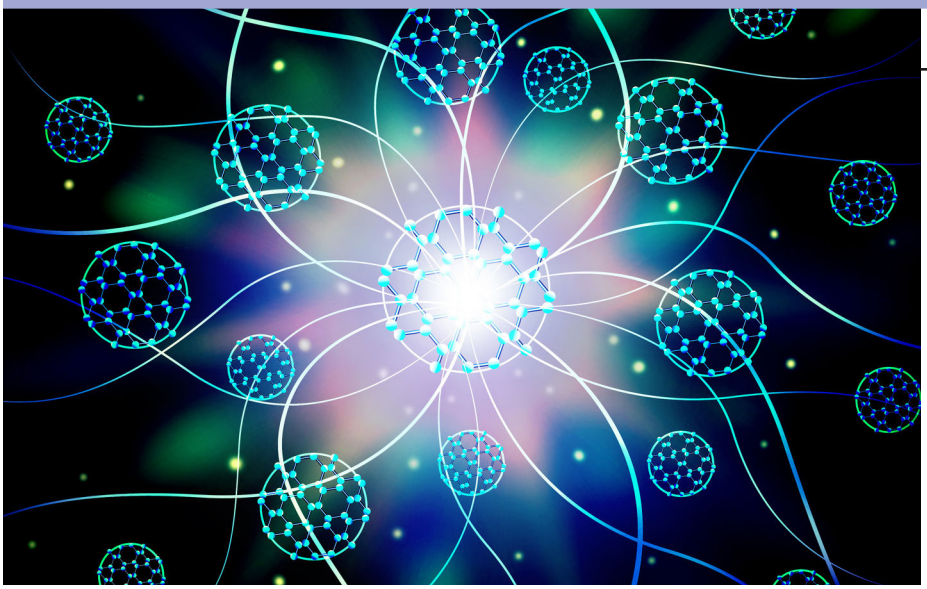
ISCBNEWSLETTER



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ISMB/ECCB 2019 Arriving Soon in Basel

Cutting-edge science, knowledge building hands-on tutorials, community-based networking, student-focused symposium, these are the ingredients to the perfect computational biology enriched gathering. You will find these and a few other surprises at ISMB/ECCB 2019!

ISMB is the premier event in the bioinformatics calendar, and the 2019 iteration with ECCB in the beautiful city of Basel aims to provide an exciting line up of talks, workshops and networking opportunities. Integration of COSI sessions with the conference and the inclusion of special sessions on new hot topics means participants will be able to indulge in cutting edge science and new technology developments in their field of interest, as well have exposure to other fields and newly trending topics. We are excited to welcome you to Basel and look forward to hearing about your research. - Nicola Mulder & Torsten Schwede, Conference Co-Chairs

The 2019 Intelligent Systems for Molecular Biology (ISMB) conference, in conjunction with the European Conference in Computational Biology (ECCB), will be held in Basel, Switzerland, July 21-25, 2019.

Under the direction of Torsten Schwede, Biozentrum, University of Basel & SIB Swiss Institute of Bioinformatics, Switzerland, and Nicola Mulder, University of Cape Town, South Africa, conference chairs, the ISMB/ECCB conference will be the largest and most high profile meeting of scientists working in computational biology held in 2019.

ISMB/ECCB provides an intense multidisciplinary forum for disseminating the latest developments in bioinformatics/computational biology, fosters fresh dialogues and perspectives to learn about and shape the future of the field. In response to the increasing interest in the activities of the ISCB's Communities of Special Interest (COSIs) the conference is organized with the active participation of the COSIs in the development of the program and highlights emerging or "hot" research areas providing an outstanding scientifically effective program.

The conference format features proceedings talks and abstract presentations that include highlights (previously published research) and late-breaking research. Each day of the five-day conference includes outstanding keynote lectures, technical tracks, COSI track presentations, a variety of workshops and tutorials, special sessions, equal opportunities activities, a students' council day and other focused presentations on other important research area topics in computational biology.

The 2019 COSI track areas are:

- Structural Bioinformatics and Computational Biophysics
- BIOINFO-Core
- Bio-Ontologies
- Biological Data Visualizations
- Critical Assessment of Massive Data Analysis
- Computational Biology and Bioinformatics Education and Training
- Computational Mass Spectrometry
- Computational Modeling of Biological Systems
- Evolution & Comparative Genomics
- Gene and Protein Function Annotation
- General Computational Biology Research

- BOSC - Bioinformatics Open Source Conference
- High Throughput Sequencing Algorithms & Applications
- Integrative RNA Biology
- Machine Learning in Computational and Systems Biology
- Microbiome
- Network Biology
- Regulatory and Systems Genomics
- Translational Medicine Informatics & Applications
- Variant Interpretation

The bulk of the ISMB/ECCB program will be determined by abstract and proceedings submissions. Abstract submissions are still being accepted.

We expect to schedule approximately 600 talks and 900. In addition to the selected talks, the conference will also offer Comp Bio Ignite talks.

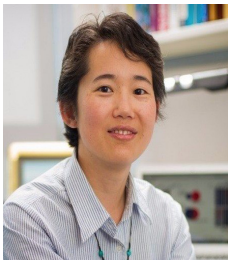
Comp Bio Ignite is a presentation opportunity that is organized using the un-conference approach. Delegates who are registered for the conference who are not presenting oral presentations in the tracks of the meeting will have the opportunity to sign up for a slot to present their research in lighting style talks lasting five minutes each.

Even though most of the program is developed through submissions, we do have a few highlights to share with you about the upcoming meeting.

ISCB Congratulates the 2019 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. During the 2009 inaugural year of the program, the ISCB Board of Directors unanimously conferred Fellows status on the seven winners-to-date of the ISCB Accomplishment by a Senior Scientist Award. 2019 marks the 10th anniversary of the program. Each year since 2010, ISCB has sought Fellows nominations from our members, with eligibility restrictions based on selection criteria focused most heavily on the significance of scientific contributions, and service to our field and to ISCB.

Vineet Bafna, Professor, Computer Science and Engineering, University of California, San Diego, United States, an innovator who developed many bioinformatics algorithms for solving important biological problems and a leading researcher in the area of Cancer Genomics, Population Genetics, and Proteogenomics. His research is marked by deep insights into fundamental problems that were ignored by others.



Xiaole Shirley Liu, Professor, Biostatistics, Harvard T.H. Chan School Of Public Health, Harvard School of Public Health; Co-director, Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, United States, an innovative and prolific computational cancer biologist. Her research focuses on algorithm development and integrative modeling of high throughput data to understand the specificity and function of regulator genes in tumor development, progression, drug response and resistance, resulting in many highly cited papers.

Eleazar Eskin, Professor, Computer Science, Human Genetics, University of California, Los Angeles, United States, a leading computer scientist working in computational problems in human genetics, especially in terms of human disease. He has developed advanced educational programs for computer scientists, biologists, and statisticians, in computational biology, especially through his leadership activities at the NSF Center for Pure and Applied Mathematics (IPAM) at UCLA.

Marie-France Sagot, Director of Research (DR1) INRIA, Head of BAOBAB Team, INRIA Grenoble Rhône-Alpes & Laboratoire de Biométrie et Biologie Évolutive (LBBE), Université Claude Bernard, Universite Claude Bernard, France, a key figure linking the South-American and European bioinformatics communities. She is best known for her sharp algorithmic work. Specifically, her work on exact algorithms for structured or approximate motif search using suffix trees was foundational in the analysis of transcriptional regulatory sequences.

Congratulations, 2019 Class of Fellows!

ISMB/ECCB Distinguished Keynotes

ALEXIS BATTLE, BIOMEDICAL ENGINEERING AND COMPUTER SCIENCE

JOHN HOPKINS UNIVERSITY, BALTIMORE, UNITED STATES

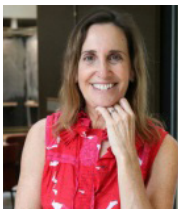
Alexis Battle is an Associate Professor of Biomedical Engineering and Computer Science at Johns Hopkins University, and a 2016 Searle Scholar. Her research group focuses on understanding the impact of genetic variation on the human body, using machine learning and probabilistic methods to analyze large scale genomic data. She is interested in applications to personal genomics, genetics of gene expression, and gene networks in disease, leveraging diverse data to infer more comprehensive models of genetic effects on the cell. She earned her Ph.D. in Computer Science in 2013 from Stanford University, where she also received her Bachelor's degree in Symbolic Systems in 2003. Alexis spent several years in industry as a manager and member of the technical staff at Google, Inc.

NIKOLAUS RAJEWSKY, MAX-DELBRÜCK-CENTRUM FOR MOLECULAR MEDICINE IN THE HELMHOLTZ ASSOCIATION, BERLIN-BUCH, GERMANY

Nikolaus Rajewsky combines computational approaches (Informatics, Statistics, Theoretical Physics) with Biochemistry and Molecular Biology. His research is about understanding how differentiated cells can become totipotent and vice versa.

Nikolaus Rajewsky is a member of numerous international advisory boards (for example of the MRC Clinical Sciences, London) and has served as a referee for all major journals in the life sciences (Science, Nature, Cell etc.). His peer-reviewed publications have been cited more than 33,000 times. His research is or has been supported by grants from the EC, German Ministry of Science, Senate of Berlin, DFG, NIH, GIF, and others. He has given more than 170 invited talks at international meetings during the past years. Nikolaus has conceived, initiated and directs a new branch of the MDC, the "Berlin Institute for Medical Systems Biology (BIMSB)", endowed with 20 Million Euros per year to fund ~25 new group leaders. BIMSB has received funding for a new building in the Center of Berlin and has already recruited 17 group leaders, most of them from abroad.

ISCB Award Keynotes



BONNIE BERGER, SIMONS PROFESSOR OF MATHEMATICS AND PROFESSOR OF ELECTRICAL ENGINEERING & COMPUTER, MASSACHUSETTS INSTITUTE OF TECHNOLOGY, UNITED STATES

RECIPIENT OF ISCB ACCOMPLISHMENTS BY A SENIOR SCIENTIST AWARD

The ISCB Accomplishments by a Senior Scientist Award recognizes leaders in the fields of computational biology and bioinformatics for their significant research, education, and service contributions. Bonnie Berger is being honored as the 2019 winner of the ISCB Accomplishments by a Senior Scientist Award.

Professor Bonnie Berger is the Simons Professor of Mathematics with a joint appointment in Computer Science, and Associate Member of the Broad Institute at Massachusetts Institute of Technology (MIT), Cambridge, MA, United States. She is also Faculty of Harvard and MIT Health, Science and Technology. She received her Ph.D from MIT in 1990 in computer science and completed a postdoctoral fellowship in applied mathematics in 1992.

After beginning her career working in algorithms at MIT, she was one of the pioneer researchers in computational biology and, together with the many students she has mentored, has been instrumental in defining the field. She continues to lead efforts to design algorithms to gain biological insights from recent advances in automated data collection and the subsequent large data sets drawn from them. Dr. Berger works on diverse areas, including Compressive Genomics, Network Inference, Structural Bioinformatics, Population Genomics, and Genomic Privacy.

She has co-authored over 185 scholarly research articles and has been invited to present at conferences in fields ranging from randomized algorithms and graph theory to computational Molecular Biology. Dr. Berger was recently elected to serve as a Member-at-Large of the Section on Mathematics at American Association for the Advancement of Science (AAAS). Over the years, she has received numerous honors including: election to the American Academy of Arts and Sciences, the NIH Margaret Pittman Director's Award for Outstanding Scientific Achievement & Lectureship, Biophysical Society's Dayhoff Award, Technology Review Magazine's inaugural TR100 as a top young innovator, ACM Fellow, ISCB Fellow, American Institute for Medical and Biological Engineering Fellow, American Mathematical Society Fellow, NSF Career Award and Honorary Doctorate from EPFL.

CHRISTOPHE DESSIMOZ, SNSF PROFESSOR, UNIVERSITY OF LAUSANNE; ASSOCIATE PROFESSOR, UNIVERSITY COLLEGE LONDON; GROUP LEADER, SWISS INSTITUTE OF BIOINFORMATICS

RECIPIENT OF THE ISCB OVERTON PRIZE

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. Christophe Dessimoz is being recognized as the 2019 winner of the Overton Prize.

Christophe Dessimoz is a SNSF Professor at the University of Lausanne; an Associate Professor at the University College London; a Group Leader at the Swiss Institute for Bioinformatics. Christophe obtained his Master in Biology (2003) and PhD in Computer Science (2009) from ETH Zurich, Switzerland. After a postdoc at the European Bioinformatics Institute near Cambridge (UK), he joined University College London as Lecturer (2013) and was promoted to a Reader in 2015. He joined the University of Lausanne as a SNSF Professor in 2015. With 70 papers published, Christophe has made varied and sustained contributions to bioinformatics.

He is renowned for his contributions to and subsequently management of the OMA resource providing high quality information on orthologous proteins. OMA is a very highly regarded resource with important applications in protein function prediction.

Another important thread across Christophe's work has been his pursuit of benchmarking. Christophe's rigorous approach to benchmarking had a major impact on three key subfields of computational biology: orthology inference, sequence alignment, and gene ontology.

WILLIAM STAFFORD NOBLE, PROFESSOR, DEPARTMENT OF GENOME SCIENCES, DEPARTMENT OF COMPUTER SCIENCE AND ENGINEERING, DIRECTOR, COMPUTATIONAL MOLECULAR BIOLOGY PROGRAM, UNIVERSITY OF WASHINGTON, UNITED STATES

RECIPIENT OF THE ISCB INNOVATOR AWARD

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. William Stafford Noble is the 2019 winner of the ISCB Innovator Award.

Dr. Noble is a Professor in the Department of Genome Sciences and in the Paul G. Allen School of Computer Science and Engineering at the University of Washington, United States. He received the Ph.D. in computer science and cognitive science from University of California, San Diego in 1998. After a one-year postdoc with David Haussler at University of California, Santa Cruz, he became an Assistant Professor in the Department of Computer Science at Columbia University. In 2002, he joined the faculty of the Department of Genome Sciences at the University of Washington where he now is a Professor and the Director of the Computational Molecular Biology Program.

Noble's research applies statistical and machine learning methods to the analysis of complex biological data sets. He has extensive experience developing novel analytical methods, creating user-friendly software implementing those methods, and collaborating with experimentalists. The most notable areas of research for Noble and his group are sequence analysis methods for DNA and proteins, kernel methods for learning from heterogeneous data, semi-automated genome annotation, the 3D structure of the genome and machine learning and statistical methods for analyzing shotgun proteomics data.

He is the author of >230 peer reviewed publications and has advised 27 postdoctoral fellows and 24 graduate students. William is the recipient of an NSF CAREER award, is a Sloan Research Fellow, is on the Clarivate Analytics list of "Highly cited researchers," and is a Fellow and former member of the Board of Directors of the International Society for Computational Biology.

Youth Bioinformatics Symposium 2019

On Saturday, January 12 of this year ISCB held its second Youth Bioinformatics Symposium (YBS). Co-organized by George Mason University and held on their campus in Innovation Hall in Fairfax, Virginia. In attendance were over 100 middle and high school students and their parents from the Washington DC, Maryland, and Virginia areas.

Dr. David Fenstermacher kicked off the event as the keynote speaker. Inspiring the students by telling the story of his career path and encourage them to consider various career opportunities in computational biology. Students then had the opportunity to participate in 4 workshops run by teams from George Mason University, The George Washington University, University of Maryland, and Thomas Jefferson High School for Science and Technology. The Workshops explored Neuroscience, Artificial Intelligence and Machine Learning in Bioinformatics, Biomedical Bioinformatics, as well as Forensics with DNA and Bioinformatics.

The day ended with a panel comprised of students, postdocs, and professionals studying and working in different areas of computational biology. Our moderator, Dr. Quattrochi, asked questions, fostered healthy debate and encouraged the students to ask questions of the panelists.

Mark Your Calendars for GLBIO 2019!

The 13th Great Lakes Bioinformatics Conference: GLBIO 2019! An official conference of the International Society for Computational Biology and organized by the Great Lakes Bioinformatics Consortium, is scheduled to be held May 19-22 this year in Madison, Wisconsin. Hosted by the University of Wisconsin-Madison.

The conference program will include 6 outstanding keynote speakers from the Great Lake region, oral and poster presentations as well as a variety of special sessions and workshops. From novice to expert, attendees have the opportunity to participate in a variety of workshops, presentations, networking events, recruiting events and exhibits.

GLBIO has established a strong reputation for building relationships among a nationally prominent bioscience research community, showcasing the North American Great Lakes region as a perfect place to conduct computer-aided research. There will be an opportunity to recruit talent as well as seek a positon during the Lunch N' Learn Recruitment Roundtable on Monday. There are also two networking opportunities this year – the Welcome Reception and the Game Night Networking events – both excellent opportunities to see old friends, meet new friends, build relationships, and create opportunities to collaborate on future projects. We look forward to seeing YOU in Madison in May!

For more information please visit: www.iscb.org/glbio2019

ISMB/ECCB 2019 Tutorials and Hands-on Training

The conference will feature eight tutorial workshops. The purpose of the Tutorials program is to build knowledge and provide hands-on training in "cutting-edge" topics relevant to the bioinformatics field and the COSI communities. Tutorials offer participants an opportunity to get an introduction to important established topics in bioinformatics, to learn about new areas of bioinformatics research, or to develop advanced skills in areas about which they are already knowledgeable. Tutorials also serve to bring together people and COSI communities with common interests to discuss, debate and problem-solve defined topics. The 2019 workshops are:

INTERPRETABILITY FOR DEEP LEARNING MODELS IN COMPUTATIONAL BIOLOGY

The recent application of deep neural networks to long-standing problems such as the prediction of functional DNA sequences, the inference of protein-protein interactions or the detection of cancer cells in histopathology images has brought a break-through in performance and prediction power. However, high accuracy often comes at the price of loss of interpretability, i.e. many of these models are built as black-boxes that fail to provide new biological insights. This tutorial focuses on illustrating some of the recent advancements in the field of Interpretable Artificial Intelligence. We will show how explainable, smaller models can achieve similar levels of performance than cumbersome ones, while shedding light on the underlying biological principles driving model decisions.

This tutorial will demonstrate how to build and extract knowledge using interpretable approaches in two different domains of computational biology: the functional analysis of raw DNA sequencing data and drug sensitivity prediction models. The choice of these two applications is motivated by the availability of adequately large datasets that can support deep learning approaches and by their high relevance for personalized medicine. We will exploit both publicly available deep learning models as well as in-house developed models.

The tutorial is aimed to strike the right balance between theoretical input and practical exercises. The tutorial has been designed to provide the participants not only with the theory behind deep learning and interpretability, but also to offer a set of frameworks, tools and real-life examples that they can implement in their own projects.

RECENT ADVANCES IN STATISTICAL METHODS AND COMPUTATIONAL ALGORITHMS FOR SINGLE-CELL OMICS ANALYSIS

Single-cell genomics is the study of individual cells using omics approaches, which circumvents averaging artifacts associated with traditional bulk population data and yields new insights into cellular heterogeneity. The field has seen rapid development in both technologies and statistical methods and computational algorithms, leading to improved data analysis. This tutorial is focused on advanced statistical and computational methods that are recently developed for single-cell omics data. The first half of the tutorial will include a brief introduction, followed by “generalized” methods and workflows for scRNA-seq data, including data normalization, visualization, batch correction, and denoising. The second half of the tutorial will be on “specific” topics and applications in the single-cell domain, including pseudotime reconstruction, simultaneous measurements of single-cell transcriptomic and V(D)J profiles, multimodal alignment of single-cell transcriptomic and epigenomic data, as well as single-cell inference of tumor heterogeneity.

Website: https://github.com/rhondabacher/ISMB2019_SingleCellTutorial

BUILDING A DISTRIBUTED KNOWLEDGE GRAPH TO ASSIST WITH COMPUTATIONAL DRUG DISCOVERY

Drug discovery pipelines are expensive in time and resources, which are wasted if a drug is rejected due to toxicities discovered in late stages. Computational investigation of the different entities (proteins, diseases, pathways, ...) that are involved in drug discovery could help provide a better understanding of the dynamics governing their relations and the downstream effects of targeting proteins with drugs. Using various data sources, including the UniProt Knowledgebase, disease ontologies, the DrugBank database and protein interactions and pathways data, we present data integration approaches to build a distributed knowledge graph (DKG) that will assist with computational discovery of drugs.

In this tutorial, the participants will be introduced to two emerging tools in the field of big data, namely the Apache Spark computing framework and the Apache Zeppelin interactive analytics framework. Spark can be used from within Zeppelin and coupled with other back-end languages and tools to provide deeper insights. Participants will also learn about data structures for representing knowledge graphs (GraphFrames) and building machine learning (ML) models.

A PRACTICAL INTRODUCTION TO REPRODUCIBLE COMPUTATIONAL WORKFLOWS

This hands-on tutorial teaches participants the key requirements and practical skills to setup a reproducible and reusable computational research environment. The tutorial is intended for Python and R users, and anyone interested in using Jupyter Notebooks, which supports over 50 programming languages. We will work through a few bioinformatics use cases step by step, including biological visualization and machine learning. We will then share the results using Binder (mybinder.org), a publicly hosted environment to run Jupyter Notebooks in a fully reproducible and interactive manner. We also cover collaborative development practices. After attending this workshop, participants should be able to set up their own projects by applying the principles and techniques learned and publish reproducible research protocols.
Audience

This course is designed for everyone who would like to gain hands-on experience in setting up reproducible computational environments to their own projects. Introductory level Python skills are required and R skills are optional.

BIOMARKER DISCOVERY AND MACHINE LEARNING IN LARGE PHARMACOGENOMICS DATASETS

Over the past decade there has been an explosion in the availability of massive datasets combining drug screening with high-throughput molecular profiling in cancer model systems. These datasets have become a rich community resource which can be leveraged for biomarker discovery, in-silico validation, drug repurposing, drug method of action prediction, and to train statistical machine learning models for drug response prediction. However, this data poses unique challenges during analysis and requires methods that are robust to the noise inherent in the drug sensitivity assays. Furthermore, irreproducibility of some findings across studies strongly motivates integrative analysis across studies. Fortunately, tools have been developed implementing bioinformatics and machine learning methods designed specifically for the analysis of pre-clinical pharmacogenomics data.

In this tutorial, participants will become familiar with common preclinical cancer models (such as cell-line, patient derived xenografts and organoids) and publicly available large pharmacogenomics datasets. Next, in the hands on session, they will be introduced to the tools and packages published for analysis of these datasets, with a focus on tools written in R. Furthermore, after becoming familiar with the challenges posed by the noise in the pharmacological assays observed in high-throughput pharmacogenomics, participants will gain hands on experience using these datasets for the purpose of biomarker discovery and validation as well as building machine learning models predictive of drug response. A focus will be on translational research, validating discoveries from in vitro datasets using in vivo pharmacogenomic and clinical datasets. The hands on sessions will be conducted primarily in R and RStudio.

VISUALIZATION OF LARGE BIOLOGICAL DATA

The aim of this tutorial is to familiarize the participants with modern visual analytics methodologies applied to biological data and to provide simple hands-on training. Questions such as what is data visualization, what is visual analytics, and how can large-scale biological data be visualized to gain insight will be addressed, so that hypotheses can be generated or explored and further targeted analyses can be defined. The tutorial will cover the basics that are necessary to create visualizations for biological data. This includes a general introduction to visualization, basics of visual design, and fundamentals of human color perception. Based on these generally applicable principles, various examples of visualizations and visual analysis tools for biological data that adhere to the aforementioned fundamentals and best practices will be presented and discussed. A specific focus will be laid on visualization approaches of large-scale (omics) data. Finally, attendees will have the opportunity to get first hands-on experience in creating their own interactive web-based visualization application using modern web technologies like HTML5, JavaScript, and D3.

Topics include:

- Digital/Electronic visualization of data
- Understanding color
- Visual Design Principles
- Examples of visualization of biological data
- Challenges of large-scale biological data visualization
- Introduction to web-based visualization for biological data

BASEL
JULY 21-25
ISMB ECCB 2019
iSCB

NEW THIS YEAR

COMP BIO IGNITE PRESENTATIONS

Comp Bio Ignite is a presentation opportunity at ISMB/ECCB 2019 that is organized using the un-conference approach. Delegates who are registered for the conference who are not presenting oral presentations in the tracks of the meeting will have the opportunity to sign up for a slot to present their research in lighting style talks lasting five minutes each. Delegates may present using the PechaKuchaor Ignite talkspresentation style or a single slide or PDF. All talks will be over the lunch period in a dedicated open theater space. Talks are given on a first come first serve basis and can be requested in the evening of Sunday, Monday, and Tuesday for presentation on Monday, Tuesday, and Wednesday by submitting an talk title, abstract, and author list. There is no scientific review of abstracts for this presentation type. Organization of the schedule will be based on topic. All schedules will be posted on the ISMB/ECCB Conference website in the CompBio Ignite section of the program along with the submitted abstract.

#ISMBECCB2019

RECOMB 2019
May 5 – 8, 2019
Washington, USA
HTTPS://RECOMB2019.ORG

GLBIO 2019
May 19 - 22, 2019
Madison, Wisconsin, USA
HTTPS://WWW.ISCB.ORG/GLBIO2019

ISMB/ECCB 2019
July 21-25, 2019
Basel, Switzerland
HTTPS://WWW.ISCB.ORG/ISMBECCB2019

RECOMB/ISCB REGULATORY AND SYSTEMS GENOMICS CONFERENCE WITH DREAM
Nov 4 - 6, 2019
New York, New York

ISCB-AFRICA ASCBC CONFERENCE ON BIOINFORMATICS
Nov 11 - 15, 2019
Kumasi, Ghana, Africa

ADVANCES IN COMPUTATIONAL BIOLOGY - FOSTERING COLLABORATION AMONG WOMEN SCIENTISTS
Nov 28 - 29, 2019
Barcelona, Spain

ROCKY 2019
Dec 5 - 7, 2019
Snowmass, Colorado

TOOLS FOR REPRODUCIBLE RESEARCH

The typical data analyst must simultaneously juggle multiple projects, each having its own duration and software requirements. As few analysts have any formal training on structuring or even writing the code necessary to perform an analysis, it is unsurprising that the iterative analytic process can produce a wide assortment of almost identically named files (e.g., "final_results.txt", "final_results.version2.txt", "final_results.really_final.txt"), all with unclear origins and produced with a hodge-podge of similarly poorly named scripts. The near impossibility of tracing a results file to the exact process that produced it creates untold difficulties both when it comes time to publish results as well as when planning subsequent experiments months or years later (afterall, which of the "final_results" files was really the "right one"?). These issues are further compounded by software paths and other similar assumptions being hard-coded into scripts, preventing easy analysis replication elsewhere. Performing analyses in a reproducible and traceable manner is clearly needed to combat such problems.

In this hands-on tutorial, we demonstrate how Conda can be used to deploy specific software versions easily, reproducibly, and without administrator credentials. Moreover, we demonstrate how Conda's ability to create isolated software environments helps to avoid side-effects between different analyses or different steps of the same analysis. Attendees will also learn how to create conda recipes themselves, so they can contribute new packages to projects such as Bioconda. We further demonstrate how Snakemake can be used in combination with Conda and Containers to create reproducible analyses workflows and executed them on any platform from workstations to clusters and the cloud. Finally, using snakePipes as an example, we demonstrate how Conda and Snakemake can be used to define reproducible and flexible workflows for complex genomics analysis.

SKILLS GAINED FROM ATTENDING ISMB/ECCB TUTORIALS PROGRAM WILL BETTER EQUIP ANY RESEARCHER TO SOLVE CURRENT AND FUTURE CHALLENGES IN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY.

ISCB Code of Ethics and Professional Conduct

ISCB has grown significantly since its founding in 1997. Over the course of the past 22 years, we have gained knowledge, adapted to our changing world, and evolved to meet the needs of our members and greater community. ISCB's goal is to be the leading organization for all those who call computational biology and bioinformatics home. To do this, we need to be willing to set the example for others and uphold ourselves in the highest regard.

Science is best advanced when there is mutual trust, based upon honest behavior, throughout the community. Our scientific Society thus expects all of our members to adhere to the highest standards of honesty and integrity in all their actions, whether inside or outside ISCB. Honesty must be regarded as the cornerstone of ethics in science. Professional integrity in the formulation, conduct, interaction, and reporting of bioinformatics and computational biology activities reflects not only on the reputation of individuals and their organizations, but also on the image and credibility of the profession as perceived by scientific colleagues, government, and the public. It is important that the tradition of ethical behavior be carefully maintained and transmitted with enthusiasm to future generations.

On February 14, 2019, the ISCB Board of Directors adopted the Code of Ethics and Professional Code. Each researcher, practitioner, technician, student, and supplier within the field is a citizen of the community of science. Each shares responsibility for the welfare of this community. The guiding principles set forth in the ISCB Code of Ethics and Professional Conduct are meant to protect the community of science. The guidelines are not meant to be a complete list of all ethical issues. They may be modified and amplified by events and experience. Society members have an individual and a collective responsibility to ensure that there is no compromise with these guidelines.

The Code of Ethics and Professional Conduct applies to all participants of all ISCB related activities, including:

- conferences, affiliated groups, communities of special interest (COSIs), workshops, and events sponsored, co-sponsored, or in cooperation with
- exchanges among committees or other bodies associated with ISCB
- communication sent through ISCB communication channels and associated social media
- communications of press/media pass holders who are communicating through their own blogs/communication platform while in attendance of ISCB events or activities

ISCB desires to maintain an environment that allows science and scientific careers to flourish through respectful, inclusive, and equitable treatment of others and is committed to providing a safe place for its members and nonmember participants. In addition to the Code of Ethics and Professional Conduct, the ISCB Board of Directors also adopted the ISCB - Safe Place statement.

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

The Code of Ethics and Professional Conduct as well as the Safe Place statement aim to foster a culture that creates a safe and open working environment for all who are participating in ISCB activities, conferences, and programs.

We encourage our members, colleagues, and friends to take the time to review the ISCB Code of Ethics and Professional Conduct and stand with ISCB as we work to create a better world.

ISMB/ECCB 2019 Special Sessions

SOCIAL MEDIA MINING FOR DRUG DISCOVERY RESEARCH: CHALLENGES AND OPPORTUNITIES OF REAL WORLD TEXT

Social media mining in biomedicine is a research area that marries biomedical natural language processing (BioNLP) techniques with the biomedical sciences. This field has been of growing interest since the popularization of microblogs and disease-related forums and blogs. Because it involves handling Real World Data (RWD), it poses unique challenges in comparison to other BioNLP applications such as the mining of scientific documents. Some of these challenges are: higher prevalence of non-English content, use of colloquial and lay language, abundance of noise and junk content, and source format variability. Despite these challenges, social media can bring a unique perspective and knowledge about patients as well as their caregivers, family and friends. In fact, it presents an unfiltered access to the patient's view on a wide range of topics, including politically incorrect and socially embarrassing ones, while bypassing traditional information gatekeepers such as healthcare providers and patient organizations.

This special session will include the following topics: patient outcomes research, patient journey, unmet medical need, symptom and daily-life-impact disease models, evaluation of and compliance with current therapies, adverse-event and signal detection, evaluation of existing standards of care, assessing cultural differences between patients, recruitment optimization, patient burden and disease work, and disease-coping strategies.

REPRODUCIBILITY OF FINDINGS FROM BIG DATA - FROM VISION TO REALITY

Scientific output is growing at a fast pace (United Nations Educational Scientific and Cultural Organization, 2015) but standards for transparency and reporting of data are often lagging. This lack of transparency can lead to challenges in extracting- and building upon relevant knowledge and following reproducibility issues frequently highlighted in past years (Begley and Ellis, 2012; Begley and Ioannidis, 2015; Button et al., 2013).

While knowledge may be extracted both from structured or unstructured text in scientific articles and from data, it is often difficult to keep track and reconcile all of it. Ideally, all of the existing knowledge should be modeled and used together in a way that enables tracing the origin of the data and support for the conclusions. The context in which the results have been obtained should be captured alongside the findings. It is particularly relevant in cases when findings in the literature may appear contradictory. While the insufficient quality of the experiment, i.e., a lack of reproducibility, may explain such discrepancies, it is also possible that a specific mechanism varies depending on the temporal, spatial, or pathological context. Therefore, infrastructure and guidelines that facilitate aggregating well-annotated data and information are needed to enable scientists to harness the power of the data generated globally. Indeed, new and better data sharing and interoperability practices must be put forward and embraced by all stakeholders to realize the full potential of big data in a shared analytical effort by the scientific community (Dinov, 2016; Sansone et al., 2012).

Provided the relevant tools are in place, one can consider how to obtain relevant information to understand our environment and its influence on physiology and pathology. While clinical data is invaluable to reach those objectives, it is often advantageous to first use more accessible and controllable in vitro and in vivo systems to gather preliminary evidence. It is essential before drawing definite conclusions to determine the extent to which one can translate specific mechanisms relevant for human health or the ecosystem from the knowledge gained in model systems.

This session will include the following:

- From literature to computable knowledge: BEL and BioDati, William Hayes, BioDati, USA
- Zebrafish: a model organism to model adverse outcome pathways, Anze Zupanic, EAWAG, Switzerland
- GladiaTOX: developed by industry and packaged for the scientific community to analyze high content screening data, Vincenzo Belcastro, PMI
- Methods benchmarking in metagenomics – CAMI & sbv IMPROVER challenges, Alice McHardy, Helmholtz Centre for Infection Research, Germany
- INTERVALS – a platform for data transparency, a mine of data, Stéphanie Boué, PMI
- Towards creating an engine of scientific discovery, Samik Ghosh, SBX Corporation, Tokyo, Japan
- Panel discussion– transparency, crowdsourcing…stronger together

CAID: THE CRITICAL ASSESSMENT OF INTRINSIC PROTEIN DISORDER

Intrinsically disordered proteins and protein regions (IDPs/IDRs), characterized by high conformational variability, cover almost a third of the residues in Eukaryotic proteomes (Perdigão et al., 2015; Mistry et al., 2013). As major players in protein homeostasis (Iakoucheva et al., 2004) and cellular signaling (Iakoucheva et al., 2002), IDPs are involved in numerous diseases. Over the last two decades, IDPs have developed from being bespoke projects of biophysicists interested in protein (non-)folding to being recognized as a major determinant in cellular regulation (Guharoy et al., 2015; Chouard, 2011). One of the key problems with IDPs was the lack of a clear definition of the phenomenon (Dunker et al., 2001; Uversky, 2002; Wright and Dyson, 1999) as different authors have used it to mean somewhat different things (Orosz and Ovádi, 2011). This reflects on automatic detection methods for intrinsic disorder. A recent evaluation of these prediction methods on new DisProt examples showed there is a significant room for improvement. A large fraction of IDRs still goes virtually undetected and many predictors appear to confound ID and regions outside X-ray structures (Necci et al., 2017).

IDR prediction has been a challenge in CASP but only for few editions due to the difficulty in generating a blind benchmark. With CAID we aim at assessing prediction methods for intrinsic disorder leveraging the manual curation of IDP from DisProt (Piovesan et al., 2017).

CAID (Critical Assessment of Intrinsic Disorder) is a community wide experiment to determine and advance the state of the art in the detection of intrinsically disordered residues forms the amino acid sequence. Participants are invited to submit new software, which is executed locally by the assessors and evaluated mainly on new experimental disorder evidence from the DisProt database. Each round of DisProt annotation produces a new dataset of IDPs, which are used to assess prediction methods' performance in a so-called blind test.

The first edition of CAID started with the submission of prediction methods during September 2018 and produced preliminary results presented at CASP 13. Final results will be presented at ISMB/ECCB during this special session.

SCALABLE PLANT-RESEARCH IN CLOUD ENVIRONMENTS

Plant research needs to cope with the major challenges of population growth and climate change adaptation. Sequencing of the DNA and RNA of crop and forest plants, as well as their pathogens and pests, has generated enormous quantities of data. High-throughput "omics" technologies are widely used and increasingly important to support plant biology research and breeding of diverse plant species for production of food, feed, fibre and other biomaterials, and bio-energy. Much of this data is found in well-established repositories and data resources. However, large-scale automated phenotyping is now possible under controlled and field conditions, and there is classical phenotyping data available in literature and in dispersed databases. This data is heterogeneous, described in diverse ways, and difficult to find and re-use.

Significant advances in plant science can be obtained by integrating available genomic and genotyping data with diverse types of phenotyping data, including field and greenhouse experimental data, molecular, -omics and image data. Although most -omics data, and especially phenomic data, are being generated at an increasing scale from public and private research organizations, the dispersion of datasets and metadata among multiple repositories and their often poor description and annotation, make their use and exploitation still challenging or even unapproachable.

To help unlock the full potential of a multi-omics approach to plant science, it is essential to make plant data interoperable in accordance with the FAIR principles (i.e. Findable, Accessible, Interoperable and Reusable). Several standards have been built for the annotation of data sets.

This session will give participants an introduction to what is needed to use and create cloud-enabled bioinformatics pipelines. Speakers from several projects that are already using cloud computing to solve plant related research questions will be featured. Based on their hands-on experience, speakers will showcase usage of cloud computing in their projects, including bottlenecks and learned best practices. We will introduce participants to usage of established as well as emerging data repositories and standards. The focus will be on accessing and using these resources for FAIR data management strategies and integrative analysis leveraging the power and scalability of cloud computing.

At the end of the session participants will be able to leverage cloud computing and data resources for their research questions according to best practices, using established production platforms.

COMPUTATIONAL ONCOLOGY – HETEROGENEITY AND IMMUNE DEFENCE

Cancer is one of the main causes of morbidity and mortality worldwide. Although chemotherapeutic drugs and new targeted treatments have resulted in improved quality of life and prolonged survival for many patients, most tumors and especially metastases still have a severe impact on human health.

Cancer constitutes a group of diseases characterized by abnormal cell growth, stage-wise progression, genomic and cellular heterogeneity, and potential to develop resistance to therapies. All these aspects are consequences of the evolutionary nature of cancer and, consequently, the study of somatic evolution in cancer constitutes a tremendously promising approach to precision oncology, carrying a huge potential medical impact. This is accentuated by the frequent failure of current biomarker and treatment concepts to achieve durable drug response and long-term survival for cancer patients. Simultaneously, the immune system, in particular, antigen-specific T- cells, constitutes an essential component of a tumor's environment and is an important determinant of the selective pressure acting on it during its evolution. Computational methods play an increasingly important role to address these challenges and have given rise to the field of computational oncology.

This special session will cover two interrelated and clinically important problems in computational oncology, namely, the assessment and interpretation of intra-tumor molecular heterogeneity and the role of immune responses in cancer treatment. Until recently, the dominant method for studying a tumor's heterogeneity consisted of first obtaining bulk DNA-seq data and then deconvoluting this signal in order to identify a few dominant subpopulations, using computational methods. Today, the heterogeneity is preferably studied based on single-cell data. There are a growing number of methods for analyzing cancer transcriptional and genomic heterogeneity, including reconstruction of tumor phylogenies, from scRNA-seq and scDNA-seq data, respectively, from the ISMB community and beyond.

Moreover, studies of the immune system and cancer-immune interactions have become increasingly interesting, since the field of tumor immunotherapy has proven to be an enormous success in the past decade with multiple therapeutic interventions leading to functional cures in several disparate types of cancer.

OMICS DATA FORMATS, COMPRESSION AND STORAGE: PRESENT AND FUTURE

In 2003 the first human genome assembly was completed. It was the end of a project that took almost 13 years to complete and cost 3 billion dollars (around $1 per base pair). This milestone ushered in the genomics era, giving rise to personalized or precision medicine. Fortunately, sequencing cost has drastically decreased in recent years. While in 2004 the cost of sequencing a whole human genome was around $20 million, in 2008 it dropped to a million, and in 2017 to a mere $1000. As a result of this decrease in sequencing cost, as well as advancements in sequencing technology, massive amounts of genomic data are being generated. At the current rate of growth (sequencing data is doubling approximately every seven months), more than an exabyte of sequencing data per year will be produced, approaching the zettabytes by 2025 [1]. As an example, the sequencing data generated by the 1000 Genomes Project (www.1000genoms.org) in the first 6 months exceeded the sequence data accumulated during 21 years in the NCBI GenBank database [2].

The generation of other types of omics data are also experiencing rapid growth. This situation calls for state-of-the-art, efficiently-compressed representations of massive biological datasets, that can not only alleviate the storage requirements but also facilitate the exchange and dissemination of these data. This undertaking is of paramount importance, as the storage and acquisition of the data are becoming the major bottleneck, as evidenced by the recent flourishing of cloud-based solutions enabling processing the data directly on the cloud. For example, companies such as DNAnexus, GenoSpace, Genome Cloud, and Google Genomics, to name a few, offer solutions to perform genome analysis in the cloud.

This special session will cover current efforts in this area, as well as future challenges. This is of importance to biologists and researchers alike that work with omics data, as the developed tools will soon become part of their standard pipelines.

ISMB/ECCB 2019 Special Sessions Preview, cont

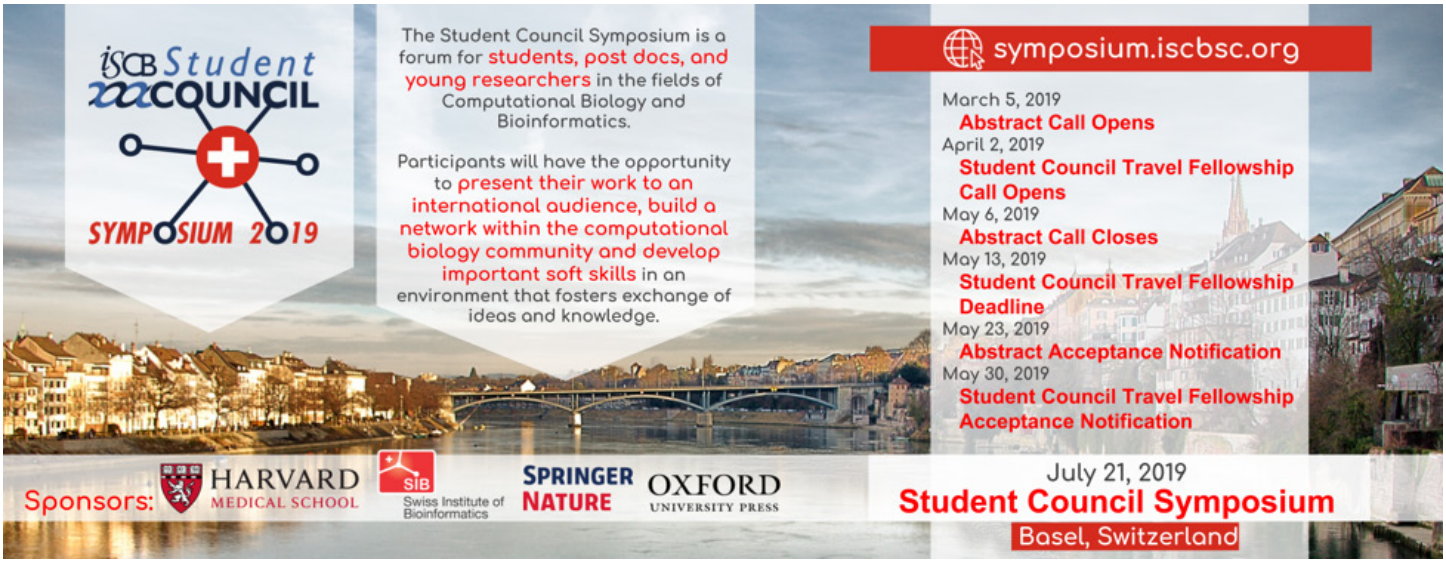
TEXT MINING FOR BIOLOGY AND HEALTHCARE

Text mining methods for biology and healthcare have matured significantly in recent years. The quality of text mining systems has improved considerably not only in terms of accuracy, but also in interoperability, scalability, and a lower barrier of entry for non-specialists. Much of current research in text mining is published as open source software, making state-of-the-art tools (e.g. PubTator) widely available. Moreover, the use of text mining methods to support other research in the biological and medical sciences has been increasing. Numerous databases use text mining — either to speed up curation (e.g. UniProt) or for directly integrating evidence (e.g. STRING) — and literature databases (e.g. PubMed) have a long history of using text mining techniques to improve search capabilities.

The previous BioLINK special interest group (SIG) successfully organized meetings at ISMB and collaborations with other SIGs for many years. Since the time that the BioLINK SIG was discontinued, however, biomedical text mining has advanced significantly. The use of textual genres outside of published literature has greatly expanded, including patents, drug labels, social media and, most notably, clinical records. At the same time, a number of new computational technologies have emerged that have led to improved accuracy, increased scalability and expanded the number of applications and use cases (e.g. accelerating drug discovery). Interest in text mining at ISMB has continued: ISMB has consistently published text mining research, even without a specific community of special interest (COSI).

Given the lack of a specific community of special interest (COSI), we propose a special session to be held at ISMB 2019 on Text Mining for Biology and Healthcare, to meet the increasing need/interests of computational biologists in such areas, and to bring 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 goal of the session is therefore 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), and biomedical text mining specialists who develop new methodologies to advance the state of the art. We therefore propose focusing on text mining use cases (concrete problems with scientific importance) in addition to methodology development.

ISCB Student Council Symposium 2019!



The ISCB Student Council is delighted to announce the 15th edition of the ISCB Student Council Symposium (SCS), which will be held on the 21st July 2019, in Basel, Switzerland, directly preceding the ECCB/ISMB 2019. The SCS 2019 is organized by young scientists coming from all disciplines in the field and different countries around the globe. The main aim of this symposium is to give the opportunity to students and young scientists to present their work to an international audience from a variety of subfields of bioinformatics and computational biology, fostering the exchange of ideas and knowledge, and helping to build the networks within the community. Abstract submission is now open until 6th May 2019 for those wanting to participate by giving oral or poster presentations. Travel Fellowships will also be available and all candidates with submitted abstracts are encouraged to apply.

More details are available at http://symposium.iscbsc.org. We would like to say thanks to our confirmed sponsors in this edition: Harvard Medical School, Swiss Institute of Bioinformatics, Springer Nature and Oxford Academic for their generous support to our Symposium!

You can help us spread the word by letting your colleagues know about the SCS 2019, referring to our website and using the hashtag #SCS19 on social media.

We look forward to welcome you in Basel this summer!

ISMB/ECCB 2019 Community of Special Interest (COSI) Tracks

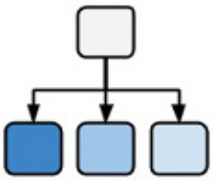
The organized community sessions (COSI tracks) includes area specific keynote presentations, a selection of talks, which are featured in OUP Bioinformatics in the ISMB/ECCB 2019 Proceedings supplement, as well as highlight and late-breaking research talks. The 2019 COSI Tracks feature the following communities of special interest:

3DSIG: STRUCTURAL BIOINFORMATICS AND COMPUTATIONAL BIOPHYSICS

It is impossible to fully understand biological systems without understanding the 3D structure of their constituting parts and their interactions. 3Dsig focuses on structural bioinformatics and computational biophysics and has become the largest meeting in this growing field.

Keynote speaker:
Torsten Schwede, Biozentrum, University of Basel & SIB Swiss Institute of Bioinformatics, Switzerland

BIO-ONTOLOGIES



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

BIOVIS: BIOLOGICAL DATA VISUALIZATION

The BioVis track showcases new and ongoing research in computational biology and computer science that highlight or address problems in biological data visualisation. Submissions for talks closes 11th April.

BOSC: BIOINFORMATICS OPEN SOURCE CONFERENCE

Since 2000, BOSC has provided a forum for developers and users to interact and share research results and ideas in open source bioinformatics and open science. BOSC's broad spectrum of topics includes practical techniques for solving bioinformatics problems; software development practices; standards and ontologies; approaches that promote open science and reproducibility; and ways to grow open source communities.

CAMDA: CRITICAL ASSESSMENT OF MASSIVE DATA ANALYSIS

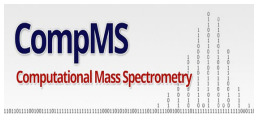
CAMDA puts a spotlight on the successful analysis and integration of the massive data sets now prevalent in the life sciences. This year, the CAMDA scientific committee offers three analysis contests:

Metagenomic Forensics Challenge
Hi-Res Cancer Data Integration Challenge
CMap Drug Safety Challenge

Leading scientists present their best methods and analyses. Extended papers are then published in the open access, fully indexed conference proceedings at Biology Direct.

EXTENDED ABSTRACT DEADLINE:
MAY 12

COMPMS: COMPUTATIONAL MASS SPECTROMETRY



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.

EDUCATION: COMPUTATIONAL BIOLOGY EDUCATION

Education-COSI focuses on bioinformatics and computational biology education and training across the life sciences with a goal to foster a mutually supportive, collaborative community in which bio scientists can share bioinformatics education and training resources and experiences, and facilitate the development of education programs, courses, curricula, etc., and teaching tools and methods.

EVOLUTION AND COMPARATIVE GENOMICS

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 SIG: GENE AND PROTEIN FUNCTION ANNOTATION

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. The Function COSI features the Critical Assessment of Function Annotation, an ongoing community challenge aimed at improving methods for protein function prediction.

Keynote speaker: Lucy Colwell, Google AI Research and Cambridge University, UK

HITSEQ: HIGH-THROUGHPUT SEQUENCING

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.

JUNIOR PRINCIPAL INVESTIGATOR (JPI)

Transitioning from a post-doc to a junior PI can be a challenging process requiring careful planning. Once running a group, junior PIs are faced with many new tasks, some of which are learnt on the job. The Junior Principal Investigators group (JPI) aims to provide support during this process via a community of peers.

MICROBIOME

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.

MLCSB: MACHINE LEARNING IN COMPUTATIONAL AND SYSTEMS BIOLOGY

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.

NETBIO: NETWORK BIOLOGY

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.

Invited Speakers:
Christian von Mering, University of Zurich, Switzerland
Laura I. Furlong, Research Programme on Biomedical Informatics (GRIB), Hospital del Mar Medical Research Institute (IMIM), Department of Experimental and Health Sciences (DCEXS), Pompeu Fabra University (UPF), Spain

RNA: COMPUTATIONAL RNA BIOLOGY – INTEGRATIVE RNA BIOLOGY

RNA 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 in both normal and disease conditions.

Invited Speakers:
Mihaela Zavolan, University of Basel, The Center for Molecular Life Science
Ana Claudia Marques, Department of Computational Biology, Université de Lausanne
Prof. Uwe Ohler, Max-Delbrück-Centrum für Molekulare Medizin (MDC) in Berlin

REGSYS: REGULATORY AND SYSTEMS GENOMICS

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.

Confirmed invited speakers (with more to come) include:

Eileen Furlong, EMBL
Stein Aerts, KU Leuven & VIB
Robin Andersson, University of Copenhagen
Bart Deplancke, EPFL & SIBd
Barbara Treutlein, Max Planck Institute for Evolutionary Anthropology,
Julia Zetlinger, Stowers Institute, Missouri

SYSMOD: COMPUTATIONAL MODELING OF BIOLOGICAL SYSTEMS

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.

Invited Speakers:
Edda Klipp, Humboldt-Universität zu Berlin, Germany (https://rumo.biologie.hu-berlin.de/tbp/index.php/en/)
Douglas Lauffenburger, Massachusetts Institute of Technology, USA (http://web.mit.edu/dal-lab/)
Jörg Stelling, ETH Zürich, Switzerland (http://www.csb.ethz.ch)

TRANSMED: TRANSLATIONAL MEDICAL INFORMATICS

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.

VARI: VARIANT INTERPRETATION

The VarI-COSI track discusses recent advances in methodology for the annotation and analysis of genetic variants. Discussion span applications in genomics, population genetics, phylogenetics and human disease including cancer.

ISMB/ECCB 2019 Career Fair

Job seeking or talent searching, ISMB/ECCB 2019 will once again host a career fair event at the conference. Scheduled over the lunch period on the last day, those we are searching for talented student, postdoc, and professionals may host a table to talk to those seeking new career opportunities. Last year, eighteen organizations participated in event where, they had the opportunity to speak to and promote their job openings to nearly 300 students, postdocs, and professionals.

The career fair is free to any registered delegate who is seeking new opportunities and tables, including access to the CV/resume repository, can be reserved for those searching for new talent for a nominal fee. Outside of the organized fair, recruiters also have the opportunity to post jobs on the jobs board located in the exhibit hall or online via the virtual jobs board.

Plan to join us for this exciting way to connect!

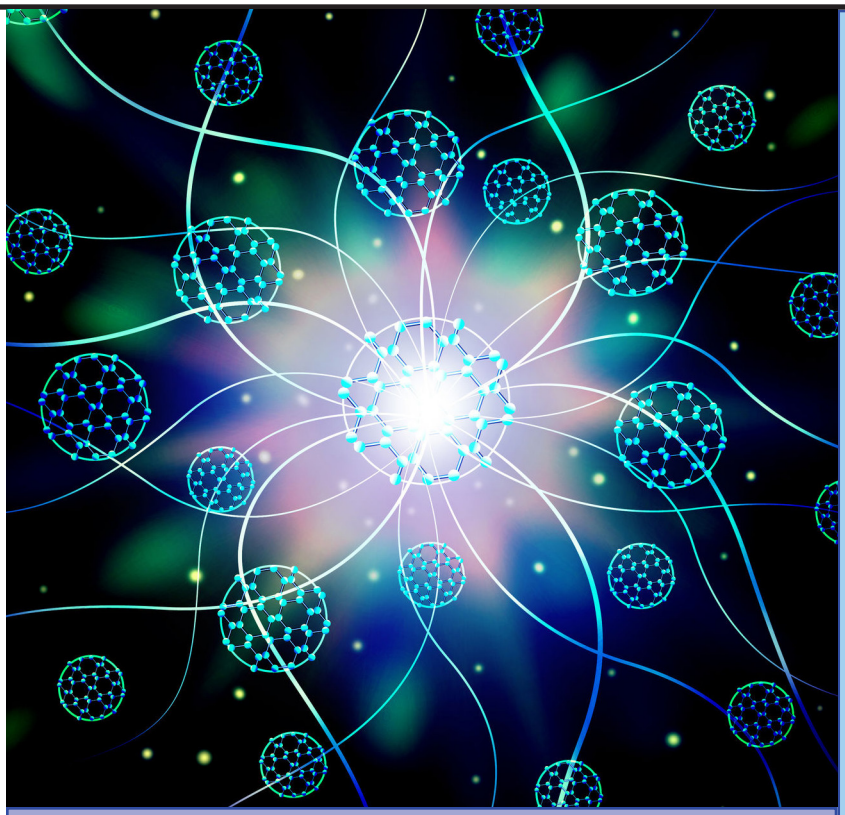
ISMB/ECCB 2019 Special Tracks

ELIIXR- GA4GH STRATEGIC PARTNERSHIP WORKSHOP

Securely accessing personal genomic data at a population scale, and across national borders, is an enormous challenge that will require significant investments in national and international infrastructure. The scope and complexity of this infrastructure is beyond the capacity — and jurisdiction — of any single organisation; international collaboration is needed to provide recognised, secure, standardised, documented, and interoperable services. Building on the current Collaboration Agreement between ELIXIR and GA4GH, the ELIXIR::GA4GH Strategic Partnership will coordinate the generation and implementation of the GA4GH suite of interoperable standards and policy frameworks to overcome the technical and regulatory hurdles to genomic data sharing with a focus on Europe. In this session we will describe this Strategic Partnership in both high-level and intricate detail, including presentations from some of the constituent projects.

BIG DATA TO KNOWLEDGE TRACK

Big Data to Knowledge (BD2K) is a trans-NIH initiative established to enable biomedical research as a digital research enterprise, to facilitate discovery and support new knowledge, and to maximize community engagement. The BD2KCCC aims to sustain the impact of BD2K achievement within the global biomedical community and the public domain through innovative solutions in resource indexing and knowledge management



Ucoming Affiliate Conferences

7TH ANNUAL LA CONFERENCE ON COMPUTATIONAL BIOLOGY & BIOINFORMATICS

Apr 05, 2019 through Apr 06, 2019
ISCB Member Discount: 99 percent
Event URL: ***https://lbrn.lsu.edu/conference-on-biology-and-bioinformatics.html***

DREAM CHALLENGES@RECOMB

May 04, 2019 through May 04, 2019
Event URL: ***https://dream.recomb2019.org***

BIOINFORMATICS EDUCATION SUMMIT

May 14, 2019 through May 17, 2019
Event url: ***https://www.h3abionet.org/categories/training/bioinformatics-education-summit***