ISCB

ANNUAL REPORT

2020

INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY

MESSAGE FROM THE CHIEF EXECUTIVE OFFICER

2020 saw the changing of the world as we knew it. COVID19 disrupted not only our lives but also how we navigate the world around us. The world paused and then we continued on. We came together and faced the situation head on. We faced not only personal challenges but also societal challenges across the board. Together we took each one in stride, adapting to our new environments, technologies, and creating solutions. Though we saw a dip in membership numbers, we also saw our largest flagship conference, ISMB, reach the widest swath of attendees from across the globe. The 100% virtual interface offered a greater international reach to audiences who never were able to attend an ISMB conference, and the thoughtful World Bank economic pricing, coupled with more than $15,000 USD in funding made it affordable for any member to attend. Practices that will be continued in the future.

2020 also saw the creation of committee driven groups. ISCB in partnership with All Things Small and Green and Trees for Life, launched ISCB groves to offset carbon emissions caused by ISCB activities such as those emitted during the conferences, workshop or panel meetings that it organizes. Looking internals as well to the social realization of systemic discrimination with the focus of the continuation and goal of creating a safe, inclusive, and equal society for all our members, the ISCB Board of Directors approved ISCB’s first Equity, Diversity, and Inclusion Strategic Plan as proposed by ISCB Equity, Diversity, and Inclusion Committee.

As a Society, we strive to enhance scientific networking and research dissemination opportunities for its membership.

One way we did this was through the creation of the COVID-19 Section, a collection of COVID-19 related materials for education and training purposes, allowing the ISCB scientists to respond to the respective challenges by offering its expertise to the scientific community. ISCB also launched the new ISCBacademy webinar series which hosted over 20 webinars throughout the year on a plethora of topics. All of which were archived as part of ISCBtv allowing open access to the entire community to view the content

Though 2020 was a year for the books delivering countless challenges, both professional and personal, it was also a year that forced profound growth for ISCB. We grew as an organization because of our dedicated members. This statement is more true today than ever. We continue to grow, supporing one another as we work towards our goal to be the leading professional society for participants in the field of computational biology and bioinformatics, serving researchers, practitioners, technicians, students, and suppliers worldwide. Thank you for sticking with us and we hope you have taken advantage of the many resources provided from the virtual format of conferences to the webinars to the ISCB COVID-19 Section. Your continued faith in us has enabled our numerous successes this year.

We advance as an organization because of our dedicated members. It is a pleasure for our societal staff to work daily for these amazing volunteers. As you continue to read this annual report, know that the lifeblood of our organization sincerely is its members who work tirelessly to advance our science.

Consider continuing the journey with us by volunteering, renewing your membership, and helping to grow our community by inviting a friend. I look forward to meeting many of you at the upcoming ISCB conferences. I also welcome your feedback and suggestions anytime. Please feel free to reach out to me at executive.office@iscb.org.
Sincerely,

Diane E. Kovats, CAE, CMP, DES
Chief Executive Officer

ISCB FACES 2020

The International Society for Computational Biology (ISCB)

is the leading bioinformatics society worldwide. ISCB brings together a global community of scientists from computer science, molecular biology, mathematics, statistics and related fields.

CONNECTING

TRAINING

EMPOWERING

WORLDWIDE

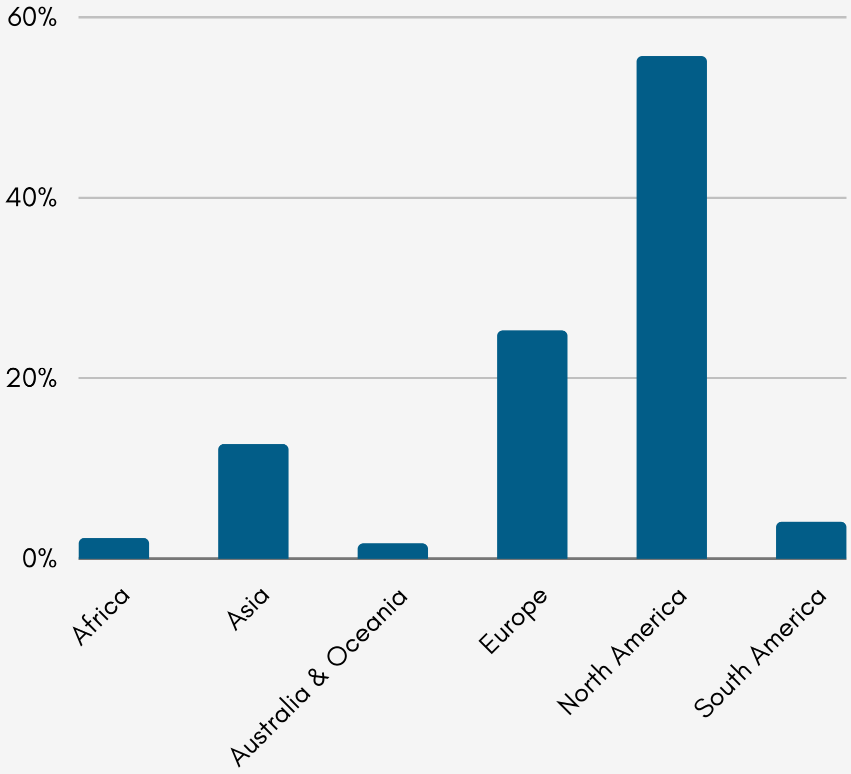
ISCB thrives on the dedication of its volunteer members. Their passion and commitment to the ISCB mission is evident each year as the Society continues to grow and offer more programs and benefits to its members. We hope you enjoy reading through the highlights and some of the major achievments of the Society throughout 2020.

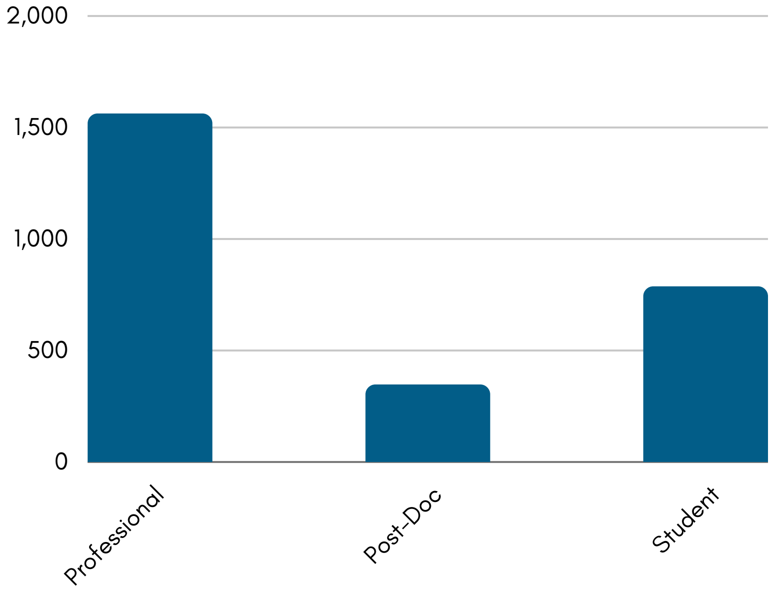
THE STATE OF ISCB

Members are the lifeblood of ISCB, recruiting and maintaining active members is essential to the vitality of this Society. At the close of 2020, ISCB stood at 2,687members,a decrease from the year prior.

MEMBERSHIP BY REGION

Members hailed from 78 countries. The two largest representations come from North America at 47%, primarily from the United States, and Europe at 33%. The truly global nature of the discipline and the Society is reflected in the number of members coming from countries in Africa, Asia, Australia and Oceania, and South America. ISCB's worldwide presence is also shown by its support of 20 affiliate societies from around the world.





MEMBERSHIP BY TYPE

ISCB supports members of the computational biology community at all stages of their career and offers three types of membership: professional, postdoctoral, and student/trainee. More than half of the Society's members are professional scientists from academic, government, or industry settings. Trainees are also represented well in the ISCB membership, with post-doc and student members representing 40% of the membership.

The Board of Directors of the International Society for Computational Biology (ISCB) is pleased to announce the results of the recent elections.
The ISCB members elected Alex Bateman as Vice President and Michelle Brazas as Seecretary. Their terms began in January 2021. Congratulations to them all.

ISCB 2020 LEADERSHIP ELECTION RESULTS

ALEX BATEMAN
Vice President

Alex Bateman has been elected to the officer position of Vice President. As an officer, Alex will also serve as a member of the Board of Directors. He will serve a three-year term. Christine is the first woman to serve in the Presidential role of ISCB. Alex is the Head of Protein Sequence Resources at EMBL-EBI. Dr Alex Bateman joined EMBL-EBI as the Head of Protein Sequence Resources in 2012. He took over from Rolf Apweiler as the PI for the UniProt grant (an international collaboration between EBI, SIB and PIR) and has oversight for protein and ncRNA related databases at EMBL-EBI. Prior to that he managed the production of numerous popular biological databases such as Pfam and Rfam at the Sanger Institute. Alex has been a member of the Board of Directors since 2013 and has served on various committees.

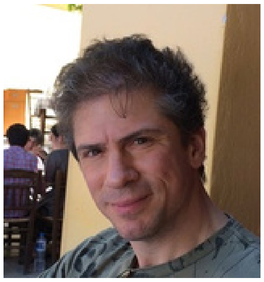
MICHELLE BRAZAS
Secretary

Michelle Brazas has been elected to the officer position of Secretary, where she will also serve as a member of the Board of Directors. She will serve a three-year term. Michelle is the Senior Program Manager for Adaptive Oncology at the Ontario Institute for Cancer Research (OICR), a program encompassing a wide variety of projects from imaging, informatics, genomics and diagnostic development. She is also the Project Manager for the Cancer Genome Collaboratory project (cancercollaboratory.org), an academic compute cloud environment for analysis across the ICGC dataset. Previously, she was the Lead for Bioinformatics.ca, a national bioinformatics continuing education program and a faculty member in Biotechnology at BCIT. She founded and runs the Toronto Bioinformatics User Group (TorBUG). Michelle is also on the Executive Board of the Global Organization for Bioinformatics Learning, Education & Training (GOBLET) and has led the tutorials and workshop development for ISMB since 2018.

ISCB CLASS OF 2020 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. 2020 marks the 11th 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.

In 2020, we were pleased to receive many excellent nominations, and the Fellows Selection Committee members carefully considered each one. Ultimately, four nominees were elected as this year's newest Fellows:

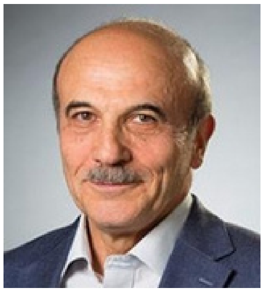


SERAFIM BATZOGLOU

Stanford University, DNAnexus, Illumina, Insitro, for foundational and innovative contributions to computational genomics in both academia and industry, through his visionary research, mentoring of young leaders and his own leadership and service to the community.

JUDITH BLAKE

The Jackson Laboratory, for her many contributions to bioinformatics over her distinguished career, most notably the Gene Ontology and the Mouse Genome Databases. These two resources are fundamental pieces of scientific infrastructure serving as foundational tools on which so much of genome-scale science is built.



MARK BORODOVSKY

Georgia Tech University, for his influential research in developing algorithms of genome analysis as well as recognized leadership in education and community development.

RITA CASADIO

University of Bologna, as one of the pioneers of machine learning based approaches for predicting protein structures, protein function and the impact of genetic variation. The methods from her group have been highly ranked in international competitions assessing prediction of protein structure (CASP), function (CAFA) and variant impact (CAGI).

PAUL FLICEK

EMBL-EBI, as a leading figure in the field of genomics and for his tireless efforts advocating for open data and equal opportunities for women in science, including the Earth BioGenome Project in which he advocates workable data sharing practices.

OSAMU GOTOH

Osamu Gotoh, Kyoto University, a pioneer in computational biology and an exemplary professional researcher, specifically for his contribution to sequence alignment through the development of what is now known as the Smith-Waterman-Gotoh algorithm.

RAFAEL IRIZARRY

Dana-Farber Cancer Institute / Harvard T.S. Chan School of Public Health, for his pioneering work in expression analysis and development of statistical methods for expression analysis which are some of the most impactful in the entire field. He is one of the leaders of the open-source Bioconductor project since its beginning.

LAXMI PARIDA

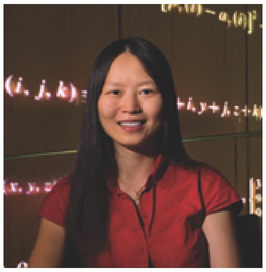
Laxmi Parida, IBM, for her breakthrough contributions to algorithms across diverse applications with impact to human health and society through IBM and clients. She was instrumental in the design of the core engine and accuracy of Watson for Genomics offering in precision oncology.

KATHERINE POLLARD

Gladstone Institutes, University of California, a world leader in developing statistical models and opensource bioinformatics software for biological big data, with an emphasis on genomics. She has uncovered biomedical knowledge that would be missed without her rigorous computational approaches.

BEN RAPHAEL

Princeton University, as a widely acknowledged leader in the area of computational and mathematical aspects of cancer genomics, with special emphasis on inferring tumor phylogenies.



ZHIPING WENG

University of Massachusetts Medical School, for her seminal contributions to computational biology and bioinformatics, specifically in structural biology (widely-used ZDOCK suite of protein-protein docking algorithms), regulatory genomics (pipelines for analyzing genomic and epigenomic data from ENCODE and PsychENCODE Consortia) and small-RNA biology (piRNAs).

XUEGONG ZHANG

Tsinghua University, for the development of computational methods for analyzing transcriptomic and RNA-seq data including the methods DEGseq, DEsingle, SCRL, scFly, and establishing an influential graduate program, educating a generation of students, and promoting the field of computational biology and bioinformatics in China.

Congratulations, 2020 Class of ISCB Fellows!

ISCB CONGRATULATES ITS SENIOR MEMBERS

In an effort to find ways to further highlight the achievements of our members and reward members for their support and dedication to ISCB, in 2014, ISCB introduced the ISCB Senior Member designation. A successful candidate for Senior ISCB Member designation must have demonstrated sustained contributions to the field of computational biology or to ISCB. Thank you to our Senior Members for the continued contributions to the science and Society.

Peter Karp
SRI International

David Rocke
University of California, Davis

Hershel Safer
Consultant

Robert F. F Murphy
Carnegie Mellon University

Satoru Miyano
The University of Tokyo

Torsten Schwede
SIB Swiss Institute of Bioinformatics &
University of Basel

Ivet Bahar
University of Pittsburgh, School of Medicine

James Foster
University of Idaho

Russ B Altman
Stanford University

Victor Jongeneel
Retired

Andy Baxevanis
National Institutes of Health

Alexander Hartemink
Duke University

David Eisenberg
UCLA-DOE Institute for Genomics and Proteomics

Gunnar von Heijne
Stockholm University

Iddo Friedberg
Iowa State University

Martin Vingron
Max-Planck-Institute for Molecular Genetics

Rolf Apweiler
EMBL-EBI

John Kececioglu
The University of Arizona

Cathy Wu
University of Delaware

Brent Richter
Partners HealthCare/Harvard Medical School

Thomas Lengauer
Max Planck Institute for Informatics

Eugene Myers
Max Planck Institute of Molecular Cell Biology and Genetics

Søren Brunak
Novo Nordisk Foundation Center for Protein Research

Alfonso Valencia
Barcelona Supercomputing Center -
Centro Nacional de Supercomputacion (BSC)

Michael Waterman
University of Southern California

Chris Rawlings
Rothamsted Research

Raffaele A Calogero
University of Torino

Dominic A Clark
Cambridge Alliance Management Ltd

Martin Reese
Omicia Inc.

Donna K Slonim
Tufts University

Ewan Birney
EBI

Gary Stormo
Washington University Medical School

Lawrence Hunter
University of Colorado

Pavel Pevzner
University of California at San Diego

Minoru Kanehisa
Kyoto University

Nir Friedman
Hebrew University

Michael Ashburner
University of Cambridge

Wyeth Wasserman
University of British Columbia

Olga Troyanskaya
Princeton University

Bruno Gaeta
University of New South Wales

Pierre Baldi
University of California, Irvine

Ron Shamir
Tel Aviv University

Janusz Bujnicki
Intl. Institute of Molecular and Cell Biology (IIMCB)

Julio Collado-Vides
National University of Mexico

Michael J Wise
University of Western Australia

Judith Anne Blake
The Jackson Laboratory

Sarah Teichmann
Wellcome Sanger Institute

William Noble
University of Washington

Li-San Wang
University of Pennsylvania

Anna Tramontano
University of Rome

David Haussler
Howard Hughes Medical Institute/
UC Santa Cruz Genomics Institute

Steven Brenner
University of California, Berkeley

Andrew Su
The Scripps Research Institute

Liping Wei
Peking University

Dong Xu
University of Missouri-Columbia

Olga Vitek
Northeastern University

Ramana V Davuluri
Northwestern University

Scott Markel
Dassault Systèmes BIOVIA

Reinhard Schneider
LCSB

Chris Sander
Harvard Medical School and
Dana-Farber Cancer Institute

David Sankoff
University of Ottawa

Haim Wolfson
Tel Aviv University

Janet Kelso
MPI for Evolutionary Anthropology

Fran Lewitter
Whitehead Institute for Biomedical Research

Bonnie Berger
MIT

Ralf A Bundschuh
The Ohio State University

Richard Durbin
University of Cambridhe

Burkhard Rost
TUM Munich/Columbia Univ NYC

Jill P Mesirov
UC San Diego

Russell Schwartz
Carnegie Mellon University

Anil G Jegga
Cincinnati Childrens Hospital

Predrag Radivojac
Northeastern University

Lukasz Kurgan
Virginia Commonwealth University

Jake Chen
University of Alabama at Birmingham

Weichuan Yu
The Hong Kong University of Science and
Technology

Alex Bateman
EMBL- EBI

Aviv Regev
Broad Institute

Hagit Shatkay
University of Delaware

Janet M Thornton
EMBL-EBI

Yana Bromberg
Rutgers University

Dmitry Korkin Worcester
Polytechnic Institute

Max Alekseyev
George Washington University

Lonnie Welch
Ohio University

Desmond G Higgins
Conway Institute

Carl Kingsford
Carnegie Mellon University

Temple F. Smith
Boston University

Stephen Ramsey
Oregon State University

Philip Bourne
University of Virginia

Louxin Zhang
National University of Singapore

Ana Maria Rojas
CSIC-CABD

Christine Orengo
University College London

Webb Miller
Pennsylvania State University

Ernest Fraenkel
MIT

Ivan Erill
UMBC

Paul C Boutros
University of California, Los Angeles

David Posada
Universidad de Vigo

T. M. Murali
Virginia Tech

Francisco De La Vega
Fabric Genomics

Steven Salzberg
Johns Hopkins University

Dan Gusfield
UC DAVIS

Vicky Schneider
EMBL Australia Bioinformatics Resource

Shoshana Wodak
Vlaamse Inst. of Biotechnology,
Flemish Free Unversity of Brussels

Michael Levitt
Stanford School of Medicine

Mark Gerstein
Yale University

Amos Bairoch
Swiss Institute of Bioinformatics

Andrej Sali
University of California San Francisco

Ruth Nussinov
National Cancer Institute

Anatoly Sorokin
Institute of Cell Biophysics RAS

Robert Gentleman
23andMe

Pankaj Agarwal
GlaxoSmithKline

David Lipman
Impossible Foods

Criteria for the Elevation to a Senior member Status:

An ISCB professional member can self-nominate via an online form for elevation to senior member status or be nominated by any of the eligible endorsers. After the ISCB staff verifies that a candidate meets the first criteria, all endorsers are given an opportunity to endorse the candidate. Each eligible candidate securing three or more endorsements (excluding self) will be elevated to the status of senior member. As the endorsers are not required to participate in voting, senior member candidates are encouraged to contact a small number of eligible endorsers to secure their support through personal interaction.

Maintaining and Re-establishing the Senior Member Status:

The senior ISCB member must remain in good standing to retain his or her status. If good standing is not maintained, the senior member status becomes invalid. Senior member status is automatically re-established when the member returns to good standing. However, if a senior member has more than a one-year lapse in membership and returns to good standing, he/she will not receive the 10% registration discount to ISCB official conferences unless he/she remains in good standing for two-consecutive years.

Benefits to Senior Member Status:

- Recognition on the ISCB website featuring our Senior Members
- Special recognition ribbons at ISCB official conferences
- Opportunity to be selected for keynote speaking positions & important steering committees
- Annual 10% registration discount off the early member rate for a select ISCB official conference of choice
- Special ISCB Senior Member logo for website and CV

ISCB ADOPTS NEW POLICIES & INTRODUCES INITIATIVES

INTRODUCTION OF GREEN ISCB: ISCB GROVES

ISCB, in partnership with All Things Small and Green and Trees for Life, set up its first grove of native trees, the ISCB 2020 grove, to offset carbon emissions caused by ISCB activities such as those emitted during the conferences, workshop or panel meetings that it organizes. With this grove, ISCB members are also offered a simple and convenient way to offset their own carbon emissions such as those incurred during traveling to ISCB conferences or workshops.

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

ISCB EQUITY, DIVERSITY, AND INCLUSION

Equity and Inclusion in ISCB

The International Society for Computational Biology (ISCB) is acutely aware that global science is facing substantial challenges regarding equity and inclusion. Current science is still dominated by males and by what is shortly called "the West". In our Society, we are vigorously working to bring this skew into balance. We are actively pursuing balance in our governing bodies, most relevantly in our Board of Directors and slate of Officers. Furthermore, we have implemented processes towards achieving more balance in our suite of award winners, Fellows, and invited conference keynotes. We are guiding our affiliated conferences on the importance of diversity balance within their own programs. We also encourage our members to support these endeavors by providing nominations of excellent scientists from all corners of science and of the world to all of ISCB's programs.

At the same time, we are aware that improving equity and inclusion is a process that requires long-term dedication. Progress indicated by corresponding statistics will only be observed gradually. Moreover, while the criterion of balance is an important one it is not the only one in science.

We continually revisit our procedures for progress towards equity and inclusion and assess their efficacy. We do not think that automated procedures of assessment are appropriate for this purpose. Algorithms performing such categorization suffer from inherent limitations that distort the notion of balance we are striving for. Specifically, categorization of disjoint regional, ethnic or gender groups of scientists, while easing classification, also functions divisively.

ISCB is committed to creating a safe, inclusive, and equal society for all our members. These values are enshrined in the Society's code of conduct, values, and ethics. We acknowledge, respect, and promote the value of a diverse community as core to our international organization and culture.

ISCB continues to seek to create a diverse and inclusive environment where all can come together, meet, exchange ideas, and work toward goals in an atmosphere of safety, respect and civility. The ISCB Board of Directors approved ISCB's first Equity, Diversity, and Inclusion Strategic Plan as proposed by ISCB Equity, Diversity, and Inclusion Committee.

Diversity_Strategic_Plan_Approved2020.7.pdf
Click here to visit the page.

ISCBACADEMY WEBINAR SERIES

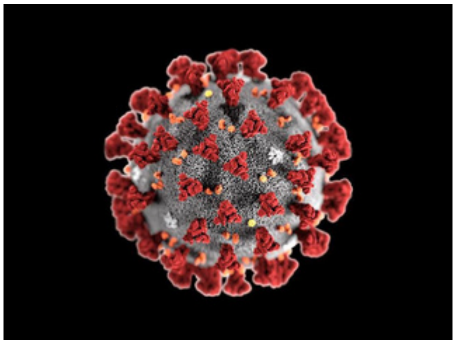
2020 saw the creation and growth of the ISCBacademy webinar series. In conjunction with the communities of special interest (COSIs), 23 select presentations were given via a live-streamed talk about specific research.

Access to the webinar series is complimentary for all.

INTRODUCTION OF THE ISCB COVID-19 SECTION

In response to the unprecedented impact of the COVID-19 pandemi, ISCB introduced the COVID-19 section.

The COVID-19 pandemic is both severely affecting our lives and impacting our science. ISCB responds to the respective challenges by offering its expertise to the scientific community and empowering scientific networking. The ISCB COVID-19 Section offers four lines of this initiative:



ISCB COVID-19 Statements. Here you find statements on the ongoing pandemic that have been issued by ISCB.

ISCB COVID-19 Webinar collection. Here you find webinars specific to the topics of COVID-19 and Sars Cov-2 that are organized by ISCB.

ISCB COVID-19 Science collection. Here you find materials specific to the topics of COVID-19 and Sars Cov-2 that have been submitted by ISCB members. This collection has three subsections for (i) scientific articles, (ii) scientific data sets and, (iii) proposals of community science projects.

ISCB Tutorial collection. Here you find tutorials that present basic or advanced computational biology content for biologists and computational biologists in these times of increased digital education activity. The tutorials have been (i) presented at recent ISCB conferences and (ii) suggested by ISCB members.

CALL FOR SUBMISSIONS

If you are a member of ISCB we encourage you to submit entries to the Science collection and Tutorial collection. Your submission entails a pointer to the science content, a short description of background or purpose (two lines) and lists your name as submitter. Submission will be subjected to a basic check of scope and purpose.

CONTINUED GROWTH OF COSIS & ISCB CONNECT

ISCBconnect continues to maintainin an active ISCB Communities of Special Interest (COSI) online community group. COSIs are member communities of shared interest that have self-organized and have multiple activities or interactions throughout the year, rather than solely meeting during the COSI Track of the ISMB/ECCB conference. An important goal of any COSI is to foster a topically-focused collaborative community wherein scientists communicate with one another on research problems and/or opportunities in specific areas of computational biology.

Such communication is often in the form of meetings, but can also be through other social media tools that allow for vibrant participation in a virtual environment. This virtual communication has been given a greater voice through the creation and implemention of the ISCBconnect, which allows each COSI to easily communicate, engage, share and connect in an easy to use online forum. Each COSI has a customized homepage through which topical discussions are created, events are marketing,and information is easily disementiated.

Consider joining one of these dynamic groups today:

3D-SIG: Structural Bioinformatics and Computational Biophysics

3Dsig focuses on structural bioinformatics and computational biophysics and has become the largest meeting in this growing field.

BIOINFO-CORE

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

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

BioVis: Biological Data Visualizations

Data visualization cuts across all areas of computational biology. On the one hand, sophisticated data visualization techniques are required to allow the biologist to explore their large/complex datasets and gain insight from them. On the other hand, this approach can lower the black-box nature of complex (bioinformatics) algorithms. The goal of BioVis is to bring together researchers from the visualization, bioinformatics, and biology communities with the purpose of educating, inspiring, and engaging bioinformatics and biology researchers in state-of-the-art visualization research, as well as visualization researchers in problems in biological data visualization.

BOSC: Bioinformatics Open Source Conference

Since its inception in 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 sharing of data, reproducible results and software; and ways to grow open source communities while promoting diversity within them. BOSC is run by the Open Bioinformatics Foundation (OBF).

CAMDA: Critical Assessment of Massive Data Analysis

CAMDA presents a crowd sourcing and open-ended data analysis challenge format which focuses on big heterogeneous data sets that are increasingly produced in several fields of the life sciences.

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. The CompMS initiative aims to exploit synergies between different application domains, in particular proteomics and metabolomics.

Education: Computational Biology and Bioinformatics Education and Training

The ISCB EDUCATION COSI focuses on bioinformatics and computational biology education and training across the life sciences. A major goal of this COSI is to foster a mutually supportive, collaborative community in which bioscientists can share bioinformatics education and training resources and experiences, and facilitate the development of education programs, courses, curricula, etc., and teaching tools and methods.

EvolCompGen: Evolution & 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. At the same time, evolutionary and comparative genomics are inherently “transversal” disciplines in that work in many other biological areas of research have some evolutionary component (e.g. cancer genomics, epidemiology, toxicology, population genetics, functional genomics, structural biology just to name a few). The scope of this COSI is intentionally kept broad. The track will feature a mix of proceedings, highlight, and invited talks. Priority will be given to contributions which are relevant to more than a single area of application, or to contributions which are not covered by more specialised COSIs.

Function: Gene and Protein Function Annotation

The accurate annotation of protein function is key to understanding life at the molecular level. The Function SIG COSI brings together computational biologists, experimental biologists and biocurators who are dealing with gene and gene product function prediction, to share ideas and create collaborations. The Function-SIG holds annual meetings and conducts the multi-year Critical Assessment of protein Function Annotation, or CAFA, experiment.

HiTSeq: High Throughput Sequencing Algorithms & Applications

HiTSeq is devoted to the latest advances in computational techniques for the analysis of high-throughput sequencing data including novel algorithms, analysis methods and applications in biology where high-throughput sequencing data has been transformative. It provides a forum for in depth presentations of novel algorithms, analysis methods, and applications in multiple areas of biology that HTS is transforming.

IRB: Integrative RNA Biology

The Integrative RNA Biology (IRB) group organizes the RNA SIG session at ISMB. The group aims to bring together experts in computational and experimental aspects of research in RNA Biology to cover new developments across this broad field of research. The RNA SIG session at ISMB focuses on two major areas: (1) the development of computational and high-throughput experimental methods, and (2) the application of such methods to break new grounds in the study of RNA biology and disease. We aim to educate and inspire researchers in the field, novice and seasoned alike, by meshing together different aspects of Computational RNA Biology, and promoting cross-disciplinary collaborative research.

JPI: Junior Principal Investigators

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.

MLCSB: Machine Learning in Computational and Systems Biology

MLCSB is a community for researchers interested in the interface of data sciences and life sciences, in particular the method development and application challenges that arise for Machine Learning in Computational and Systems Biology.

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. It therefore guides users in the selection and application of methods and in their proper interpretation. Furthermore, the COSI provides a platform for exchange and networking between method developers, and provides valuable information allowing them to identify promising directions for their future work.

NetBio: Network Biology

As more research fields turn to network visualization and analysis for perspective, our Network Biology Community serves to introduce novel methods and tools, identify best practices and highlight the latest research in the growing and interconnected field of network biology.

RegSys: Regulatory and Systems Genomics

The Regulatory and Systems Genomics Community of Special Interest focuses on computational methods that are important in the study of regulation of genes and systems. The RegSys COSI organizes the following activities: (1) ISMB Regulatory Genomics SIG Meeting, (2) RECOMB/ISCB Conference on Regulatory and Systems Genomics and DREAM Challenges, and (3) Top Ten Papers in Regulatory and Systems Genomics.

SysMod: Computational Modeling of Biological Systems

The SysMod Community of Special Interests aims at bridging the gap between bioinformatics and systems biology modeling. Recently, aspects of the two fields have converged. Systems modeling has become more reliant on bioinformatic network inference to build models and has begun to use transcriptomics and proteomics data to train models. In addition, more communication between systems modellers and bioinformaticians is needed to build models of whole cells, organs and organisms. Furthermore, the promises of precision medicine lie, in part, on the interplay between bioinformatics-based analysis of patient data and model-based predictions of treatments.

TransMed: Translational Medicine Informatics & Applications

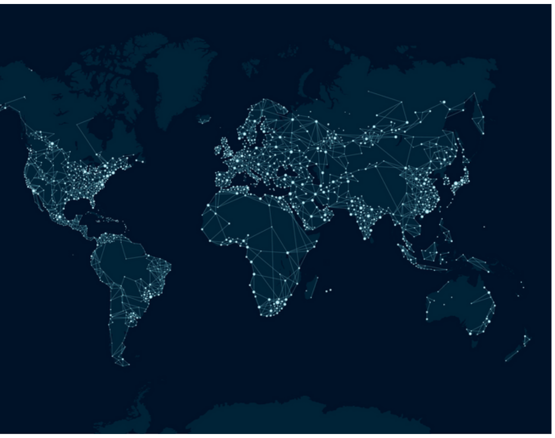
Knowledge-based translational medicine is a rapidly growing discipline in biomedical research and aims to expedite the discovery of new diagnostic tools and treatments by using a multi-disciplinary, highly collaborative, "bench-to-bedside" approach. It involves the integration of multiple high dimensional datasets that capture the molecular profiles of patients, as well as detailed clinical information. Within public health, translational medicine is focused on ensuring that proven strategies for disease treatment and prevention are actually implemented within the community, and on progressing towards data-educated personalised therapy. To genuinely realise the promise of Big Data in healthcare, we must consistently collate the data, annotate it with consistent and useful ontologies, apply sophisticated statistical analysis and translate these findings to the clinic. As a community, we will explore the current status of computational biology approaches within the field of clinical and translational medicine. In this COSI we will bring scientists from both academia and industry to exchange knowledge and foster networking, to help in building up of the translational medicine community.

VarI: Variant Interpretation

The Variant Interpretation Community of Special Interest (VarI-COSI) is a community of scientists interested in “breaking” the genomic code. The main goal of our COSI is to promote the formation of a collaborative network of scientists interested in the understanding of the meaning of genomic variation as applied to a range of questions, including population studies, functional and evolutionary impacts, and disease.

ISCBconnect is an interactive community platform, which allows you to have continuous dialogue within the ISCB COSIs. To join a community, click on the ISCBconnect icon.

FOSTERING RELATIONSHIPS THROUGH AFFILIATED GROUPS



The Affiliates Committee continues to foster interactions between the Society and its affiliated regional and institutional groups. ISCB now has 19 active affiliated groups with more in the application and evaluation process. Once confirmed their information will be listed on the website and conferences included on our conference calendar and added to our affiliate marketing schedule.

ISCB continues to strengthen its ties with affiliated groups by providing an annual review of the website content posted on ISCB to ensure organization information is accurate. Additionally, ISCB offers a bulk membership option for affiliated groups. This bulk membership drive allows these regional and institutional groups to establish a group membership for their individual organization and ISCB and simplifies the registration process with ISCB.The Affiliates Committee also introduced a reorganization of the affiliated group structure to remove entry barriers during the application process. The new structure features different tiered levels of affiliation and removed the two-year waiting period to for application.

WHY SHOULD MY ORGANIZATION BECOME AN ISCB AFFILIATE?

One voting seat in the Affiliates Committee for recommendations to the ISCB Affiliates Task Force or Board of Directors on affiliate matters

Authorization to use a special “ISCB Affiliate” logo on affiliate’s website and promotional materials

Potential pool of ISCB member volunteers, editorial assistance for papers / reports / web page content

Listing of the affiliate’s meeting(s) within the Affiliated Conferences section of the ISCB website

Possibility of ISCB professional help in organization of the meeting
This might include registration fee collection (not always possible and may involve impediments involving country/currency/tax limitations), marketing, use of abstract submission system, conference planning consulting, sponsorship, fellowship, etc.

Listing on the Affiliates page of ISCB website, including link to Affiliated Group’s site

One page of content on the ISCB web site managed by the affiliate (optional)





2020 ISCB AWARD WINNERS

The International Society of Computational Biology (ISCB) announced the winners of the 2020 Accomplishments by a Senior Scientist Award, Overton Prize, Innovator Award, and Outstanding Contributions to ISCB Award. “The ISCB awards program highlights scientists in our field who are beacons at the junior, mid-term and senior career stage and scientists who have shown extraordinary commitment to our Society and the field at large,” said ISCB President, Thomas Lengauer. “Our awards committee under the leadership of Ron Shamir has thoughtfully and in an established process selected this year's awardees and has come up with a very impressive slate. I congratulate all award winners for their achievements and the awards committee for doing a fabulous job.”

Congrtulations to all the 2020 ISCB Awardees and Competition Winners!

Steven L. Salzberg, PhD

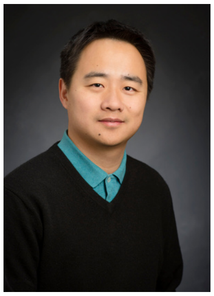
Bloomberg Distinguished Professor, Professor of Biomedical Engineering, Computer Science, and Biostatistics, Director, Center for Computational Biology, McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine

Recipient of ISCB Accomplishments by a Senior Scientist Award

Jian Peng, PhD

Assistant Professor, Department of Computer Science, College of Medicine (by courtesy), Institute of Genomic Biology (affiliate) Cancer Center at Illinois (affiliate), National Center of Supercomputing and Applications (affiliate), University of Illinois at Urbana-Champaign

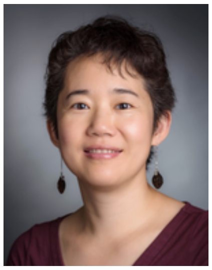
Recipient of the ISCB Overton Prize



Xiaole Shirley Liu, PhD

Professor, Biostatistics, Harvard T.H. Chan School of Public Health; Co-director, Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute

Recipient of ISCB Innovator Award



Judith Blake, PhD

Professor, The Jackson Laboratory

Recipient of the ISCB Outstanding Contributions Award

2020 ISCB WIKIPEDIA COMPETITION WINNERS

ISCB held its ninth international competition to improve the coverage on Wikipedia of any aspect of computational biology. A key component of the ISCB's mission to further the scientific understanding of living systems through computation is to communicate this knowledge to the public at large. Wikipedia has become animportant way tocommunicate all types of science to the public and Wikidata plays an increasingly growing role in that. ISCB aims to further its mission by increasing the quality of Wikipedia and Wikidata coverage of Computational biology, and by improving accessibility to this information via Wikipedia and its sister sites. The competition is open to students and trainees at any level either as individuals or as groups.

Each winner was awarded a one year complimentary ISCB membership and a monetary award announced at the first ever virtual ISCB Town Hall at ISMB 2020.

1st PLACE

Diego Mariano

For ‘structural bioinformatics’ in both English and portugese

2nd PLACE

tiago Lubiana

For ‘obo foundry’ and ‘list of obo foundry ontologies’

3rd PLACE

Darko Durovski

For ‘transcriptomics’

The competition aims to improve the coverage on Wikipedia of any aspect of computational biology.

2020 ISCB SOFTWARE PRIZE

The ISCB Student Software Prize was created to recognize the development of excellent bioinformatics software by students and postdocs that are members of the International Society for Computational Biology.

PROSPECTIVE FUTURE IMPACT AWARD WINNER

Robert Ietswaart

Genewalk

1ST PLACE

FloRian Schmidt

TEPIC

ISCB ART IN SCIENCE WINNERS

Finding the beauty of science through art!

The winning image was announced during the virtual ISCB Town Hall and presented with a $200 USD prize, as well as being the feature cover image for the ISCB 2020 Fall Newsletter.

To showcase your art, submit to the Art in Science competition: https://www.iscb.org/iscb-art-in-science-competition

FALL 2020 | ISSUE 3

FALL NEWSLETTER

Cover Image:

2020 Art in Science winner,
Dr. Zdenko Herceg,
Art of Epigenetics

Contents:

That's a Wrap on Virtual ISMB 2020
virtualHackathon@ISMB2020
Mark Your Calendars
Congratulations to the ISMB 2020 Awardees
COSI Highlights
Student Award Season is Open
ISCBs Initiative Corner
ISCB ANNUAL AWARDS - Call for Nominations
Fellows Nominations
Upcoming Events of Interest

HTTPS://WWW.ISCB.ORG

ISCB ART IN SCIENCE 1ST PLACE

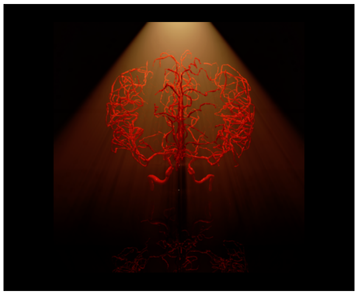
Art of Epigenetics
TDR. HERCEG, ZDENKO

ISCB ART IN SCIENCE 2ND PLACE

impact
JOSHUA BUGBEE

ISCB ART IN SCIENCE 3RD PLACE

Brain Vasculature
MARWAN ABDELLAH



SOCIETY CONFERENCES & COSI REPORTS

ISMB 2020

Nearly 2400 participants gatherd virtually July 13- 16 for ISMB 2020 virtual, ISCB's first ever ful-scale virtual conference. COVID- 19 disrupted not only our lives but also how we navigate the world around us. ISCB faced the situationhead on and instead of canceling or postponing ISMB 2020, the conference was moved to a 100% virtuallandscape offering a greater international reach to audiences who never were able to attend before the ISMBconference. Though we missed Montreal, the opportunities a virtual ISMB 2020 offered were numerous. Those whohave attended in the past found what they have grown to expect through live sessions, poster “halls”, visits to thevirtual ISCB Booth and so much more from the comfort of their homes.

The movement of the ISMB 2020 conference to a virtual landscape required an extreme restructuring of the conference. It was essential that all of the robust scientific content that the conference was known for was retained and delivered tothe community to the best of our technical capabilities. In addition, the conference steering committee wanted to ensurerelevance and goals to provide cutting-edgecontent by introducing a new track showcasing research on SARS-Cov-2 / COVID-19.

Virtual ISMB 2020 brought together the perfect recipe of cutting-edge science, knowledge building, tutorials, community based and onlinenetworking opportunities, and so much more for the perfect computational biology enriched online experience.

At the heart of the conference scientific program were the ISCB's Communities of Special Interest (COSIs), enabling intensified community involvement and bolstering its reputation as a conference with a strong scientific and technical program, which showcases thebest international developments in the field. This year ISMB showcased 22 COSIs participating with major computational biology themesensuring a greater connection to researchers sharing common interests and an ability to come together and listen to exciting newdevelopments in those areas of research. Each COSI ran their sessions (COSI tracks or workshops) as part of the conference. All attendeeshad the opportunity to attend any of these sessions in an either Live or via an on- demand format ensuring all time zones had equalaccess.

Throughout the four-day conference, attendees had the opportunity to hear and interact live with speakers delivering 5 renowned keynotespeakers, 3 of which were ISCB Award Winners.

The conference opening keynote was Elaine Mardis who gave an engaging and enthusiastic keynote address on Computational Analysis inPediatric Cancer Precision Medicine.

The first award winning keynote was the ISCB innovator Award awarded to Xiaole Shirley Liu, PhD, Professor, Biostatistics, Harvard T.H.Chan School of Public Health. Her dynamic presentation focused on Computational modeling of tumor immunity. ISCB Overton Award was given to the third keynote of the conference, Jian Peng, PhD, University of Illinois at Urbana-Champaign. His engaging presentation focused on Machine learning for structural and functional genomics. Distinguished Keynote Laxmi Parida, IBM, who gave an engaging presentation on Combinatorics, Statistics andTopology enabling Genomics was the final mornings keynote.

The final keynote of the conference, ISCB Accomplishments by a Senior Scientist Award Keynote, Steven L. Salzberg, Johns HopkinsUniversity. His energetic and fascinating talk focused on Bioinformatics and genomics: a virtuous cycle driven by technology.

In addition to phenomenal keynote presentations, the virtual conference offered over 400 talks in the Community of SpecialInterest (COSI) tracks, Special Sessions, Technology Tracks, as well as a plethora of Workshops including Workshop on BioinformaticsEducation (WEB), a Lunch and Learn showcasing The Black Women in Computational Biology Network. Finally, all attendees had accessto the 700 posters in the virtual Poster Hall, where authors were able to engage with live question and answer chat sessions.

As is the goal every year, ISMB brought together scientists from computer science, molecular biology, mathematics, statistics and relatedfields, and provided an intense multidisciplinary forum for disseminating the latest developments in bioinformatics/computational biology ina virtual environment. The virtual platform of the conference fostered fresh dialogues, collaboration, and learning opportunities.

We of course want to extend our appreciation to our conference sponsors and exhibitors for their ongoing support during these tryingtimes. This year's virtual exhibition section was a key feature for attendees to learn more about publishing opportunities, services, tools, and job openings. ISMB 2020 showcased the strength and resilience of its community. Thank you to all its members and attendees for their support andhelp in making ISMB 2020 such a success!

We look forward to seeing you online in Juy for an even more robust ISMB/ECCB 2021!

ISB-LA SOIBIO BIONETMX 2020 CONFERENCE

Attracting 137 attendees from 26 countries worldwide, ISCB-Latin America SolBio BioNetMX Symposium on Bioinformatics 2020, organized by the Bioinformatics Network Mexico (BioNetMX) together with the Iberoamerican Society of Bioinformatics (SolBio) and the International Society for Computational Biology (ISCB) aimed to promote scientific and professional exchange in bioinformatics across Latin America.

Over the course of the meeting, delegates had the opportunity to participate in tutorials, hear from 6 renown keynote speakers, get the latest updates in research sessions, and explore 30+ posters.

RECOMB/ISCB CONFERENCE ON REGULATORY AND SYSTEMS GENOMICS, WITH DREAM CHALLENGES 2020

Now in its thirteenth year, the RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges, is one of the premier annual meetings in the fields of regulatory genomics, systems biology, and network visualization. This multidisciplinary conference brings together both computational and experimental researchers from across the world to discuss recent discoveries about genomic and molecular regulatory networks as well as innovative, integrative methods for developing a systems-level understanding of biological activity.

The conference was virtually. The conference represented 242 total attendees representing 24 total countries worldwide. Over the course of the meeting, delegates had the opportunity to participate in tutorials, hear from 8 renown keynote speakers, 86 Posters, and 42 total oral presentations.

COSI REPORTS FROM 2020...

3D-SIG: Structural Bioinformatics and Computational Biophysics
COSI representative to committee: Rafael Najmanovich
Pull text from ISMB recap ---COSIsubmission reportt is lacking

Bio-Ontologies
COSI representative to committee: Michel Dumontier
Bio-Ontologies (#bioontologies; http://www.bio-ontologies.org.uk/) is an ISMB Community of Special Interest (COSI) that covers the latest and most innovative research in the application of ontologies and the organisation, presentation and dissemination of knowledge in biomedicine and the life sciences. Bio-Ontologies celebrated its 23rd year at ISMB 2020, held virtually on July 13-16, 2020. Bio-Ontologies provides a vibrant environment for reporting novel methods and sharing experiences on the construction and application of ontologies in health care and the life sciences. The COSI run track offers a constructive environment to nurture discussion of innovative and scientifically sound work that range from preliminary to completed, from both young and experienced investigators alike. Bio-Ontologies participants also benefit from a strongly interdisciplinary setting, where ISMB attendees intermingle with members from American Medical Informatics Association (AMIA), the W3C's Healthcare and Life Sciences Community Group (HCLSCG), and the National COVID Cohort Collaborative (N3C) thereby increasing impact through new collaborations and broader dissemination.

Day 1 of the Bio-ontologies track included 2 keynotes: The first keynote was delivered by Dr. Michael Gruninger on "Bio-Ontologies Keynote: The crisis of content" where he shared his ideas for a novel approach for designing ontologies, which formalizes ontology semantics in order to guarantee shareability and reusability. In the second keynote, Dr. Karin Verspoor presented on "Bio-Ontologies Keynote: COVID-SEE: Enabling scientific evidence exploration through semantics in a time of crisis" where she discussed the development of COVID-SEE (Scientific Evidence Explorer), a novel NLP system designed to improving the processing and representation of COVID-19 related literature. Both talks drew sizable crowds and elicited lively discussions.

Bio-ontologies also featured many exciting talks on the application of ontologies and knowledge graphs in computational biology. The day featured 10 regular talks covering different uses of ontologies for COVID-19 (i.e. development of new ontologies, methods for modeling quantitative traits, and collection and analysis of animal hosts and diagnosis), FAIR (i.e. ensuring reproducible data analysis and metadata standards for sharing knowledge graph embeddings), text mining (i.e. ontology-based information extraction and fact-tracking), data analysis (ontology-wide association studies to enrich traditional GWAS analyses), knowledge representation (for human pluripotent stem cell lines, and for physician suicide claims as nanopublications), and the development of biomedical knowledge graph construction software.

Day 2 (half day) of the Bio-ontologies track featured 5 talks primarily focused on the development of novel ontology-based tools designed to detect Gene Ontology misannotations, improve the ontology development process, model biological phenomena, and enrich models of human disease. The session closed with a call to participate in the 2021 proceedings and in further development of the COSI's planned activities.

Bio-Ontologies cont'd...

This year's talks had a clear new trend topic: "COVID-19/infectious diseases" due to the challenge posed by the COVID-19 pandemic, which is consistent with the massive amount of research effort the scientific community is devoting to meet this urgent societal need and highlights the importance of ontologies in biomedical research. The kind of papers presented covered a wide range of biomedical areas, from clinical to omics, and applications, from NLP to FAIR enabler. Best talk was awarded to Runar Reve for his work on Applying GWAS on UK Biobank by using enhanced phenotype information based on Ontology-Wide Association Study and best poster was awarded to Toshiyuki T. Yokoyama and Simon Heumos for their work on Semantic Variation Graphs: Ontologies for Pangenome Graphs.

BIOINFO-CORE

COSI representative to committee: Brent Richter

The bioinfo-core COSI held a heavily attended session at ISMB exploring both present and perennial topics, including machine learning, single cell analysis, conda/bioconda for software management and reproducibility, project tracking tools, training, and nf-core (community nextflow pipelines). In small breakout groups, participants were able to meet colleagues from diverse cores, functions and background and discuss these topics in greater depth. Please see our wiki for more details, slides and notes. (http://bioinfo-core.org/)

Regarding diversity of our speakers, we had seven total speakers. Three of these were women, and we had a variety of ethnicies represented as well.

We held two social events at ISMB: the markthalle event organized by ISCB and a joint dinner with AEBC2. Both were well attended and lively events with a lot of informal discussion and networking.

Shortly after ISMB, we set up a bioinfo-core slack as an alternative form of communication to our email list.

Besides ISMB, in November of 2018 we had a zoom call with a nextflow demo presented by Alexander Pelzer. We are currently planning a zoom call for this November about single-cell analysis and trajectory analysis.

BioVis: Biological Data Visualizations

COSI representative to committee: Kay Nieselt

Highlights of the scientific/enabling themes from the meeting (i.e., the half page article for the Society pages, newsletter, and annual report):

The 10th edition of BioVis (http://biovis.net/2020/program_ismb/) attracted over 380 unique viewer participants and there were 335 registrants showing interest in BioVis. Along this year's theme of "Integrating visualization and machine learning and explainable AI for biological analysis", we had two great keynotes by Hendrik Stobelt (IBM Research & MIT) and Marinka Zitnik (Harvard Medical School). We started with Hendrik's talk on the importance of visualization for human-AI collaboration where he presented projects from the IBM Explainability Team. In the afternoon, Marinka gave an inspiring and very popular talk on Machine Learning for Drug Repurposing and presented an impressive range of projects that sparked several questions and a lively discussion. There were over 150 live participants during Marinka's talk.

The program featured a further 2 full papers presenting innovation in visualisation, 14 abstract talks and 17 poster presentations concerning the latest developments in visual analysis systems that tackle biological data, from phylogenetic trees to SNP data. The award for the best poster went to Kari Lavikka and colleagues for their work titled "Grammar-Based Interactive Genome Visualization". The "interactive" sessions following the talks were very popular and several participants carried out their discussions in the Zoom calls in-between the sessions. The social channel was particularly busy after Marinka's talk.

BOSC (Bioinformatics Open Source Conference) / OBF (Open Bioinformatics Foundation)

COSI representative to committee: Peter Cock

Accomplishments of the OBF over the past year include Clarificattion of the process of becoming an OBF Affiliated Project (https://github.com/OBF/obf-docs/blob/master/Affiliated-Project-Policy.md)

The OBF Participated in Google Summer of Code 2020 (https://summerofcode.withgoogle.com/archive/2020/organizations/4595548239167488/. 8 students worked on open source bioinformatics-related projects, with 18 mentors and four organisation admins managing the program and work. (https://www.open-bio.org/2020/11/04/google-summer-of-code-2020-wrap-up/)

Notable. OBF Travel Fellowships included the. following:

In December 2019, Malvika Sharan took over as OBF Travel Fellowship chair, replacing previous chair Farah Khan (https://www.open-bio.org/2019/12/21/travel-fellowship-december-2019/)

OBF Expanded the Travel Fellowship program (now renamed the OBF Event Fellowships) to cover costs associated with participating in online events such as virtual conference fees, headsets, high speed internet, etc. (https://www.open-bio.org/event-awards/)

TheOBF Revised the Event Fellowship application calendar; applications are now reviewed twice a year (April and October). In the past year, 7 people were awarded funds to attend in-person or virtual events. 2 applicants received funding in the December 2019 round, 4 in the April 2020 round (https://www.open-bio.org/2020/05/08/obf-travel-fellow-2020-1/), and 1 in the October 2020 round.

We Developed an OBF-wide Code of Conduct that apply to in-person and virtual events organised and led by OBF, and can be adopted by member projects if they choose. The proposed Code of Conduct is still open for community comments at https://github.com/OBF/obf-docs/pull/78

BOSC accomplishments over the past year include the development of a comprehensive document covering the BOSC abstract review process: https://github.com/OBF/bosc_materials/blob/master/BOSC_review_process.md

Most years, BOSC has been part of ISMB, but in 2018, and again in 2020, BOSC partnered with the Galaxy Community Conference (GCC). This year (in July 2020), the BOSC + GCC conference was called the Bioinformatics Community Conference (BCC2020, bcc2020.github.io). More than 800 people from 61 countries registered for at least part of the online meeting, which was held mostly in the Remo.co video-conferencing platform. Keynote speakers were Abigail Cabunoc Mayes, Lincoln Stein, and Prashanth Suravajhala. The BOSC 2020 schedule can be found at https://www.open-bio.org/events/bosc/schedule/. A report about BOSC 2020 can be found on F1000: https://f1000research.com/articles/9-1160

CAMDA

COSI representative to committee: David P Kreil

The challenges for CAMDA 2020 were advertised early in the year and included:

The Hi-Res Cancer Data Integration Challenge presents clinical and matched molecular profiles, with read level data for individual genomes. Explore non-standard genomes and splicing events for better prognosis. Where download is not feasible, data can be made available on hard-disk by courier.

The CMap Drug Safety Challenge presents clinical toxicity results, cellular and molecular responses to hundreds of drugs. Compare and integrate a range of cell line assays to predict the severity of the drug induced liver injury in humans.

The Metagenomic Geolocation Challenge presents thousands of city microbiome profiles in context of climate data. Construct multi-source microbiome fingerprints and predict the ecological niche or exact geographical origin of mystery samples.

This year, CAMDA with ISMB for the first time ran as a virtual conference due to the recend pandemic. Virtual CAMDA 2020 took off to a full house, with the almost 200 delegates likely grateful that they didn't have to cram into a real room, while reducing their carbon footprint by 100 tons of carbon dioxide.

Opening the session, former NSF director Prof. Rita Colwell show-cased in her keynote on cholera the power of multi-level analyses ranging from microbial meta-genomics via public health to climate-scale

CAMDA, cont'd...

effects, which was followed by a variety of contributions by CAMDA delegates dissecting the interactions of urban microbial meta-genomics and ecological climate niches. Daena Farber's Aedin Culhane started the second day of CAMDA with a much-anticipated keynote on cancer single-cell -omics data-integration and factor analyses, giving a practical tour de force of current algorithmic alternatives, which was followed by contributions of CAMDA delegates on challenging cancer data sets and drug safety predictions. While the traditional real-world CAMDA dinner was sorely missed this time, as every year, the last session closed with a ceremony where promising young scientists accepted the treasured CAMDA Awards, which was nicely put into context by Joaquin Dopazo marking the CAMDA 2000-2020 anniversary with a perspective of how the 'Critical Assessment of Massive Data Analysis' pioneered the crowd-sourcing of science, showing the way with open ended questions in scientific data analysis competitions, which naturally segued into Wenzhong Xiao leading a discussion of current challenges in Big Data analyses for CAMDA 2021 and beyond.

CompMS: Computational Mass Spectrometry

COSI representative to committee: Wout Bittremieux

The CompMS COSI received 49 abstract submissions this year, up from 10 and 21 abstract submissions in 2018 and 2019, respectively. This prompted us to expand the CompMS program at ISMB to two days for the first time. The first day was focused on proteomics applications and included a mix of eight short (10 minutes) and nine long (20 minutes) presentations on various topics, including public data repositories, mass spectrometry imaging, spectral clustering, and spectrum identification and quantification. A very timely keynote was delivered by Dr. Anne-Claude Gingras on the SARS-CoV-2 virus-host interactome.

The second day was focused on metabolomics applications and was guest hosted by Dr. Shuzhao Li and Dr. Jeff Xia. It included five short talks and four long talks. Keynote presentations were delivered by Dr. David Wishart on computational tools to identify the dark metabolome and by Dr. Gary Siudzak on repository-scale metabolomics analysis. Getting more engagement from the metabolomics community has been a goal for the CompMS COSI, and we are delighted that we were able to devote an additional day to metabolomics topics for the first time.

Besides the oral representations, 27 abstracts were selected as poster presentations. Two of the poster presentations were awarded a best poster prize and two oral presentations were awarded a best presentation prize (one proteomics and one metabolomics poster/oral presentation each).

The CompMS session was well attended, with the number of participants on each of the two days hovering around 60 people. Break-out sessions in addition to the officially scheduled presentations were only sparsely attended, although some interesting discussions took place. Given the unprecedented number of abstract submissions, session attendees, and the expansion of the CompMS program from one to two days, despite the challenges posed by the SARS-CoV-2 pandemic, this year's CompMS COSI session was very successful.

Besides the CompMS COSI session at ISMB 2020, the May Institute on Computation and Statistics for Mass Spectrometry and Proteomics was sponsored by CompMS and attracted over 100 participants.

Education: Computational Biology and Bioinformatics Education and Training

COSI representative to committee: Russell Schwartz

The COSI works to bring bioinformatics education to the agenda of the ISCB community and to export it to education efforts in computational biology and life sciences internationally. It started with an agenda of specifically bringing together the ISCB Education community with the Global Organisation for Bioinformatics Learning, Education & Training (GOBLET), although it has since broadened its mission to be an interface between the ISCB education community and the international bioinformatics education community broadly defined..

Education Cont'd...

The largest single effort of the COSI each year is the ISCB educational program and associated activities, where the COSI seeks to create a community discussion on education within ISMB, bring in voices from outside ISCB to work with us, and highlight some of the most exciting work in the field each year. The COSI also works with the Workshop on Education in Bioinformatics (WEB) to offer an integrated ISMB program in recent year. As in previous years, this combined COSI program led to a vibrant program 1.5-day program of invited and submitted talks, posters, and workshop sessions. COSI members also contributed to organizing the tutorial program at ISMB.

The COSI also works to bring education topics to other meetings of the community. While 2020 has been a bad year for meetings and opportunities and our opportunities have been fewer, we have remained active in encouraging members to bring education topics to other meetings they attend. Examples include Schwartz ensuring that education would be covered as part of a panel discussion on the Future of Algorithms in Biology at RECOMB when he served as RECOMB PC Chair this year.The COSI has also been very active in a series of collaborative education initiatives organized around what has become an annual Bioinformatics Education Summit, held virtually this year. The summit, led by Nicky Mulder, has been organizing several prominent efforts in bioinformatics education now to define and improve standards for bioinformatics education, to produce papers and other resources and training materials for the community, and to work with the ISCB on initiatives such as the short course affiliation and degree program endorsement processes now being put in place. The COSI is one of several sponsoring groups of this summit and active in its organization and planning and running sessions, developing the materials it has produced, and working offline on continuing to refine that work and prepare it for dissemination.

EvolCompGen: Evolution & Comparative Genomics

COSI representative to committee: Nadia El Mabrouk

The Evolution and Comparative Genomics (EvolCompGen) COSI hosted a one day-session at ISMB 2020. The session featured a stimulating mix of proceedings and contributed talks on a wide variety of topics, befitting the central role of evolution in the biological sciences. The talks touched on timescales as short as those for viral epidemics and the progression of cancer to those as long as the complete history of life on Earth Computational topics included species tree estimation, phylogenetic tree comparison, modeling protein sequence evolution, and reconstructing genome rearrangements.

The COSI (and in particular Aida Ouangraoua) was instrumental in helping ISCB to set up its webinar series on evolution and comparative genomics topics in collaboration with the Society of Molecular Biology and Evoluion (SMBE). In the past year, our COSI hosted four talks. Importantly, the participation is free for any members of ISCB and SMBE.

Function: Gene and Protein Function Annotation

COSI representative to committee: Iddo Friedberg

The CAFA competition was published in Genome Biology, with 167 co-authors, most of which are COSI members. We had 3 kenote speakers, including a Nobel Prize laureate (Rich Roberts), and a woman from a US EpscoR state (Carolyn Lawrence-Dill, Iowa).

We were impressed by the growing level of interest in the CAFA challenge and the Function COSI. We have recently applied for continuing NSF funding based on the community growth, with 72 letters of support we solicited from the labs participating in the CAFA challenge and the Function COSI.

HiTSeq: High Throughput Sequencing Algorithms & Applications

COSI representative to committee: Francisco De La Vega
Mostly focused on organizing the ISMB session of HiTSeq. We explored the idea of having affiliated local meetings, but with COVID we have not been able to explore this much. Nevertheless, HiTSeq held an online regional meting in the Bay Area in conjunction with the Bay Area Bioinformatics Forum group, and Stanford University, on COVID Bioinformatics.
(https://www.meetup.com/BayBIFX/events/270179841/). This is adoption that we want to explore further.

IRNA: Integrative RNA Biology

COSI representative to committee: Yoseph Barash
The 2020 iRNA COSI track brought together world experts in diverse aspects of computational RNA biology from RNA structure, RNA-seq, RNA splicing and RNA processing to non-coding RNAs and RNA networks. The iRNA COSI aims also to promote interactions between computational and experimental RNA biologists and encourages participation from groups that are more experimental in nature. The 2020 RNA COSI track featured 18 talks (including 3 keynotes) highly computational in nature and 9 talks (including 1 keynote) with stronger experimental input.
This year we had an exciting line-up of 4 keynotes that covered transcriptomics (including a keynote presentation by Ana Conesa from the University of Florida), noncoding RNA biology, RNA metabolism (with a keynote from Athma Pai from the University of Massachusetts Medical School), RNA alignments and structure prediction (with a keynote presentation from Jérôme Waldispühl from McGill University) and RNA subcellular localization (with a keynote from Éric Lécuyer from the Montreal Clinical Research Institute). These keynotes invigorated very exciting sessions with talks from selected abstracts and proceedings in these and other topics, including tools and analyses of alternative splicing, RNA editing, RNA family classification, RNA-protein interactions, single cell and long-read sequencing analyses and methods for RNA secondary structure prediction.
Despite the difficulty in organizing such an event virtually, the iRNA COSI carried out a successful interactive poster session with presenters in breakout rooms and participants visiting rooms, leading to stimulating discussions with up to 6-7 people. In addition, while no in person conference dinner took place, we had a fun cocktail session at the end of our first day, complete with our traditional quiz, which participants enjoyed. Finally, a highlight of this year’s iRNA COSI was definitely our live and animated panel discussion on long read RNA-seq, which was well attended and led to very insightful exchanges on a subject of wide current interest.

JPI: Junior Principal Investigators

COSI representative to committee: Shaun Mahony
JPI's activities focus on peer mentoring and resource sharing for junior faculty in computational biology. We primarily carry out these activities on dedicated channels in the New PI Slack group. For example, we have 34 ISCB members in the New PI Slack #iscb_jpi channel. This year, we had additionally planned a "Birds-of-a-Feather" session at ISMB, which was to be focused on funding opportunities for junior faculty. Unfortunately, most of our speakers (program officers at various funding agencies) cancelled due to COVID-related disruptions. Instead, we ran several Zoom-based social activities at ISMB 2020. We hope to resume informational sessions at ISMB 2021.

Microbiome

COSI representative to committee: Prof. Alice McHardy

We organized and continue to organize the second round of CAMI benchmarking challenges, as well as organized a CAMI challenge evaluation workshop in Brunswick in March 2020.

MLCSB: Machine Learning in Computational and Systems Biology

COSI representative to committee: Magnus Rattray

We have hosted two ICSB webinars: April 22, 2020 - DNCON2: improved protein contact prediction using two-level deep convolutional neural networks by Jianlin Chen, University of Missouri; August 11, 2020 - Protein Function Prediction using Graph Convolutional Networks with Language Model Features by Vladimir Gligorijevic, Flatiron Institute.

NetBio: Network Biology

COSI representative to committee: Natasa Przulj

We had a large number of quality submissions at our NetBio COSI at ISMB 2020, much larger than usual. Hence, we held it for a day and a half for the first time, while previously it was one day only. We are vary happy about the expansion of the community and believe that we need to obtain a 2-day slot for the next year's NetBio COSI at ISMB 2021.

SysMod: Computational Modeling of Biological Systems

COSI representative to committee: Tomáš Helikar

The SysMod community is still transitioning to become an umbrella organization that integrates more specialized bio-modeling communities. This transition has included co-advertising activities with related communities such as the CoLoMoTo Consortium meetings for logical modeling and the online seminars of the Center for Reproducible Biomedical Modeling. Further communities of relevance include the COVID-19 Disease Map consortium, the COBRA community, and the COMBINE consortium. A new article about SysMod has been submitted to Bioinformatics at the COSI's fifth anniversary (see the preprint at doi: 10.5281/zenodo.4245269). This article aims to promote interaction among these communities and help the communities recruit researchers to participate in their activities.

The primary activity of SysMod for the past year was the annual meeting at the ISMB conference. Because of the COVID-19 pandemic, the fifth annual SysMod was held as a virtual meeting. The new format also caused some changes in the structure. This year, SysMod took place over two days. The fewer number of submissions can be explained by potential insecurity given the pandemic situation. Some potential authors might not have submitted their work. However, the number of attendance was comparably high as in previous years. The meeting featured three keynote talks, twelve contributed talks, and 14 posters. Throughout the virtual SysMod meeting, Ph.D. students and postdocs lively discussed efforts to integrate further -omics data aiming to improve mechanistic understanding of biological processes. Over the past year, SysMod has also continued to maintain a community discussion list (e.g., the announcement of impactful new research, meetings, job opportunities, etc.) and a community calendar (e.g., conferences, workshops, schools).

RegSys

COSI representative to committee: Lonnie R Welch

We had a large number of quality submissions at our NetBio COSI at ISMB 2020, much larger than usual. Hence, we held it for a day and a half for the first time, while previously it was one day only. We are vary happy about the expansion of the community and believe that we need to obtain a 2-day slot for the next year's NetBio COSI at ISMB 2021.

Text Mining for Healthcare and Biology

COSI representative to committee: Robert Leaman

ISMB 2020 text mining track was well attended: 90-110 during keynotes, 50-90 during talks. Presented a tutorial at ISMB 2020: A practical introduction to biomedical text mining in the era of deep learning. This tutorial covered introductions to biomedical text mining and deep learning, applying deep learning methods to text using word embeddings and state-of-the-art transformer models, common challenges in biomedical text mining, and constructing standard datasets to support further methods improvement.The COSI track was centered on applications of text mining. Recurring themes included supporting biocuration, literature indexing and search and pathway construction; other topics included genotype/phenotype associations, using social media and identifying cell types from single cell RNA sequence data.

TransMed: Translational Medicine Informatics & Applications

COSI representative to committee: Venkata Satagopam

VarI: Variant Interpretation

COSI representative to committee: Emidio Capriotti

This year we celebrated the 10th anniversary of the Variant Interpretation community. All the members of the committee started acknowledging Yana Bromberg who significantly contributed to the organization of the meeting since 2011. At VarICOSI 2020, we heard from a fantastic array of speakers on challenges for clinical and evolutionary variant interpretation. Our agenda included three keynote speakers, two proceedings talk, 10 (7 short +3 long) talks from submitted abstracts and a talk from our sponsor, Variantyx.

The VarICOSI was divided into a morning and afternoon session. In the morning session a keynote talk from Kelley Harris presented the results of a study on the mutation rate as a trait in human populations. In the afternoon Lincoln Stein, spoke about novel insights on cancer mutations from the PanCancer study including over 2500 tumor whole genomes. Finally, Fritz Roth described the development and application of Tileseq to systematically probe the landscape of mutations across genetic background and environmental condition. The organizers thank all of our speakers and sponsor for making this another great VarICOSI at ISMB.

The VarICOSI executive committee invited the community to provide feedback regarding meeting content and format, as well as to participate in future sessions of the meeting.

ISCB THANKS THE FOLLOWING SPONSORS FOR THEIR GENEROUS SUPPORT OF MEETINGS AND CONFERENCES:

ISMB 2020

National Institutes of Health
GLBIO
Harvard Medical School
Janssen Immunology

RSG DREAM 2020

Memorial Sloan Kettering Cancer Center
Sage Bionetworks
IBM Research

ISB-LA SOIBIO BIONETMX 2020

International Laboratory for Human Genome Research
CONACYT

ISCB RECOGNIZES THE INDIVIDUALS BELOW FOR THEIR GENEROUS VOLUNTEER SERVICE THAT ENABLED ISCB TO FACE THE CHALLENGES OF 2020 HEAD ON!

ISMB 2020

Conference Chairs

Honorary Conference chair: David Sankoff
University of Ottawa, Canada

Conference Co-chair: B.F. Francis Ouellette
Canadian Bioinformatics Workshops
Montreal, Canada

Conference Co-chair: Shoshana Wodak
VIB-VUB Center for Structural Biology
Brussels, Belgium

ISMB 2020 Steering Committee

Nadia El-Mabrouk, Proceedings Chair,
    Université de Montréal, Canada
Bruno Gaeta, Treasurer,
    University of New South Wales, Australia
Janet Kelso, Conference Advisory Council Co-chair,
    Max Planck Institute for Evolutionary Anthropology, Germany
Diane E. Kovats,
    ISCB Executive Director, United States
Steven Leard,
    ISMB Conference Director, Canada
Thomas Lengauer, President, ISCB,
    Max Planck Institute for Informatics, Germany
Christine Orengo, Conference Advisory Council Co-chair,
    University College London, United Kingdom
Francis Ouellette, Conference Co-chair,
    Canadian Bioinformatics Workshops, Canada
Pat Rodenburg,
    Conference Administrator, Canada
David Sankoff, Honorary Chair,
    University of Ottawa, Canada
Donna Slonim, Proceedings Co-chair,
    Tufts University, United States
Shoshana Wodak, Conference Co-chair,
    VIB-VUB Center for Structural Biology, Belgium

COSI TRACK LEADS & ABSTRACT CHAIRS

3D-SIG: Structural Bioinformatics and Computational Biophysics

Iris Antes,
    Technical University of Munich, Germany
Rafael Najmanovich,
    University of Montreal, Canada

BIOINFO-CORE

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

Bio-Ontologies
Robert Hoehndorf,
    King Abdullah University of Science & Technology, Saudi Arabia
Michel Dumontier,
    Maastricht University, Netherlands

BioVis: Biological Data Visualizations
Danielle Albers,
    University of Colorado at Boulder, United States
Cagatay Turkay, City,
    University of London, United Kingdom
Thomas Höllt,
    Leiden University Medical Center, The Netherlands
Michael Krone,
    University of Tübingen, Germany
Michel Westenberg,
    Eindhoven University of Technology, The Netherlands

CAMDA: Critical Assessment of Massive Data Analysis
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

CompMS: Computational Mass Spectrometry
Wout Bittremieux,
    University of California San Diego, United States
Oliver Kohlbacher,
    Universität Tübingen, Germany
Shuzhao Li,
    Emory University, United States
William S. Noble,
    University of Washington, United States
Timo Sachsenberg,
    Universität Tübingen, Germany
Olga Vitek,
    Northeastern University, United States
Jeff Xia,
    McGill University, Canada

Education: Computational Biology and Bioinformatics Education and Training
Annette McGrath,
    Australian Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia
Patricia M. Palagi,
    SIB Swiss Institute of Bioinformatics, Switzerland
Venkata Satagopam,
    University of Luxembourg

EvolCompGen: Evolution & Comparative Genomics
Lars Arvestad,
Stockholm University, Sweden
Edward L. Braun,
University of Florida, United States
Christophe Dessimoz,
University of Lausanne, Switzerland

Function: incorporating CAFA 4: Gene and Protein Function Annotation
Iddo Friedberg,
Iowa State University, United States
Mark Wass,
University of Kent, United Kingdom
Kimberly Reynolds,
University of Texas Southwestern Medical Center, United States

HiTSeq: High Throughput Sequencing Algorithms & Applications
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
Gang Fang,
Mount Sinai School of Medicine, United States
Kjong Lehmann,
ETH-Zürich, Switzerland
Layla Oesper,
Carleton College, United States

iRNA: Integrative RNA Biology
IYoseph Barash,
University of Pennsylvania, United States
Klemens Hertel,
University of California, Irvine, United States
Michelle Scott,
Université de Sherbrooke, Canada

MLCSB: Machine Learning in Computational and Systems Biology
Christoph Lippert,
University of Potsdam, Germany
Sara Mostafavi,
University of British Columbia, Canada

Microbiome
Aaron Darling,
University of Technology Sydney, Australia
Alice McHardy,
Helmholtz Centre for Infection Research, Germany
Fernando Meyer,
Helmholtz Centre for Infection Research, Germany
Alexander Sczyrba,
Bielefeld University, Germany

NetBio: Network Biology
Martina (Tina) Kutmon,
Maastricht University, Netherlands
Tijana Milenkovic,
University of Notre Dame, United States
Natasa Przulj,
Barcelona Supercomputing Center, Spain

RegSys: Regulatory and Systems Genomics
Ferhat Ay,
La Jolla Institute, United States
Ziv Bar-Joseph,
Carnegie Mellon University, United States
Anaïs Bardet,
CNRS - Université de Strasbourg, France
Mathieu Blanchette,
McGill University, Canada
Raluca Gordan,
Duke University, United States
Shaun Mahony,
Penn State University, United States
Anthony Mathelier,
University of Oslo, Norway
Alejandra Medina-Rivera,
National University of Mexico
Judith Zaugg,
EMBL, Germany

SysMod: Computational Modeling of Biological Systems
Matteo Barberis,
University of Surrey, United Kingdom
Laurence Calzone,
Institut Curie, France
Andreas Dräger,
University of Tübingen, Germany
Tomas Helikar,
University of Nebraska-Lincoln, United States
Jonathan Karr,
Icahn School of Medicine at Mount Sinai, United States
Juilee Thakar,
University of Rochester Medical Center, United States

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

TransMed: Translational Medicine Informatics & Applications
Wei Gu,
University of Luxembourg
Stephen MacKinnon, Cyclica, Canada
Venkata Satagopam,
University of Luxembourg
Mansoor Saqi,
Kings College London, United Kingdom
Maria Secrier,
University College London, United Kingdom

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

General Computational Biology
Virginie Uhlmann,
European Bioinformatics Institute (EMBL-EBI), United Kingdom
Xuegong Zhang,
Tsinghua University, China

COVID-19 Abstract Committee
Nadia El-Mabrouk,
Université de Montréal, Canada
Bruno Gaeta,
University of New South Wales, Australia
Janet Kelso,
Max Planck Institute for Evolutionary Anthropology, Germany
Thomas Lengauer,
Max Planck Institute for Informatics, Germany
Stephen MacKinnon,
Cyclica, Canada
Christine Orengo,
University College London, United Kingdom
Aida Ouangraoua,
Université de Sherbrooke, Canada
Francis Ouellette,
Canadian Bioinformatics Workshops, Canada
Vladimir Reinharz,
Université du Québec à Montréal, Canada
Sushmita Roy,
University of Wisconsin-Madison, United States
David Sankoff,
University of Ottawa, Canada
Russell Schwartz,
Carnegie Mellon University, United States
Donna Slonim,
Tufts University, United States
Shoshana Wodak,
VIB-VUB Center for Structural Biology, Belgium
Yu Xia, McGill University, Canada
Fellowship Committee
Chair: Lucia Peixoto, Washington State University, United States
Co-chair: Dimitri Perrin, Queensland University of Technology, Australia
Co-chair: Catherine Putonti, Loyola University Chicago, United States

Proceedings Reviewers
Stein Aerts,
VIB, Belgium
Tatsuya Akutsu,
Kyoto University, Japan
Max Alekseyev,
George Washington University, United States
Can Alkan,
Bilkent University, Turkey
Manimozhiyan Arumugam,
University of Copenhagen, Denmark
Lars Arvestad,
Stockholm University, Sweden
Kiyoshi Asai,
The University of Tokyo, Japan
Ferhat Ay, La Jolla Institute, United States
Erman Ayday,
Case Western Reserve University and Bilkent University, Turkey
Vikas Bansal,
University of California San Diego, United States
Jan Baumbach,
Technical University of Munich, Germany
Robert Beiko, Dalhousie University, Canada
Tim Beissbarth,
University Medicine Göttingen, Germany
Asa Ben-Hur,
Colorado State University, United States
Nir Ben-Tal, Tel-Aviv University, Israel
Mathieu Blanchette, McGill, Canada
Isabell Bludau, ETH Zurich, Switzerland
Nils Blüthgen, Charite, Germany
Sebastian Böcker,
Friedrich Schiller University Jena, Germany
Richard Bonneau,
New York University, United States
Karsten Borgwardt,
ETH Zurich, Switzerland
Christina Boucher,
University of Florida, United States
Alan Boyle, University of Michigan, United States
Edward Braun, Univeristy of Florida, United States
Steven Braun,
Northeastern University, United States
Michael R. Brent, WUSTL, United States
Yana Bromberg, Rutgers University, United States
Juan Caicedo,
Fundación Universitaria Konrad Lorenz, Colombia
Tolga Can,
Middle East Technical University, Turkey
Hannah Carter,
University of California San Diego, United States
Mark Chaisson,
University of Washington, United States
Cedric Chauve,
Simon Fraser University, Canada
Jianlin Cheng,
University of Missouri Columbia, United States
Rayan Chikhi, CNRS, France

Maria Chikina,
Mount Sinai School of Medicine, United States
Leonid Chindelevitch,
Simon Fraser University, Canada
Hyunghoon Cho,
Schmidt Fellow at the Broad, United States
Meena Choi,
Northeastern University, United States
Olivia Choudhury,
IBM Research, United States
A. Ercument Cicek,
Bilkent University, United States
Joseph Cohen,
University of Montreal, Canada

Phillip Compeau, Carnegie Mellon University, United States
Ana Conesa, University of Florida, United States
Juan Cortés, LAAS, CNRS ; Université de Toulouse, France
James Costello, University of Colorado Anschutz Medical Campus, United States
Miklós Csürös, University of Montreal, Canada
Aedin Culhane, Dana-Farber Cancer Institute, Harvard School of Public Health, United States
Thomas Dandekar, University of Würzburg, Germany
Noah Daniels, The University of Rhode Island, United States
Jeroen de Ridder, Delft Bioinformatics Lab, Netherlands
Dan DeBlasio, University of Texas at El Paso, United States
Alain Denise, CNRS - Univ. Paris-Sud & IGM, France
Viraj Deshpande, Illumina Inc., United States
Christophe Dessimoz, University College London, United Kingdom
Alexander Diehl, University at Buffalo, United States
Robin Dowell, University of Colorado Boulder, United States
Jingcheng Du, UTHealth, United States
Ingo Ebersberger, Goethe University, Germany
Mohammed El-Kebir, University of Illinois at Urbana-Champaign, United States
Jason Ernst, USLA, United States
Dirk Evers, Molecular Health GmbH, Germany
Gang Fang, Mount Sinai School of Medicine, United States
Selene Fernandez-Valverde, Advanced Genomics Unit / Langebio, Cinvestav, Mexico
Liliana Florea, Johns Hopkins University, United States
Anthony Fodor, UNC Charlotte, United States
Caroline Friedel, Ludwig Maximilian University of Munich, Germany
Fabian Froehlich, Harvard University, United States
Shilpa Garg, Harvard University, United States
Dario Ghersi, University of Nebraska at Omaha, United States
David Gifford, Massachusetts Institute of Technology, United States
Jesse Gillis, Cold Spring Harbor Laboratory, United States
Anthony Gitter, University of Wisconsin-Madison, United States
Casey Greene, Univ. Pennsylvania, United States
Gamze Gursoy, Yale University, United States
Faraz Hach, University of British Columbia and Vancouver Prostate Centre, Canada
Iman Hajirasouliha, Cornell University, United States
Will Hamilton, Stanford University, United States
Nurit Haspel, University of Massachusetts Boston, United States
Carl Herrmann, University Heidelberg, Germany
Ivo Hofacker, University of Vienna, Austria
Liisa Holm, University of Helsinki, Finland
Farhad Hormozdiari, Harvard University, United States
Larry Hunter, UC Denver, United States
Vân Anh Huynh-Thu, University of Liege, Belgium
Pierre-Etienne Jacques, Université de Sherbrooke, Canada
Lars Juhl Jensen, European Molecular Biology Laboratory, Denmark
Peng Jiang, National Cancer Institute, United States
Tao Jiang, University of California, Riverside, United States
Xiaoqian Jiang, UTHealth at Houston, United States
Yuxiang Jiang, Indiana University, United States
Lars Kaderali, University Medicine Greifswald, Germany
Andre Kahles, ETH Zurich, Switzerland
Tamer Kahveci, University of Florida, United States
Lukas Käll, KTH Royal Institute of Technology, Sweden
Emre Karakoc, University of Washington, Germany
John Kececioglu, University of Arizona, United States
Birte Kehr, Berlin Institute of Health / Charité - Universitätsmedizin Berlin, Germany
Sunduz Keles, University of Wisconsin-Madison, United States
Daisuke Kihara, Purdue University, United States
Larisa Kiseleva, OIST, Japan
Judith Klein-Seetharaman, Colorado School of Mines, United States
David Knowles, New York Genome Center, United States
Oliver Kohlbacher, University of Tübingen, Germany
Rachel Kolodny, US, Israel
Sergey Koren, NHGRI/NIH, United States
Dmitry Korkin, Worcester Polytechnic Institute, United States
Dennis Kostka, University of Pittsburegh, United States
Mehmet Koyuturk, Case Western Reserve University, United States
Roland Krause, University of Luxembourg, Luxembourg
Arjun Krishnan, Michigan State University, United States
Smita Krishnaswamy, Yale University, United States
Jack Kuipers, ETH Zurich, Switzerland
Anshul Kundaje, Stanford University, United States
Lukasz Kurgan, Virginia Commonwealth University, United States
Alain Laederach, Univ. North Carolina, United States
Manuel Lafond, Univ. Sherbrooke, Canada
Lydie Lane, SIB, Switzerland
Ben Langmead,

Keren Lasker, Stanford University, United States
Mathieu Lavallée-Adam, University of Ottawa, Canada
Heewook Lee, Carnegie Mellon University, United States
Jingyi Jessica Li, University of California, Los Angeles, United States
Ming Li, Univ of Waterloo, Canada
Qunhua Li, The Pennsylvania State University, United States
Yue Li, McGill University, Canada
Maxwell Libbrecht, University of Washington Genome Sciences, United States
Olivier Lichtarge, Baylor College of Medicine, United States
Zhiyong Lu, NCBI, United States
Gerton Lunter, University of Oxford, United Kingdom
Jian Ma, Carnegie Mellon University, United States
Francois Major, University of Montreal, Canada
Serghei Mangul, University of California, Los Angeles, United States
Guillaume Marçais, Carnegie Mellon University, United States
Florian Markowetz, University of Cambridge, United Kingdom
Deborah Marks, Harvard University, United States
Pier Luigi Martelli, University of Bologna, Italy
Manja Marz, Leipzig, Germany
Brian Matejek, Harvard University, United States
David Mathews, Univ. Rochester, United States
Shalin Mehta, Chan Zuckerberg Biohub, United States
Wouter Meuleman, Altius Institute for Biomedical Sciences, United States
Michelle Meyer, Boston College, United States
Tom Michoel, University of Bergen, Norway
Tijana Milenkovic, University of Notre Dame, United States
Emily R. Miraldi, Cincinnati Children's Hospital Medical Center, United States
Siavash Mirarab, The University of Texas at Austin, United States
Hosein Mohimani, Carnegie Melon University, United States
Alexandre Morozov, Rutgers University, United States
Quaid Morris, University of Toronto, Canada
T. M. Murali, Virginia Tech, United States
Robert Murphy, Carnegie Mellon University, United States
Chad Myers, University of Minnesota, United States
Luay Nakhleh, Rice University, United States
Leelavati Narlikar, National Chemical Laboratory, India
Kay Nieselt, University of Tübingen, Germany
William Stafford Noble, University of Washington, United States
Emmanuel Noutahi, InVivo AI, Canada
Ibrahim Numanagic, Massachusetts Institute of Technology, UnitedStates
Claire O'Donovan, EBI, United Kingdom
Layla Oesper, Carleton College, United States
Yaron Orenstein, Ben-Gurion University, Israel
Hatice Osmanbeyoglu, University of Pittsburgh, United States
Aditeya Pandey, Northeastern University, United States
Gaurav Pandey, Mount Sinai School of Medicine, United States
Laxmi Parida, IBM, United States
Benedict Paten, UCSC, United States
Rob Patro, University of Maryland, College Park, United States
Itsik Pe'Er, Columbia University, United States
Jian Peng, University of Illinois at Urbana-Champaign, United States
Yifan Peng, NIH, United States
Yasset Perez-Riverol, EMBL-EBI, United Kingdom
Theodore Perkins, Ottawa Hospital Research Institute, Canada
Dmitri Pervouchine, Skoltech, Russia
Anton Petrov, EMBL, United Kingdom
Nico Pfeifer, University of Tübingen, Germany
Roger Pique-Regi, Wayne State University, United States
Yann Ponty, CNRS/LIX, Polytechnique, France
Natasa Przulj, ICREA; Barcelona Supercomputing Center; University College London, Spain
Simon Puglisi, University of Helsinki, Finland
Qin, IMADA, Denmark
Predrag Radivojac, Northeastern University, United States
Sven Rahmann, University of Duisburg-Essen, Germany
Huzefa Rangwala, George Mason University, United States
Ben Raphael, Princeton University, United States
Magnus Rattray, The University of Manchester, United Kingdom
Tobias Rausch, EMBL Heidelberg, Germany
Vladimir Reinharz, Université du Québec à Montréal, Canada
Melissa Resnick, University at Buffalo, United States
Anna Ritz, Reed College, United States
Elena Rivas, Harvard, United States
Marc Robinson-Rechavi, Universite de Lausanne, Switzerland
David Rocke, UC Davis, United States
Cenk Sahinalp, Indiana University Bloomington, United States
Leena Salmela, University of Helsinki, Finland
Mike Schatz, Cold Spring Harbor Laboratory, United States
Alexander Schoenhuth, Vrije Universiteit Amsterdam, Netherlands
Marcel Schulz, Goethe University, Germany
Michelle Scott, University of Sherbrooke, Canada
Mingfu Shao, Carnegie Mellon University, United States
Roded Sharan, Tel Aviv university, Israel
Hagit Shatkay, University of Delaware, United States
Tal Shay, Ben-Gurion University of the Negev, Israel
Amarda Shehu, George Mason University, United States
Yang Shen, Texas A&M University, United States
Qian Shi, The Pennsylvania State University, United States
Mile Sikic, Genome Institute of Singapore, Singapore
Sean Simmons, Broad Institute, United States
Saurabh Sinha, Illinois, United States

Giltae Song,
Pusan National University, South Korea
Erik Sonnhammer,
Stockholm University, Sweden
Jens Stoye, Bielefeld University, Germany
Krister Swenson, CNRS,
Université de Montpellier, France
Marta Szachniuk, Poznan, Poland
Ewa Szczurek, University of Warsaw, Poland
Eric Tannier, INRIA, France
Jaclyn Taroni,
Childhood Cancer Data Lab, United States
Glenn Tesler,
University of California San Diego, United States
Silvio Tosatto, University of Padova, Italy
Hélène Touzet, CNRS, CRIStAL, Lille, France
Todd Treangen, Rice University, United States
Olivier Tremblay-Savard,
University of Manitoba, Canada
Alfonso Valencia,
Barcelona Supercomputing Centre BSC, Spain
Fabio Vandin, University of Padova, Italy
Mauno Vihinen, Lund University, Sweden
Martin Vingron,
Max Planck Institut fuer molekulare Genetik, Germany
Hao Wang, Carnegie Mellon University, United States
Tandy Warnow,
the university of illinois at urbana-champaign, United States
Zasha Weinberg, Univ. Leipzig, Germany
Sebastian Will, University of Vienna, Vienna
Yu Xia, McGill, Canada
Jinbo Xu,
Toyota Technological Institute at Chicago, United States
Vicky Yao, Rice University, United States
Esti Yeger-Lotem, Ben Gurion University, Israel
Peng Yu, Texas A&M University, United States
Yun William Yu,
Harvard Medical School DBMI, United States
Jianyang Zeng, Tsinghua University, China
Louxin Zhang,
National University of Singapore, Singapore
Ralf Zimmer,
Ludwig Maximilian University of Munich, Germany
Marinka Zitnik, Harvard University, United States

Special Sessions
Chair: Mathieu Blanchette,
McGill University, Canada
Co-chair: Sushmita Roy,
University of Wisconsin-Madison, United States

Technology Track Committee
Chair: Hagit Shatkay,
University of Delaware, United States

Tutorials
Chair: Michelle D. Brazas,
Ontario Institute for Cancer Research, Canada
Co-chair: Patricia M. Palagi,
SIB Swiss Institute of Bioinformatics, Switzerland
Co-chair: Annette McGrath,
Commonwealth Scientific and Industrial Research Organisation (CSIRO), Australia

RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2020

Steering Committee
Bonnie Berger,
MIT
Richard Bonneau,
NYU
Christina Leslie,
MSKCC
Andrea Califano,
Columbia University
Manolis Kellis,
MIT
Saurabh Sinha,
University of Illinois at Urbana-Champaign
Lonnie Welch,
Ohio University

Organizing Chairs
Elise Blaise,
IBM, DREAM Chair
Anshul Kundaje,
Stanford University, RSG Program Chair
Jian Ma,
Carnegie Mellon University, RSG Program Chair
Pablo Meyer,
IBM, DREAM Chair
Sushmita Roy,
University of Wisconsin RSG Program Chair

ISCB-LA SOIBIO BioNetMX 2020

Scientific Program
Alejandra Medina Rivera,
Laboratorio Internacional de Investigación sobre el Genoma Humano
Maribel Hernández Rosales,
Centro de Investigación y de Estudios Avanzados del IPN (CINVESTAV), Unidad Irapuato
Javier De Las Rivas,
Cancer Research Center (CiC-IBMCC), USAL-CSIC, Salamanca, Spain
Selene Fernández-Valverde,
Laboratoria Nacional de Genómica para la Biodiversidad (LANGEBIO)
Daniela Robles,
Laboratorio Internacional de Investigación sobre el Genoma Humano-UNAM
Ernesto Pérez Rueda,
UNAM Campus Mérida
Benilton Carvalho,
.Universidad Estadual de CampinasFederico
Sánchez Quinto,
Instituto Nacional de Medicina Genómica (INMEGEN)
Alejandro Reyes Quiroz,
Novartis Institutes for Biomedical Research (NIBR)
Maria Emilia Walter,
Universidade de Brasilia

Steering Committee

Alejandra Medina Rivera,
    Laboratorio Internacional de Investigación sobre el Genoma Humano
Maribel Hernández Rosales,
    Centro de Investigación y de Estudios Avanzados del IPN (CINVESTAV), Unidad Irapuato
Dr. Javier De Las Rivas
    Cancer Research Center (CiC-IBMCC), USAL-CSIC
Francisco Melo,
    Universidad Catolica de Chile
Dr. Alfredo Varela
    Instituto de Neurobiología, UNAM, Campus Juriquilla
Dr. Julio Collado-Vides
    Centro de Ciencias Genómicas, UNAM, Campus Morelos
Dr. Ana Tereza Vasconcelos
    Bioinformatics Laboratory - LABINFO - National Laboratory of Scientific Computation
Dr. Elizabeth Tapia
    CIFASIS - Conicet

Organizing Committee

Alejandra Medina Rivera,
    Laboratorio Internacional de Investigación sobre el Genoma Humano, Campus Juriquilla (LIIGH-UNAM)
Maribel Hernández Rosales,
    Centro de Investigación y de Estudios Avanzados del IPN (CINVESTAV), Unidad Irapuato
Diane Kovats,
    International Society for Computational Biology
Diego Ortega-Del Vecchyo,
    Laboratorio Internacional de Investigación sobre el Genoma Humano, Campus Juriquilla (LIIGH-UNAM)
Yalbi Balderas,
    Instituto Nacional de Enfermedades Respiratorias, México (INER)
Selene Fernández Valverde,
    Laboratorio Nacional de Genómica para la Biodiversidad (LANGEBIO)
Irma Martínez Flores,
    Centro de Ciencias Genómicas, UNAM campus Morelos (CCG-UNAM)
Allan Orozco,
    Autonomous University of Madrid and University of Costa Rica

2020 DONORS

ISCB thanks everyone who has made a gift in support of the Society, including the many generous donors who wish to remain anonymous!

Jesus Galaz-Montoya
Emily Kawabata
Kevin Cohen
Nilson Da Rocha Coimbra
Dr. Lukeman Shittu
Boyang Ji
Rita Stack
Khalid Mahmood
Lawrence Hunter
Achille Zappa
Didier Barradas-Bautista
Clare Sansom
Peter Ebert
Pavlo Lutsik
Prashanth Suravajhala
Jyothi Thimmapuram

Noah Daniels
Janos Binder
Ceslovas Venclovas
Peter Lackner
David Gibbs
Jens Kleinjung
Deborah Chasman
Matteo Schiavinato
William McLaughlin
Jennifer Weller
Lenore Cowen
Jesus Galaz-Montoya
Helen Berman
Davis McCarthy
Mirian Silvera
Pier Luigi Martelli
Juan Dias

Thank you for supporting ISCB!