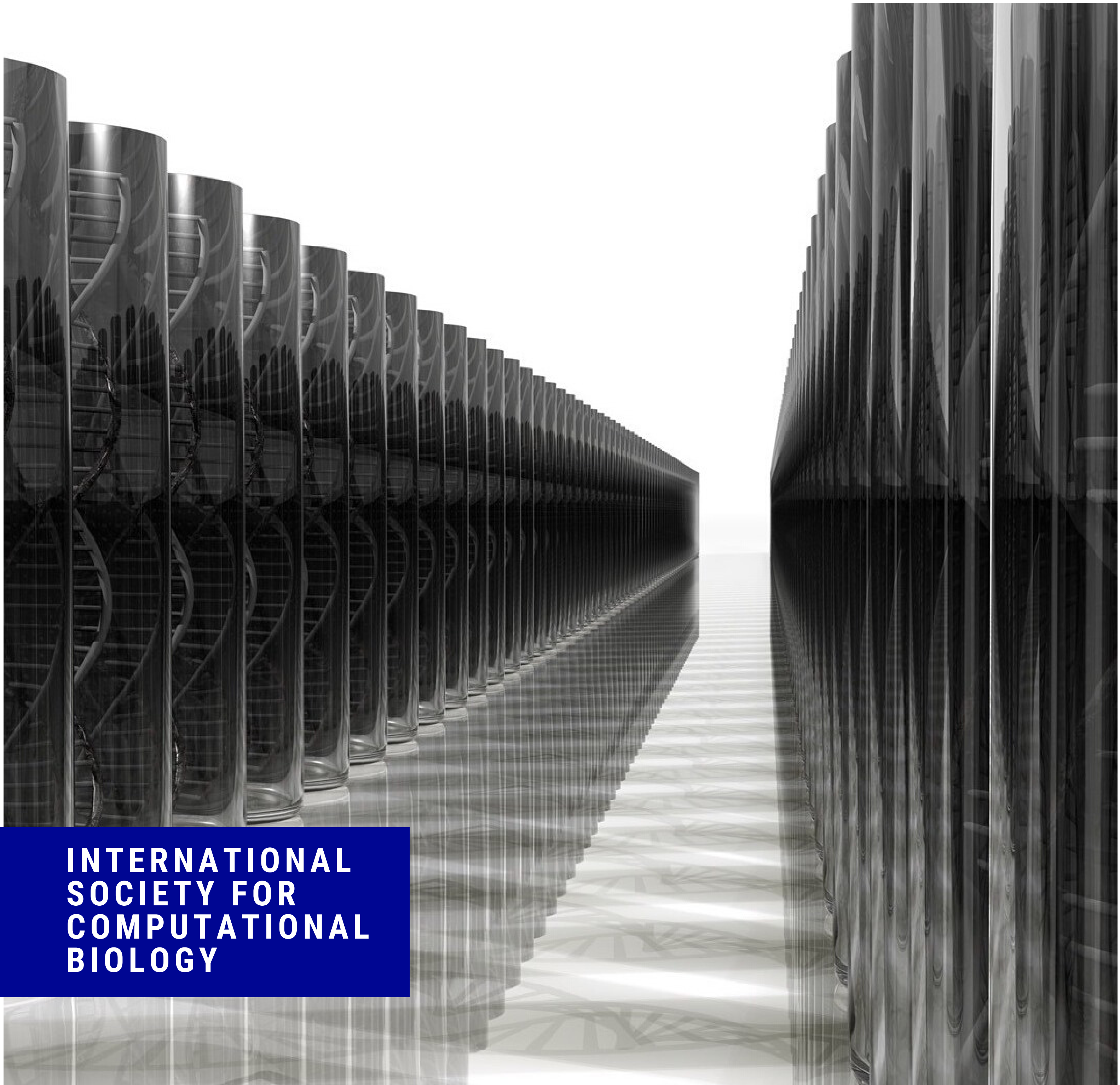
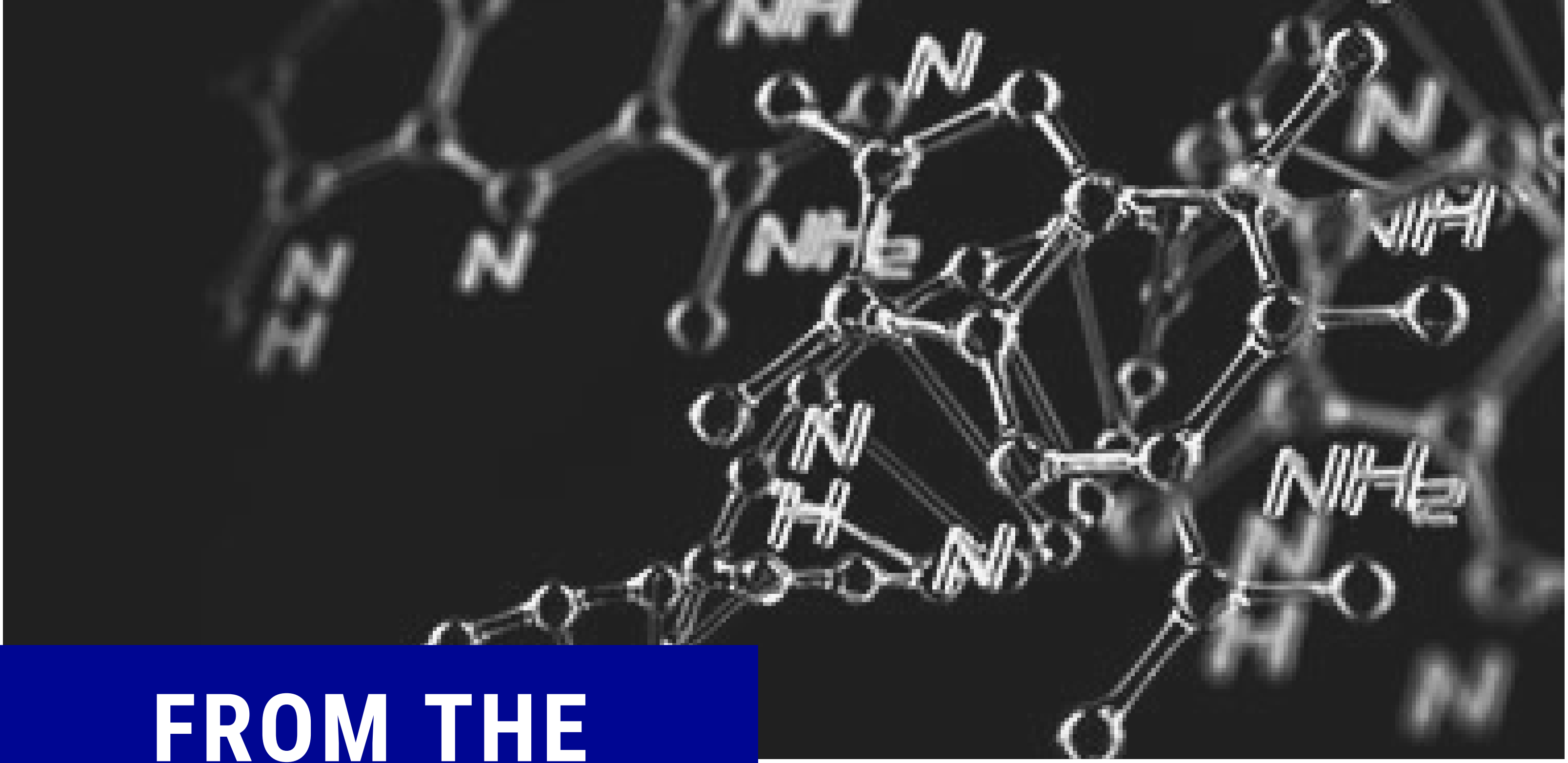
ANNUAL REPORT 2019

LEADING PROFESSIONAL SOCIETY
FOR COMPUTATIONAL BIOLOGY
AND BIOINFORMATICS

CONNECTING, TRAINING,
EMPOWERING, WORLDWIDE



INTERNATIONAL
SOCIETY FOR
COMPUTATIONAL
BIOLOGY



FROM THE EXECUTIVE DIRECTOR

2019 was a year of accomplishments for ISCB. We reached our highest membership on record, launched the new ISCBlive program, established two new committees to better serve our membership, approved an environmental sustainability policy, celebrated in Basel with a record-breaking conference attendance, and much more of which you will have the opportunity to read about in this report.

ISCB continues to grow, working 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.

Current ISCB membership is just under 3,500 members worldwide, reflecting a 7% growth in our membership compared to 2018. We are truly excited about this membership growth as it reflects the importance of our science. Over the course of 2020, we will continue to work to serve you, our members.

During the ISMB/ECCB conference in Basel, Switzerland, we piloted a new live streaming program, ISCBLive. ISCB recognized that there are members within our community that are unable to make it to the meeting in person. In order to give them the opportunity to experience the science without waiting for the content to be posted, we offered complimentary to our membership the ability to watch the conference keynotes live. A rebroadcast event was held in the evening of each day to accommodate the many time zones that are present within the membership. Almost 200 unique users participated in the live-stream and rebroadcast program. ISCB also offered the live-stream services for its ISCB-Africa ASBCB conference. As we look ahead to 2020, look for more exciting online learning and knowledge gaining sessions as we work to launch ISCB Academies, a year-round webinar series, as well as live-streamed conference content.

Recognizing that science is best advanced when there is mutual trust, based upon honest behavior, throughout the community, ISCB developed a societal-wide Code of Ethics and Professional Conduct. The guiding principles set forth in the ISCB Code of Ethics and Professional Conduct are meant to protect the community of science and are not meant to be a complete list of all ethical issues. Along with the Code of Ethics and Professional Conduct, ISCB launched ISCB – A Safe Space program. ISCB – A Safe Space works to maintain an environment that allows science and scientific careers to flourish through respectful, inclusive, and equitable treatment of others and is committed to providing a safe place for its members and nonmember participants.

Eleven staff and volunteers were also trained as Ombudsmen to assist members in need. Our community has taken this very seriously and I am pleased to report that since the launch of the program, we have received only two incident reports both which were addressed by the Ombudsmen with no further action required. To further support the importance of the highest level of ethical and professional behavior within our community, the ISCB Board of Directors also approved the establishment of an Ethics and Professional Conduct Committee.

Promoting the involvement and expanded access to leadership opportunity regardless of race, ethnicity, gender, religion, age, sexual orientation, nationality, disability, appearance, geographic location, or professional level, is a strategic goal of the organization.

To help us achieve this goal, the ISCB Board of Directors also established an Equity, Diversity, and Inclusion Committee. The ISCB Equity, Diversity and Inclusion (EDI) Committee will support the Society by identifying the inclusion and diversity strengths, issues, and opportunities within all aspects of ISCB, developing strategies and plans to examine ways in which we can become more inclusive, and systematically examining aspects of ISCB to enhance its effectiveness and ability to meet the needs of its diverse membership. We as an organization are truly looking forward to growing, enhancing, and celebration the value of diversity, equity, and inclusion of all.

We truly had a lot to celebrate in 2019 but none of these accomplishments would have been achieved without the dedication of our volunteer members. The successes and achievements are theirs to celebrate. We grow as an organization because of our dedicated members. 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
Executive Director

MEMBERSHIP

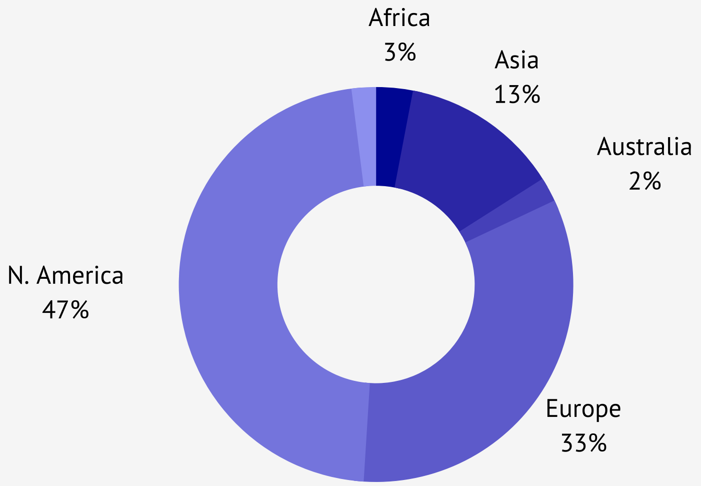
Members are the lifeblood of ISCB, and recruiting and maintaining active members is essential to the vitality of this Society. At the close of 2017 ISCB finished strong with a 6% increase of membership to 3466 members.

6%

ISCB's membership increased by 6% in 2019

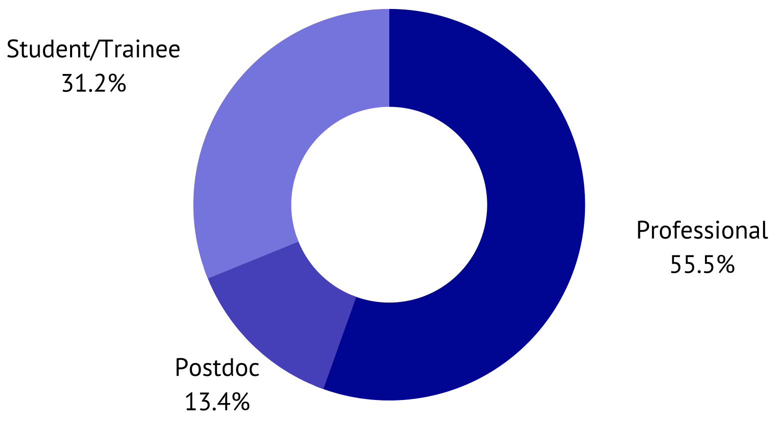
MEMBERSHIP BY REGION

Members are the lifeblood of ISCB, and recruiting and maintaining active members is essential to the vitality of this Society. At the close of 2019, ISCB finished strong with a 6% increase of membership to 3466 members. Members hailed from 77 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 25 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 45% of the membership.



SOCIETY COMMITTEE AND LEADERSHIP HIGHLIGHTS

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. The highlights of some of the major achievments throughout 2019 are featured below.

The ISCB members elected Christine Prengo as President-Elect and Yana Bromberg as Vice-president. Incoming members of the boarrd

OFFICERS

CHRISTINE ORENGO
President-Elect

Christine Orengo has been elected to the officer position of President-elect. She will serve a one-year term as President-elect, a three-year term as President, and a one-year term as Immediate Past President. As an officer, Christine will also serve as member of the Board of Directors. Christine is the first woman to serve in the Presidential role of ISCB. Christine is a Professor of Structural Bioinformatics, Division of Biosciences, University College London (UCL), whose core research has been the development of robust algorithms to capture relationships between protein structures, sequences and functions. She has built one of the most comprehensive protein classifications, CATH, used worldwide by tens of thousands of biologists, and central to many pioneering structural and evolutionary studies. Christine has been a member of the Board of Directors since 2012, served on various committees, and most recently led the integration of the Communities of Special Interest (COSI) into the ISCB flagship meeting, the Intelligent Systems for Molecular Biology (ISMB) conference.

YANA BROMBERG
Vice President

Yana Bromberg has been elected to the officer position of Vice President, where she will also serve as a member of the Board of Directors. She will serve a three-year term. Yana is an Associate Professor, Department of Biochemistry and Microbiology at Rutgers University. Her research focuses on deciphering the DNA “blueprints” of life’s molecular machinery. She develops novel bioinformatics techniques to find out where this machinery comes from and why/how it runs. Yana received her degrees from SUNY Stony Brook and Columbia University. Her work has been recognized by private and federal agencies, including NASA and NIH. She received an NSF CAREER award and is also a Fellow of the Munich Institute for Advanced Study. Her findings consistently indicate that our world functions via dependencies and interactions at all scales. Yana has served as a member of the ISCB Board of Directors, was the proceedings chair for ISMB (2017-2019), and was within the leadership of the Variant Interpretation (VarI) COSI.

ISCB BOARD OF DIRECTORS

MICHELLE BRAZAS

Michille Brazas has been re-elected for a second term 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.

CATH BROOKSBANK

Cath Brooksbank has been elected as a member of the Board of Directors. She will serve a three-year term and will be eligible for re-election. Cath is the head of the EMBL-EBI Training Programme. She joined EMBL-EBI in 2002 to develop the outreach programme, and extended her responsibilities to include training in 2006. Her team now coordinates a wide-ranging portfolio of training activities reaching tens of thousands of individuals each year. She contributes to a number of international projects including CABANA (which she leads), RItrain, CORBEL and BioExcel. She is co-chair of the Education Committee for the International Society of Computational Biology and a member of the advisory board for the Crick African Network.

HAGIT SHATKAY

Hagit Shatkay has been re-elected as a member of the Board of Directors. She will serve a three-year term. Hagit is a professor of Computer & Information Sciences and an Associate Professor of the Center for Biomechanical Engineering Research at the University of Delaware. Her research focuses on biomedical text mining, computational biology and computation methods in biology and medicine. She has served on several editorial and review boards for publications and journals involving bioinformatics, computational biology, artificial intelligence and information retrieval. Hagit was also part of the special ISCB task force that developed the ISCB Code of Ethics and Professional Conduct.

XUEGONG ZHANG

Xuegong Zhang has been elected as a member of the Board of Directors. Xuegong is a Professor of Pattern Recognition and Bioinformatics, the Director, Bioinformatics Division, TNLIST, and the Deputy Director, MOE Key Laboratory of Bioinformatics at the Tsinghua University. Xuegong Zhang is a leading computational biologist in China. He has deep background in machine learning, and has been working on bioinformatics for almost two decades. His outstanding track record of scientific productivity, teaching, leadership, community service make him one of the most respected Chinese computational biologists. Xuegong's main research focus is on developing machine learning and bioinformatics methods for transcriptomics data analyses and biological discoveries. He is the Chair of the Committee for Bioinformatics Committee in the Chinese Association for Artificial Intelligence, and the Acting Chair of the Committee of Computational Biology in the Chinese Society of Biotechnology. He hosted the RECOMB 2013 conference and RECOME-seq satellite meeting in Beijing, both of which were very successful.

WELCOME CLASS OF 2019 FELLOWS

The ISCB Fellows program was created to honor members who have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics. During the 2009 inaugural year of the program, the ISCB Board of Directors unanimously conferred Fellows status on the seven winners-to-date of the ISCB Accomplishment by a Senior Scientist Award. 2019 marks the 10th anniversary of the program. Each year since 2010, ISCB has sought Fellows nominations from our members, with eligibility restrictions based on selection criteria focused most heavily on the significance of scientific contributions, and service to our field and to ISCB.

This year 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:

VINEET BAFNA

Professor, Computer Science and Engineering, University of California, San Diego (UCSD), United States; an innovator who developed many bioinformatics algorithms for solving important biological problems and a leading researcher in the area of Cancer Genomics, Population Genetics, and Proteogenomics.

ELEAZAR ESKIN

Professor, Computer Science, Human Genetics, University of California, Los Angeles, United States; a leading computer scientist working on computational problems in human genetics and educator and developer of advanced educational programs for computer scientists, biologists, and statisticians, in computational biology.

XIAOLE SHIRLEY LIU

Professor, Biostatistics, Harvard T.H. Chan School Of Public Health, Harvard School of Public Health, Co-director, Center for Functional Cancer Epigenetics, Dana-Farber Cancer Institute, United States; an innovative and prolific computational cancer biologist.

MARIE-FRANCE SAGOT

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

ISCB CONGRATULATES ITS SENIOR MEMBERS

Peter Karp
SRI International

David Rocke
University of California, Davis

Hershel Safer
Consultant

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

Robert F. F Murphy
Carnegie Mellon University

Satoru Miyano
The University of Tokyo

Torsten Schwede
SIB Swiss Institute of Bioinformatics &

University of Basel
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

Søren Brunak
Novo Nordisk Foundation Center for Protein Research

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

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

Pierre Baldi
University of California, Irvine

Ron Shamir
Tel Aviv University

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

Scott Markel
Dassault Systèmes BIOVIA

Reinhard Schneider
LCSB

Aviv Regev
Broad Institute

H**agit 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

L**ouxin Zhang**
National University of Singapore

Ana Maria Rojas
CSIC-CABD

C**hristine Orengo**
University College London

Webb Miller
Pennsylvania State University

Weichuan Yu
The Hong Kong University of Science and Technology

Alex Bateman
EMBL- EBI

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

Ernest Fraenkel
MIT

David Lipman
Impossible Foods

Ivan Erill
UMBC

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 WORKS TO ACCOMPLISH THE GOALS OF THE STRATEGIC MAP

In 2018, the ISCB Board of Directors finalized the organizational strategic map (https://www.iscb.org/strategicmap/file). This strategic document was designed to be a road map over the next three years for the organization to follow as it worked towards it mission of advancing understanding of living systems through computation and for communicating scientific advances worldwide. Through the dedicated efforts of the many volunteers that serve ISCB, the organization has successfully meant the following outlined goals within the noted core competencies.

Communities

Through the work of a task force made of our the ISCB Community of Special Interest (COSI) leaders, the ISCB Board of Directors adopted the ISCB Community of Special Interest Guidelines. These guidelines outline the relationship of the COSIs with ISCB.

Additionally, members of the ISCB leadership meet with COSI track chairs and leader to discuss the scientific development and relationships for ISMB. Together the group works to ensure ISMB is an engaging and fruitful experience for its participants.

As we look to the future, we will be working on a resource center to assist our COSIs in achieving their individual goals and supported activities outside of ISMB as well as assessing the appropriate lifecycle of a COSI.

Education

The ISCB Education Committee and Education COSI have been done an amazing job in 2019. The Education COSI executed a full day track at ISMB on Education in Bioinformatics. They also supported the Workshop on Education in Bioinformatics, half-day program.

The Education Committee, led by chairs Cath Brooksbank, Nicola Mulder, and Venkata P. Satagopam, has been working on enhancing the ISCB Curriculum & Competency Guidelines for degree program, and developing the criteria for ISCB affiliated workshops and training.

As we move into 2020 expect to see more announcements on the outcomes of the affiliated workshops and training program as well as some exciting online learning opportunities.

Membership

Part of your membership goals are to ensure we are delivering value to our members. In 2019, ISCB offered online live streaming of its keynote speakers at ISMB. This pilot program offered complimentary access to live scientific content to those who were unable to make the event. In addition to the live streaming, ISCB conducted a rebroadcast of the session later in the day to allow our members from all time zones to partake in the content.

The program was also offered during the ISCB-Africa ASBCB program. We are working on a webinar series for 2020. This series will be complimentary for all ISCB members.

Conferences

One of the key values of ISCB membership are the discounts on conferences. ISCB strives to support the dissemination of scientific content worldwide. In 2019, ISCB supported three regional conferences and a topically conference. It also affiliated with 20 different regional conference from 17 countries.

We continue to work on developing sustainable conference models that allow our membership and participants to present their research in affordable manners.

Profession

Our profession core competency was our most ambitious as an organization. In 2019 we focused on strategic structure of organizational makeup and resources to position us to achieve our goals. The ISCB Board of Directors implemented the organization’s first Ethics and Professional Conduct Policy, instated an Ethics and Professional Conduct Committee and trained fourteen volunteers and staff as ombudsmen and allies to ensure our Safe Place policy is taken seriously.

Additionally, The Board of Directors instate an Equity, Inclusion, and Diversity committee charging them with identifying the inclusion and diversity strengths, issues, and opportunities within all aspects of ISCB; developing strategies and plans to examine ways in which we include and exclude (however unintentionally) ISCB members; and systematically examining aspects of ISCB to enhance its effectiveness and ability to meet the needs of its diverse membership.

Finally late in the year, Fran Lewitter, longtime ISCB member and former Board member, started ISCB efforts to development a resource center that will promote the value of our profession. The center will include examples of career paths within the field, guidance on setting up your own data centers, stories of start-up and much more. We are extremely excited about all of the possibilities and information this working group will bring.

CONTINUED GROWTH OF COSIS & ISCB CONNECT

ISCBconnect has 21 active ISCB Communities of Special Interest (COSI) online community groups. 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

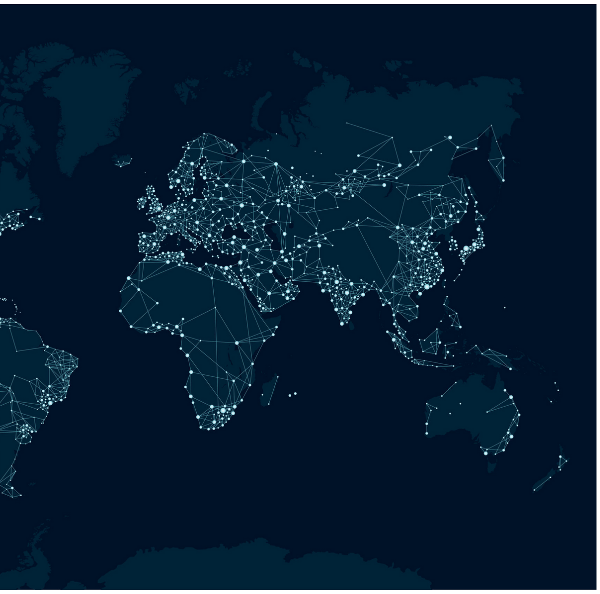
Knowledge-based translational medicine is a rapidly growing discipline in biomedical research and aims to expedite the discovery of new diagnostic tools and treatments by using a multi-disciplinary, highly collaborative, "bench-to-bedside" approach. It involves the integration of multiple high dimensional 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



IThe 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.

ISCB AFFILIATES PROGRAM GUIDELINES

The core of the International Society for Computational Biology's mission is to advance the understanding of living systems through computation. As the international membership organization of computational biologists, ISCB is committed to building bridges across the variety of not-for-profit community organizations that serve bioinformaticians/computational biologists in order to contribute to advancing the science globally.

The ISCB Affiliates Program provides an official designation of "ISCB Affiliate" to non- governmental organizations (NGO), not-for-profit organizations, or other non- commercial entities that meet the necessary criteria within the following categories:

Membership organizations are open to members from a specific geographic area representing at least three research institutions/organizations.

Institutes, Centers and Networks represent national/regional/worldwide consortia of educational institutions, and/or academic hospitals/medical centers, and/or research institutes, and (optionally) industrial partners that actively contribute to expanding the effectiveness of members in the advancement of bioinformatics/computational biology.

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)

2019 AFFILIATE REPORTS

Thank you to the ISCB Affilaites for providing detailed reports on their exciting activites throughout 2019!

ISCB - A SAFE SPACE POLICY STATEMENT

In February 2019, the ISCB Board of Directros unanimously approvd the adoption and implmentation of the ISCB Safe Program.

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

ISCB is committed to supporting a productive and safe working environment for all who are participating in ISCB activities, conferences, and programs. Incidents of inappropriate and uncivil behavior are taken extremely seriously. If an individual experiences or witnesses harassment, they should contact an ISCB Ombudsman (wearing the ISCB Ally ribbon) in person or email safeISCB@iscb.org, or use a venue phone and ask for security if they feel unsafe. All complaints will be treated seriously and responded to promptly. While ISCB is not an adjudicating body, ISCB has appointed Ombudsmen who can be consulted, give advice or help seek out appropriate authorities to further handle any form of harassment or assault. Confidentiality will be maintained unless disclosure is legally required.

ISCB CODE OF ETHICS AND PROFESSIONAL CONDUCT

In February 2019, the ISCB Board of Directros unanimously approvd the adoption of the Code of Conduct.

As the Articles of Incorporation of the International Society for Computational Biology (ISCB) state that the objective of the Society shall be to promote the application of computational methods to problems of biological significance. The mission of the Society is to advance understanding of living systems through computation and to communicate those scientific advances worldwide. These goals demand honesty and truthfulness in all activities sponsored or supported by the Society.

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

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

Guiding Principles

ISCB members

- *Aim to uphold and advance the integrity and dignity of the profession and practice of bioinformatics and computational biology.*
- *Aspire to use their knowledge and skills for the advancement of life sciences and human welfare.*
- *Strive to increase the competence and prestige of the profession and practice of bioinformatics and computational biology by responsible action and by sharing the results of their research through academic and commercial endeavors, or by public service.*
- *Seek to maintain and expand their professional knowledge and skills.*
- *Respect professional Codes of Ethics and abide by the prevailing ethical and legal norms of their profession.*
- *Endeavor for objectivity in their professional activities through recognition, acknowledgment, and mitigation of intentional and unintentional biases.*
- *Adhere to the highest standards of publication ethics in line with those documented by the Committee on Publication Ethics (https://publicationethics.org). This includes but is not limited to: timely and accurate reporting of findings; full disclosure of author contributions, sources of financial support, and any potential conflicts of interest; fair and objective peer- review.*
- *Act responsibly, honestly, and respectfully toward colleagues, government, corporate sponsors, the wider health care community and the public at large. Build public trust through accountability.*
- *Foster fair participation of all people, including those of underrepresented groups in all of the Society's activities and at all levels of its organization. Prejudicial discrimination on the basis of age, color, disability, ethnicity, family status, gender identity, labor union membership, military status, nationality, race, religion or belief, sex, sexual orientation, or any other inappropriate factor is an explicit violation of the Code. Harassment, including sexual harassment, bullying, and other abuses of power and authority, is a form of discrimination that, amongst other harms, limits fair access to the virtual and physical spaces where such harassment takes place.*
- *Treat colleagues and researchers with respect and courtesy, based on principles of equality and mutual respect for those with differing worldviews or from different cultures. Share research results and ideas honestly, giving proper credit for others' contributions to their work.*

Professional Conduct

ISCB members

- *Maintain professional competence by advancing their knowledge andunderstanding of new scientific developments and emerging areas of practice through ongoing education and training.*
- *Educate employees, students, and professionals to follow responsible research practices consistent with the highest ethical standards. Treat trainees with respect and provide them with opportunities for professional growth and development.*

- *Share knowledge in research, practice, and ethics through publication, professional meetings and conferences, and foster collaborations. Meet applicable ethical and legal standards while collaborating*
- *Foster public understanding of the nature and objectives of bioinformatics and computational biology consistent with open and responsible use of findings in science and health care.*
- *Strive for objectivity in their professional activities through recognition, acknowledgment, and mitigation of intentional and unintentional biases.*
- *Respect the confidential nature of all information and research data entrusted to them. Disclose information with proper and specific authority through the consent of the individual or where there is a legal, ethical or professional right or duty to disclose.*
- *Claim expertise only in areas where they have the necessary depth of knowledge, especially when contributing to public discussion or policy debate. Do not make statements that are false, deceptive, or fraudulent concerning research, practice, or other work activities, or those of persons or groups with whom they are affiliated. Present personal opinions as such and not as those of the Society.*
- *Disclose any potential conflicts of interest. Safeguard the quality and credibility of their professional judgment.*
- *Report findings, including negative findings, accurately, completely, without distortion and in a timely manner.*
- *Refrain from demeaning, discriminatory, or harassing behavior, conduct and speech. Make ISCB a place that is welcoming and respectful to all participants, regardless of race, gender, gender identity, age, sexual orientation, disability, physical appearance, national origin, ethnicity, or religion. Examples ofdemeaning, discriminatory, or harassing behavior, conduct and speech are:*
  - *Any action directed at an individual that (a) interferes substantially with that person's participation; or (b) causes that person to fear for his/her personal safety. This includes threats, intimidation, bullying, stalking, or other types of abuse.*
  - *Any conduct that discriminates or denigrates an individual on the basis of race, ethnicity, religion, citizenship, nationality, age, sexual or gender identity, disability, or any other characteristic protected by law.*
  - *Unwelcome sexual advances, requests for sexual favors, or other verbal/physical conduct of a sexual nature, for example:*
    - *unwelcome advances or propositions, particularly when one individual has authority over the other;*
    - *nonconsensual touching of an individual's body;*
    - *unwelcome remarks on superficial aspects not related to the work at hand (e/g a person's appearance");*
    - *using an activity-related communication channel to display or distribute sexually explicit images or messages*
- *Demonstrate professionalism and collegiality in ISCB activities and communications, including committees, task forces, forums, and events, at all times avoiding abusive, racist, sexist, harassing, or threatening speech and/or behavior towards any other ISCB volunteer, staff, contractor, member, or event participant.*

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

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

Our goal is to foster a culture that creates a safe and open working environment for all who are participating in ISCB activities, conferences, and programs. While ISCB is not an adjudicating body, ISCB has appointed Ombudspersons who can be consulted, give advice or help seek out appropriate authorities to further handle any form of harassment or assault.

In matters directly related to alleged acts of misconduct as it relates to the ISCB Ethics and Professional Code of Conduct that take place within the purview of ISCB, ISCB is committed to listening to and addressing complaints and to guiding complainants through options confidentially before the complainant decides how to proceed. This includes ISCB consulting on details for potential informal solutions or a formal complaint. The ISCB Ombudspersons can be approached and if necessary outside counsel or consultation may be sought.

ISCB ENVIRONMENTAL SUSTAINABILITY POLICY

We are living at a time of unprecedented human-driven environmental change that threatens catastrophic changes for society and the environment. Our science has great potential to contribute to environmental science and biodiversity research outcomes. We recognise that there is a cost to the environment in the way we operate both as a society and as a community of computational biology. It is ISCB's policy to conduct our business in an environmentally sustainable and accountable manner, in compliance with all relevant environmental legislation, and we are committed to reducing as much as possible adverse environmental impacts that may result from our operations.

We aim to:

Ensure sustainable consumption and production patterns by

- Avoiding use, wherever possible, of environmentally damaging substances, materials, and processes
- Working with our supply chain to identify and mitigate the environmental impacts associated with our activities
- Promoting a purchasing policy that gives preference, as far as practicable, to those products and services that cause the least harm to the environment.
- Aiming to reduce consumption of fossil fuels and identifying options to reduce travel when possible

Take urgent action to combat climate change and its impacts by

- Implementing policies and procedures that contribute to a reduction in the carbon footprint of the ISCB and all its activities. We will base our policies on sound scientific evidence in a transparent way
- Taking into account the direct environmental impact of our operations (including that of our meetings, travel, and the procurement of materials and services) and, where possible, make a positive contribution to the environment
- Improving our energy efficiency by actively managing energy in our operations and working closely with our conference venues to do the same when hosting ISCB events
- Reducing waste generation and increasing the proportion of waste that is recycled
- Measuring, monitoring and communicating the environmental performance of our activities to drive continual improvement in areas of significant risk and opportunity.

Create a global partnership for a sustainable future by

- Promoting a culture of environmental awareness among our membership and the wide computational biology community and encourage them to conduct their activities in an environmentally friendly manner
- Working with other agencies (such as funding agencies and research institutions) locally, nationally, and internationally to promote appropriate environmental policies
- Encouraging our members and the wider community to adopt and promote these aims in their own organizations

2019 STUDENT TRAVEL FELLOWSHIP CAMPAIGN

Student travel fellowships help propel young investigators toward important future discoveries. Join ISCB in giving students access to the principal role models within the field and help influence the paths of scientific careers. As government-funding opportunities continue to decline, ISCB is reaching out to the membership to help this important initiative. Each year, ISCB receives over 400 travel fellowship requests. With currently available funds, this can only support ~50% of these requests by providing partial funding to each recipient.

ISCB will continue the travel fellowhsip campaign in 2020. Consider making a donation to enable support of even more students with higer travel awards. We continue to do all we can but there is still more to do—your contributions at any level will allow us to reach more students. By donating to ISCB student travel fellowships, you are investing in the future of our science.

2019 ISCB WIKIPEDIA COMPETITION WINNERS

ISCB held its eighth 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.

2019 winners:
Felix Richter for RNA-Seq
Tiago Lubiana Alves for Multiomics
Benjamin Lee for K-mer

Each winner was awarded a one year complimentary ISCB membership and a monetary award given out at the ISCB Town Hall at ISMB/ECCB 2019.

ISCB MEMBER-GET-A-MEMBER CAMPAIGN

Personal testimony and endorsement is the highest compliment an organization could receive. Members participating in the program were rewarded with additional incentives which included discounted registrationsto ISMB/ECCB 2019, the flagship meeting of ISCB!

Winner:
Allan Orozco

Honorable Mention:
Perry Ridge
Christophe Dessimoz
Florian Klimm
Aida Ouangraoua

With the help of rresources provided by ISCB with the member toolkit (*https://www.dropbox.com/work/ISCB%20Marketing/ISCB%20Membership%20Tool%20Kit*), current ISCB members can be the force that pushes the growth of ISCB into the future.

SOCIETY CONFERENCES & HIGHLIGHTS

Live-steaming (and rebroadcast) of ISCB Conference Distinguished Keynotes:

Introduced in 2019 at ISCB's flagship meeting, ISMB/ECCB 2019, ISCB introduced ISCB Live as a way of reaching those unable to attend ISMB/ECCB 2019 spreading the scientific reach of the community. This progrram is now being used at all ISCB conferences.

As an ISCB member, this is complimentary and another member benfit and non ISCB members can register for a fee of $250 USD.

ISMB/ECCB 2019

ISMB/ECCB 2019 conference in Basel, Switzerland welcomed a recorrd breaking 2,000+ delegates! It continued to provided an intense multi- disciplinary forum for disseminating the latest developments in bioinformatics/computational biology, and foster dialogue, showcasing over 1,300 abstracts, 69 proceedings and 1,100 posters plus 19 community-led COSI tracks & workshops. Over the course of the 4 day conference, attendees had innumerable amounts of opportunities to come face to face with cutting edge science presented through outstanding keynotes (Nikolaus Rajewsky, Wil- liam Stafford Noble the ISCB Innovator Award Keynote, Alexis Battle, Christophe Dessimoz the ISCB Overton Prize Award Keynote, and Bonnie Berger the ISCB Accomplishments by a Senior Scientist Award Keynote).

As is the goal every year, ISCB strives to continually bring you the strongest and most robust flagship conference. This year ISCB introduced many new and exciting elements of the conference. ISCB was pleased to pres- ent the Live-steaming (and rebroadcast) of the ISMB/ECCB 2019 Distinguished Keynotes. ISCB members who were unable to attend the conference could watch the keynotes complimentary. Nonmembers were able to register for the ISMB/ECCB 2019 live broadcast for a nominal fee.

To help broaden the visibility of those who only submitted a poster, CompBio Ignite talks were introduced. During lunch periods over a couple days, attendees were able to present their work in 5 minute presentations.

The conference leading keynote was The Conference leading keynote was Nikolaus Rajewsky from Max-Delbrück-Centrum for Molecular Medicine in the Helmholtz Association.
Dr. Rajewsky gave a thorough and exceptional talk focusing on mapping the molecular journey of differentiating stem cells. He covered how using more genes to map the cell location within an organism makes the process easier, though current spatial cell protocols are based on those proposed in the 19thcentury. He went on to explain how temporal pathway maps determine what a cell will look like in the future, which tells you how it is differentiating. Minimal changes in RNA drive the cell cycle that they appear to be environmental genes (likely epigenetically regulated). He showed how using these techniques can map which cells are affected by genetic pathways, diagnostically relevant to cancers. He concluded that LifeTime aims to use these techniques to map disease progression to improve medicine.
The ISCB Innovator Award Keynote, William Stafford Noble, University of Washington, set the morning in motion with an engaging and enthusiastic keynote address on traveling across spaces: the power of embedding genomic and proteinic data into a latent space. His talk demonstrated how many machine learning methods work by translating data points from the space in which they reside to a new, latent space of either higher or lower dimension. His talk then focused on three settings in which a latent representation can help us make sense of complex genomic or proteomic data. In one case, they train a deep tensor factorization model to learn latent representations of genomics assay types, cell types and genomic positions. These learned embeddings then turn out to be useful not only for imputing new genomics experiments, but also for a variety of other downstream machine learning tasks. In a second setting, they train a siamese deep neural network to embed tandem mass spectra into a latent space, such that spectra generated by the same peptide are close together. This learned embedding then provides a flexible framework for jointly analyzing hundreds of mass spectrometry experiments. Finally, he described how an unsupervised embedding approach can map diverse types of single-cell measurements into a latent space, effectively providing an in silico co-assay for experiments performed on similar sets of cells but using different experimental techniques.

The third keynote of the conference wasy Alexis Battle of Johns Hopkins University in Baltimore. Her dynamic presentation focused on Modeling the complex impact of common and rare genetic variation on gene expression The talk showed how non-coding and regulatory genetic variation plays a significant role in human health, but the impact of regulatory variants has proven difficult to predict from sequence alone. Further, genetic effects can be modulated by context, such as cell type and environmental factors. We have developed computational approaches to model the effects of regulatory variation, including predicting the impact of rare regulatory variants on gene expression, modeling the interaction between environmental factors and genetic variation, and detecting regulatory effects that vary over time courses. Her talk presented recent results evaluating the complex impact of both rare and common genetic variation on gene regulation in diverse contexts including different tissue types.

The intense science continued with the ISCB Overton Prize Award Keynote, Christophe Dessimoz who gave an engaging and illuminating presentation focusing on Challenges and rewards of benchmarking --- how to cope with a biased, incomplete, or even entirely missing ground truth.   Benchmarking has often been treated as an afterthought, but many practitioners have come to the realisation that benchmarking is critical for methodological progress. It can however be challenging to identify accurate ground truth datasets, avoid confounders, and draw general conclusions from specific test sets. Throughout his talk, he discussed some of these pitfalls and ways to overcome them. In particular, he focused on demonstrating examples on benchmarking sequence alignments, phylogenetic trees, ortholog prediction, gene ontology function prediction—including several unpublished results.

The final keynote of the conference, Accomplishments by a Senior Scientist Award Keynote, Bonnie Berger of Massachusetts Institute of Technology gave an exhilarating talk on Biomedical Data Sharing and Analysis at Scale.
Researchers around the globe are gathering biomedical information at a massive scale. However, growing privacy concerns and computational overhead limit researchers' access to these data.Through her talk, novel computational approaches was presented that help overcome these barriers to improve the scalability of essential biomedical analysis pipelines. She first described how modern cryptography presents a path toward broader data sharing and collaboration in biomedicine as demonstrated by her recent work on secure genome-wide association studies (GWAS) and pharmacological machine learning. Secondly, she built upon our initial introduction of compressive genomics, which capitalized on the growing redundancy and unique structure of biological data, to accelerate and enhance computational data analysis. She demonstrated how compressive techniques can be used to build compact summaries of rapidly growing single-cell transcriptomic datasets to facilitate their sharing and analysis. These results lay a foundation for more effective and collaborative biomedical research, whereby an unprecedented scale of data can be pooled from individuals and institutes across nations to enable novel life-saving discoveries.

See you next year in Montreal at ISMB 2020!

COSI HIGHLIGHTS FROM ISMB/ECCB 2019 & BEYOND...

NetBio

COSI representative to committee: Alexander Pico

We have focused on the annual Network Biology track at ISMB (and SIG previously) for the past 9 years. The ninth edition of NetBio attracted many of the ISMB/ECCB 2019 attendees with a high-quality program (2 keynotes, 2 proceeding talks, 13 selected talks). The talks covered a broad range of network biology topics from novel methods and tools to applied research examples. The first keynote by Christian von Mering focused on STRING, a widely adopted protein-protein interaction database, and its new feature to complement functional pathway analysis. In the last presentation of the day and the second keynote, Laura I. Furlong discussed the challenges of connecting genomics and network properties relevant for disease and drug response. The day ended with deep discussions during an excellent poster session with over 60 posters. The NetBio poster prizes went to Mijin Kwon, Sara Brin Rosenthal and Yannick Mahlich. We would like to thank all presenters and the audience for making this such a successful meeting.

EvolCompGen

COSI representative to committee: Christophe Dessimoz

The Evolution and Comparative Genomics (EvolCompGen) COSI hosted a one day-session at ISMB’19 on July 23, 2019, in Basel (Switzerland). The session included eight (8) proceedings talks and eighteen (18) short contributed talks selected from eighty-one (81) submissions. The presentations demonstrated the broad relevance of evolution and comparative genomics to computational biology. Talks addressed questions ranging from the evolution of cell lineages and driver mutations in cancer to reconstructing ancient events and deep homologies. Problems at the forefront of evolution, such as reconstructing phylogenetic networks, genome rearrangements, and assembly for experimental evolution, were an important component of the session. The problem of orthology inference and its role in function prediction has been hotly debated and has inspired spirited discussions. The organizers were delighted to note that many excellent presentations were given by students.

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

COSI representative to committee: Peter Cock

The 20th annual Bioinformatics Open Source Conference (BOSC 2019) was held as a COSI during the last two days of ISMB/ECCB 2019. The meeting report can be found at https://www.open-bio.org/2019/08/01/meeting-report-bosc-2019/. The two-day meeting included a total of 46 talks and 55 posters, all of which are listed in the complete schedule (https://www.open-bio.org/events/bosc-2019/bosc-2019-schedule/). BOSC participants also organized 8 Birds of a Feather (https://www.open-bio.org/events/bosc/bofs/). This year’s keynote speaker was University of Cape Town professor Dr. Nicola Mulder, who spoke on “Building infrastructure for responsible open science in Africa” (https://www.open-bio.org/events/bosc-2019/bosc-2019-keynote/).

3DSIG

COSI representative to committee: Rafael Najmanovich

3DSIG took place over the first two days of ISMB with a very strong program and even more exciting poster session. In the first day we had the privilege of hearing from Torsten Schwede about the maturation and challenges of Swiss-Model as a homology modelling tool that matured over 25 years into an extremely valuable and a service widely used by the scientific community at large. Talks during the day discussed modelling protein complexes and their interactions while the remaining talks in the day focused on protein design as well as chemoinformatics and drug design. Fifty years ago this week mankind took a giant step in space exploration. 3DSIG's Day 2 morning session highlighted the coming of age of methods for the template-free prediction of protein structure from sequence. In the words of John Moult who chaired the session, "the resolution of the classic protein folding problem" for monomeric proteins. A giant step in computational biology that has been deemed as the holy grail in biophysics at least since the introduction by Cyrus Levinthal of the famous apparent paradox in the same year that man landed on the moon. These methods use deep learning approaches to predict contact maps using accurate sequence alignments. Let's hope to witness in a future 3DSIG in less than 50 years the resolution of the protein folding problem for proteins without homologs where sequence alignments cannot be used to accurately predict contact maps. Additional talks focused on methods to identify and exploit surface similarities and allosteric sites in protein engineering and drug design respectively.

MICROBIOME

COSI representative to committee: Prof. Alice McHardy

Based on the results and discussions of the Critical Assessment of Metagenome Interpretation (CAMI) session of the ISMB MICROBIOME track in 2018, we prepared and organized the 2nd round of CAMI challenges. CAMI is a community-driven initiative aiming to evaluate methods for metagenome analysis comprehensively and objectively by establishing standards in the design of benchmark data sets, evaluation procedures, choice of performance metrics and questions to focus on. The 2nd round of challenges comprises metagenome assembly, genome binning, taxonomic binning, and taxonomic profiling challenges across several multi-sample data sets from different environments.

-We prepared and organized the 2019 MICROBIOME track of ISMB.
-We redesigned and launched the new MICROBIOME COSI website.

Regulatory and Systems Genomics (RegSys)

COSI representative to committee: Lonnie Welch

The Regulatory and Systems Genomics Community organized many activities throughout 2019 beginning with the ISMB Regulatory & Systems Genomics 2-day Track at ISMB/ECCB 2019 in Basel. Following that event, we held activities at ISCB's RECOMB/ISCB Conference on Regulatory and Systems Genomics and DREAM Challenges, Top Ten Papers in Regulatory and Systems Genomics. RegSys contributed to the CompBio:Wiki project by claiming pages related to regulatory and systems genomics and finally, created our twitter profile at https://twitter.com/ISCB_RegSys.

RNA-COSI

COSI representative to committee: Yoseph Barash

The 2019 RNA 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 RNA COSI aims also to promote interactions between computational and experimental RNA biologists and encourages participation from groups that are more experimental in nature. The 2019 RNA COSI track featured 21 talks highly computational in nature and 15 talks with stronger experimental input. This year we had an exciting line-up of 3 keynotes that covered advances and challenges in the study of the relationship between miRNA-dependent mRNA decay and translation (Dr. Ana Claudia Marques, Université de Lausanne), the identification of RBP binding sites and the analysis of ribosome profiling (Dr. Uwe Ohler, Max Delbrück Center for Molecular Medicine), and the contribution of each position of miRNAs on mRNA decay and the wider characterization of the regulation of translation (Dr. Mihaela Zavolan, Biozentrum – Universität Basel). 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, A to I editing, alternative polyadenylation, the integration of genomic and transcriptomic data, single cell and long-read sequencing analyses, methods for RNA secondary structure prediction, as well as novel experimental and computational tools to analyze the impact of RNA on cell homeostasis.

SysMod

COSI representative to committee: Tomáš Helikar

To increase the reach and impact of SysMod, we have taken steps to turn SysMod into an umbrella organization that integrates more specialized bio-modeling communities. This transition has included co-advertising activities with related communities such as the meetings of the CoLoMoTo Consortium for logical modeling and the online seminars of the Center for Reproducible Biomedical Modeling. We aim 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. The meeting featured three keynote talks, ten contributed talks, and four lightning talks. The meeting promoted discussion among the community about two major emerging themes: how to use modeling to help understand the physiology of microorganisms and how to use modeling to help understand, diagnose, and treat human disease. The 2019 meeting was the largest SysMod meeting to date. Over the past year, SysMod has also continued to maintain a community discussion list (e.g., for the announcement of impactful new research, meetings, job opportunities, etc.) and a community calendar (e.g., conferences, workshops, schools).

Education

COSI representative to committee: Russell Schwartz

At ISMB/ECCB 2019, the Education COSI put together a schedule of contributed and invited talks, posters, and one proceedings paper. Similar to the previous year, we consider the scheduled programme a great qualitative success in sharing some of the best work going on in our community, bringing in new ideas, and engaging members of the community beyond the core of educators active through the ISCB Education Committee and other focused society education initiatives. The final program consisted of three invited talks, eight contributed abstract talks, one contributed proceedings talk, and seventeen posters, of which eight accompanied platform talks and eleven of which were poster only.

bioinfo-core

COSI representative to committee: Rodrigo Polo

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/)

MLCSB

COSI representative to committee: Karsten Borgwardt

MLCSB has a steering board consisting of the following members: Florence d'Alché-Buc (Télécom ParisTech/Institut Mines-Télécom), Chloe-Agathe Azencott (Mines ParisTech, Institut Curie and INSERM), Karsten Borgwardt (ETH Zürich), Saso Dzeroski (Jožef Stefan Institute), Pierre Geurts (University of Liege), David Knowles (Columbia & NY Genome Center), Florian Markowetz (University of Cambridge), Yves Moreau (University of Leuven), Uwe Ohler (Max Delbrück Center for Molecular Medicine & Humboldt University), Gunnar Rätsch (ETH Zürich), Magnus Rattray (University of Manchester), Dick de Ridder (Wageningen University), Simon Rogers (University of Glasgow), Juho Rousu (Aalto University), Guido Sanguinetti (University of Edinburgh), Oliver Stegle (EMBL) and Jean-Philippe Vert (Google AI). The current president is Karsten Borgwardt. David Knowles, Florian Markowetz and Oliver Stegle joined in 2018/2019. Anna Goldenberg (University of Toronto) and Manfred Claassen (ETH Zürich) were the MLCSB program chairs at ISMB 2019.

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 22nd year at ISMB 2019, held in Basel, Switzerland on July 21-25, 2019. 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) and the W3C’s Healthcare and Life Sciences Community Group (HCLSCG), thereby increasing impact through new collaborations and broader dissemination.

CompMS

COSI representative to committee: Oliver Kohlbacher

At ISMB, the CompMS track was host to four proceedings papers, three invited speakers, and two speakers who were selected based on their submitted abstracts, plus a series of lightning talks.

Function

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 provided 7 travel fellowships, and had a high profile keynote speaker from Google AI. We were impressed by the gorowing level of interest in the CAFA challenge and the Fucntion 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

COSI representative to committee: Francisco De La Vega
HitSeq 2019 hosted 25 talks in a 20 day program, 9 of which came from accepted proceeding papers and the rest selected from abstract submitted. The accepted talks were grouped loosely in the following topics: 1) Cancer; 2) Assembly, string search and alignment algorithms; 3) Metagenomics; 4) Epigenetics and chromatin structure; 5) Single cell sequencing; 6) Genome structure; 7) DNA methylation; and 8) Transcriptomics. In addition, three keynote speakers were invited: Christina Curtis (Stanford), Andrew Adey (OSHU), and Zamin Iqbal (EBI).

Junior Principal Investigators (JPI)

COSI representative to committee: Shaun Mahony
JPI exists to support the advancement of junior faculty in computational biology and related disciplines. As such, we aim to provide support and advice to relevant junior faculty via a community of peers. During the course of the year, our primary mode of communication and networking is the New PI Slack group. New PI Slack is an online community of almost 2,000 junior faculty from various disciplines and with a worldwide membership. Membership is free and available to any junior faculty member. Interactions that are particularly relevant to the mission of JPI have been formalized in two New PI Slack channels: #iscb_jpi (~30 members, focused on ISCB-relevant activities); and #computational_pis (>200 members, broad computational/genomics discussions).
JPI also ran a BoF session at ISMB/ECCB 2019, focused on discussing the ISCB code of conduct. This session was moderated by Lucia Peixoto (WSU) and Casey Greene (U Penn). We also organized and participated in several informal networking events for junior faculty at ISMB/ECCB 2019.

GLBIO 2019

The conference is organized by the Great Lakes Bioinformatics Consortium to provide an interdisciplinary forum for the discussion of research findings and methods. An important goal for the conference is to foster long term collaborative relationships and networking opportunities within the domain of computational approaches to biology.

The program attracted over 270 delegates from 8 countries. Over the course of the meeting, delegates had the opportunity to participate in tutorials, hear from renown keynote speakers, get the latest updates in research sessions, and explore nearly 100 posters.

RSG 2019

Now in its twelfth 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 held at Memorial Sloan Kettering Cancer Center, in New York City, New York. Program activities Monday, November 4, 2019 and concluded on Wednesday, November 6, 2019 attracting over 170 delegates from 11 countries. Over the course of the meeting, delegates had the opportunity to participate in tutorials, hear from 11 renown keynote speakers, get the latest updates in over 50 sessions, and explore nearly 70 posters.

AFRICA 2019

The International Society for Computational Biology and the African Society for Bioinformatics and Computational Biology joined together to host the ISCB Africa ASBCB Conference on Bioinformatics in Kumasi, Ghana, November 11 - 15, 2019. The conference workshops were held on November 14-15. This meeting constitutes the sixth joint meeting of ISCB and ASBCB, and the seventh conference of the ASBCB on Bioinformatics of Africa.

The conference attracted nearly 80 delegates from 16 countries. Over the course of the meeting, delegates had the opportunity to get the latest updates in over 29 sessions, hear from 5 renown keynote speakers, and explore various topics thorugh visiting 65 posters.

ROCKY 2019

The Rocky series began sixteen years ago as a regional conference, and has grown into an international program with a spotlight on regional development in the computational biosciences. The presenters of the Rocky conference are scientists representing a broad spectrum of universities, industrial enterprises, government laboratories, and medical libraries from around the world. The meeting is a chance to get to know your colleagues near and far, seek collaborative opportunities, and find synergies that can drive our field forward.

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BioVis: Biological Data Visualization

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BOSC: Bioinformatics Open Source Conference

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CAMDA: Critical Assessment of Massive Data Analysis

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CompMS: Computational Mass Spectrometry

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Function: Gene and Protein Function Annotation

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HitSeq: High-throughput Sequencing

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MLCSB: Machine Learning in Computational and Systems Biology

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NetBio: Network Biology

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RegSys: Regulatory and Systems Genomics

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RNA: Computational RNA Biology

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SysMod: Computational Modeling of Biological Systems

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TransMed: Translational Medical Informatics

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VarI: Variant Interpretation

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