with some facility in Python and/or R, but are not required to have extensive prior experience with metagenomics. The tutorial will mix lectures introducing important current analysis concepts with hands-on labs using pre-built cloud instances including demonstration data and bioBakery software tools. It will conclude with a discussion of gaps, needs, challenges, and potential next steps for bioinformaticians interested in the field of microbial community research.

Tutorial 8: Reproducible omics data analysis workflows with the COVID-19 Disease Map, WikiPathways and Cytoscape

Thursday, July 22, 15:00 – 19:00 UTC

Friday, July 23, 15:00 – 19:00 UTC

Presenters:

Lauren Dupuis, Maastricht University, Netherlands

John "Scooter" Morris, UCSF, United States

Martina Summer Kutmon, Maastricht University, Netherlands

During the COVID19 pandemic, an international group of over 200 researchers started a collaboration to build a comprehensive map of SARS-CoV-2 related processes from virus uptake and virus replication to host immune response. In this tutorial session, we will highlight some of the use cases of this collection of highly curated pathway models for omics data analysis using pathway and network approaches.

Given the constant influx of new knowledge and data, the development of automated and reproducible data analysis workflows is essential. After a short introduction of the COVID-19 Disease Map project and the WikiPathways community curated pathway database, the tutorial will start with a session focused on Cytoscape, one of the most popular tools for network analysis and visualization, and its automation features. During the hands-on session in the afternoon, we will instruct participants on how to make use of three automated R-based transcriptomics data analysis workflows focused on pathway enrichment, tissue-specific pathway activity, network visualization, and network extension. Importantly, while we will focus on the COVID-19 Disease Map and COVID-19 related transcriptomics datasets, the majority of the workflows can be easily utilized for other applications.

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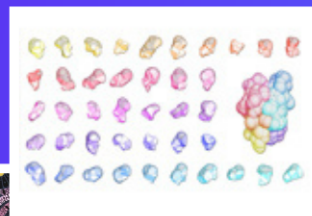*Register to attend ISMB/ECCB 2021 and SAVE!*

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