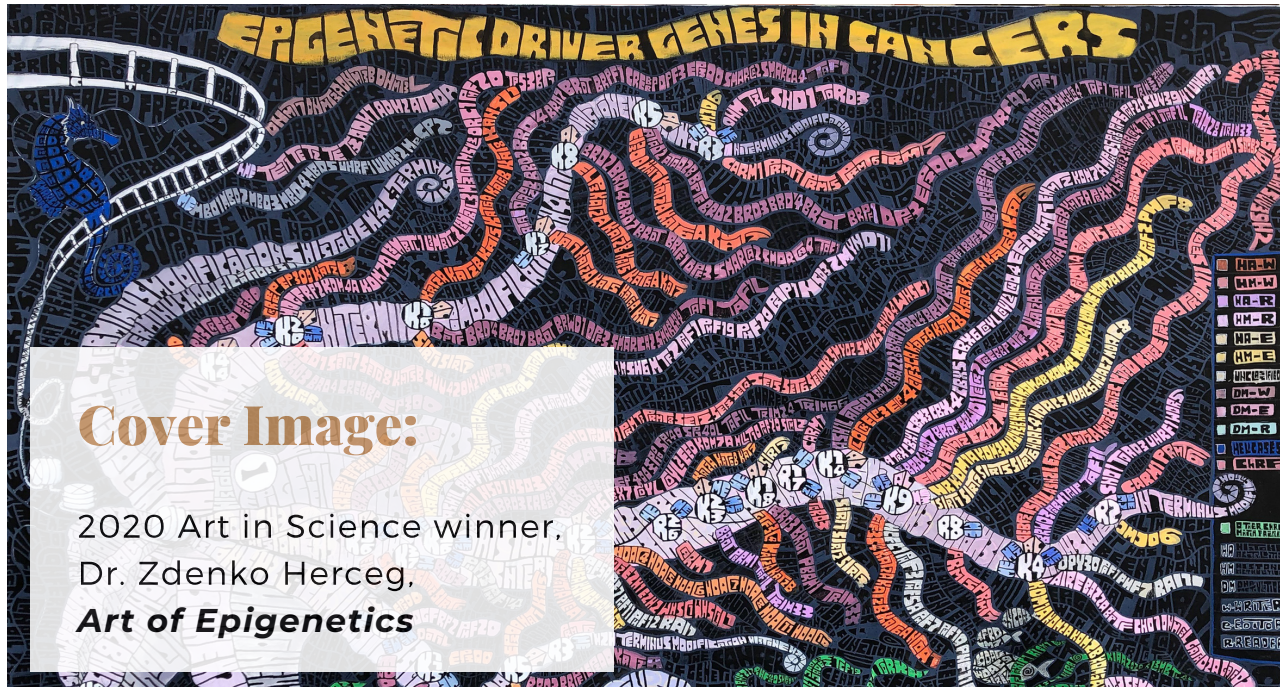


# FALL NEWSLETTER



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[HTTPS://WWW.ISCB.ORG](https://www.iscb.org)

Nearly 2400 participants gathered virtually July 13-16 for ISMB 2020 virtual, ISCB's first ever full-scale virtual conference. While it wasn't without its issue, overall attendees declared the conference a success.

2020 saw the changing of the world as we knew it. COVID-19 disrupted not only our lives but also how we navigate the world around us. ISCB faced the situation head on and instead of canceling or postponing ISMB 2020, the conference was moved to a 100% virtual landscape offering a greater international reach to audiences who never were able to attend before the ISMB conference. Though we missed Montreal, the opportunities a virtual ISMB 2020 offered were numerous. Those who have attended in the past found what they have grown to expect through live sessions, poster "halls", visits to the virtual ISCB Booth and so much more from the comfort of their homes. The first-time attendees were introduced to the cutting-edge science that makes ISMB 2020 the premier event in the bioinformatics calendar!

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 to the community to the best of our technical capabilities. In addition, the conference steering committee wanted to ensure relevance and goals to provide cutting-edge content 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 online networking 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 the best international developments in the field. This year ISMB showcased 22 COSIs participating with major computational biology themes ensuring a greater connection to researchers sharing common interests and an ability to come together and listen to exciting new developments in those areas of research. Each COSI ran their sessions (COSI tracks or workshops) as part of the conference. All attendees had the opportunity to attend any of these sessions in an either Live or via an on-demand format ensuring all time zones had equal access.

Throughout the four-day conference, attendees had the opportunity to hear and interact live with speakers delivering 5 renowned keynote speakers, 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 in Pediatric 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 and Topology enabling Genomics was the final morning's keynote.

The final keynote of the conference, ISCB Accomplishments by a Senior Scientist Award Keynote, Steven L. Salzberg, Johns Hopkins University. 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 Special Interest (COSI) tracks, Special Sessions, Technology Tracks, as well as a plethora of Workshops including Workshop on Bioinformatics Education (WEB), a Lunch and Learn showcasing The Black Women in Computational Biology Network. Finally, all attendees had access to 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 related fields, and provided an intense multidisciplinary forum for disseminating the latest developments in bioinformatics/computational biology in a 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 trying times. 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 and help in making ISMB 2020 such a success! We look forward to welcoming you to Lyon next year!



The promotional banner for ISMB ECCB 2021 Lyon features a collage of images on the left showing diverse attendees in various settings: a group discussion, a person at a computer, and a close-up of two people. The central logo for ISMB ECCB 2021 LYON includes the dates JULY 25-29. To the right of the logo, the text reads: **JOIN US AT THE PREMIER COMPUTATIONAL BIOLOGY MEETING OF THE YEAR! DISCOVER, INNOVATE AND CONNECT**. At the bottom, a dark blue banner with yellow text says: **MARK YOUR CALENDARS**. The ISCB logo is also present in the top left corner of the banner area.

“  
*The virtual landscape was*



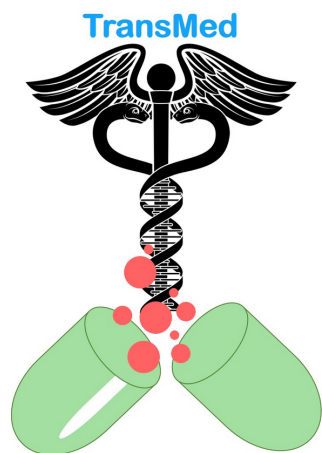
### SysMod

SysMod discussed various modeling techniques, including flux balance analysis, machine learning, and logical modeling, and their application to a multitude of biological systems. The three keynote talks focused on modeling cytokine responses, translation of observations from mouse to humans, and modeling approaches for drug discovery. Ph.D. students and postdocs gave several exciting discussions thriving to integrate more omics data to improve mechanistic understanding.



### TransMed

TransMed COSI of this year started with a very insightful keynote talk by Jason H. Moore discussing the 20 Challenges of AI in Medicine. Dr. Moore reviewed and summarised the challenges in (medical) data and machine learning methods and recommended the areas and directions of how these challenges could be tackled in the future. He emphasised that the purpose of discussion these challenges is to raise the awareness and to encourage more research in the area.

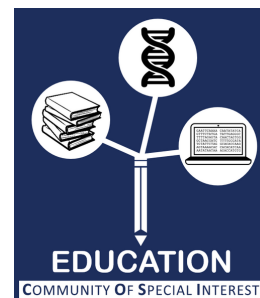


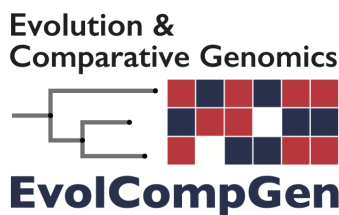
The proceedings talks as well as the talks selected from the abstracts covered different methodologies, especially machine learning and their applications in different translational medicine areas including different types of diseases (cancer, Covid-19), seasonal biological patterns, drug response, signaling networks, genotype-phenotype associations, pathways and health and lifespan in humans.

Our COSI session closed with another great keynote talk by Atul Butte on "Precisely Practicing Medicine from 700 Trillion Points of Data". Prof Butte highlighted the many freely available data resources currently existing that are still not being exploited to their full potential, including chemical information, clinical trial results and electronic health records. He advocated for the development of methods to effectively mine such datasets to extract clinically meaningful information, and discussed multiple success stories where his initial exploration of the data was converted into multi-million dollar start-ups. The impressive electronic health record database built by his group at UCSF is demonstrating the potential of such resources in predicting disease onset, evolution and outcome. Prof Butte emphasised the importance of maximising the use of data and technologies beyond scientific publications, and the fact that entrepreneurial initiatives are crucial to drive research endeavours towards societal impact.

### Education

The Workshop on Education in Bioinformatics (WEB) led off our education program Monday afternoon with a series of talks followed by group discussion and activities centered on the timely topic of moving education and training online. The Education COSI track on Tuesday then presented a broader full-day program on education in computational biology and bioinformatics with a selection of invited and contributed talks. The program included keynote talks by Bérénice Batut on building an infrastructure for comprehensive and current bioinformatics training and by Rafael Irizarry on online data science education, as well as a series of short talks on a educational experiences and strategies covering a diverse array of training environments, cohorts, and objectives.





## EvolCompGen

The Evolution and Comparative Genomics (EvolCompGen) COSI track at ISMB2020 featured a stimulating mix of proceedings and contributed talks on 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. If you would like to stay in touch with the EvolCompGen COSI, make sure to update your ISCB member profile by adding this COSI to your Interest Areas, and follow the COSI on twitter @EvolComp.

## iRNA

The iRNA COSI had a successful and lively meeting, with four invited keynotes, a live and animated panel discussion on long read RNA-seq, 18 talks from abstracts and 5 proceedings talks. 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. The iRNA COSI covered wide topics of interest for RNA computational biologists such as transcriptomics (including a keynote presentation by Ana Conesa), noncoding RNA biology, RNA metabolism (with a keynote from Athma Pai), RNA alignments and structure prediction (with a keynote presentation from Jérôme Waldspühl) and RNA subcellular localization (with a keynote from Éric Lécuyer).



## CAMDA

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 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 - join us and help shape the next competitions at [www.camda.info](http://www.camda.info)!

## MICROBIOME

The well-attended MICROBIOME COSI track featured inspiring keynotes by Niranjana Nagarajan and Amy Willis, highlighting the value of long-read sequencing for strain-level genome recovery and approaches to reduce biases in microbial abundance estimates. Talks about the second round of benchmarking challenges organized by CAMI, the Initiative for the Critical Assessment of Metagenome Interpretation, highlighted current challenges for the field.





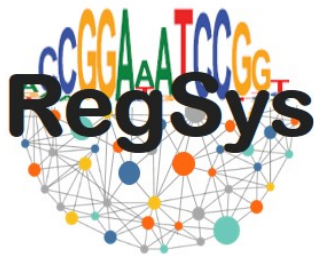
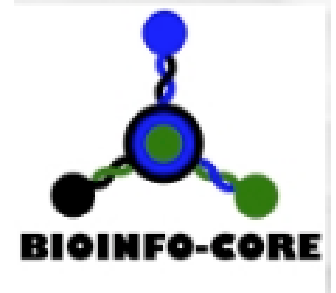


## JPI

The Junior PI COSI had two enjoyable meetups via Café Connect with our fellow new investigators. JPI discussions continue during the year as a channel within the @NewPISlack - a peer support network with over 2,000 other new principal investigators. We encourage all junior faculty and group leaders in the ISCB community to connect (<https://newpislack.wordpress.com>).

## bioinfo-core

The bioinfo-core COSI held a virtual session exploring both present and perennial topics, including spatial transcriptomics, single cell analysis, bioinformatic capacity building, and mentoring and management of bioinformatics cores. In small breakout groups, participants were able to meet colleagues from diverse cores, functions and backgrounds and discuss these topics in greater depth. The discussions were presented to the room and we look forward to our upcoming café connect zoom meetup for further sharing and brainstorming. Please see our wiki for more details, slides and notes. (<http://bioinfo-core.org/>)



## RegSys

The two days of RegSys attracted a large number of participants, with an average of 130 attendees at any given time attending each of our six sessions. We enjoyed exciting keynote talks from Wyeth Wasserman, Sara Mostafavi, Dana Pe'er, Francesca Luca, Christina Leslie, and Quaid Morris, three proceedings papers, and eleven contributed talks. Our sessions in Day 1 focused on advances in the application of interpretable deep learning approaches to problems in regulatory genomics, new methods for understanding 3D chromatin organization, innovative approaches for comparing regulatory programs across species, and advances in inferring regulatory relationships from single cell data types. Keynotes and contributed talks demonstrated cutting-edge developments in the use of neural networks for interpreting and predicting transcription factor DNA-binding sites in high resolution across cell types and species. The keynotes in particular gave wonderful overviews of progress in regulatory genomics over the past decade, while simultaneously spurring thought and discussion about future directions in the field. Day 2 focused on linking regulatory genetic variants to human diseases and phenotypes, with several talks characterizing regulatory genomic signals that explain cancer phenotypes. Presentations illustrated the power of characterizing regulatory variants in large populations of individuals or single cells, demonstrating that new technologies are enabling the detection of regulatory variants that explain complex traits. Our keynote speakers gave inspiring talks showing how to leverage large collections of regulatory genomics data to generate better understanding of the regulatory programs driven by DNA- and RNA-binding proteins. We had a very enjoyable virtual program overall, with well-attended Café Connect sessions spurring stimulating discussions.

## Text Mining

At the Text Mining COSI, keynote speaker Dr. Cathy Wu discussed her research into knowledge discovery through integrating literature mining, data mining and semantic computing. Keynote speaker Dr. Russ Altman explored advancing understanding of drug actions through mining literature and social media to support drug repositioning and analyze adverse effects. A frequent theme for both session talks and posters was applying deep learning methods to biomedical literature and social media for text classification, entity recognition and relation extraction, with additional themes in best practices for preparing text datasets for text mining - or even a single article before publication. The COVID-19 panel included demonstrations and discussions of four systems automating aspects of evidence gathering, establishing mechanisms and exploring SARS-CoV-2 related literature and social media.



## ISCB-Latin America SolBio BioNetMX 2020 Virtual Symposium Offered Train the Trainer Workshop in Native Language (Spanish)

Through a collaboration with the EBI-EMBL CABANA Project, the ISCB-Latin America SolBio BioNetMX 2020 Virtual Symposium was able to offer a train the trainer workshop conducted in Spanish. Twenty participants were provided tools, skills, guidance, and tips for developing and providing training from other trainers with the theoretical and practical understanding and adaptation to the new challenges that we are facing. Participants explored a variety of methods to enable and encourage learning, examining the requirements for a successful course, and obtain appropriate feedback. The entire workshop was held in Spanish, the native language for these participants and the region of the event. This was the first time the conference series had offered such a program and it was really exciting to see a sold-out workshop.

The CABANA Project (<https://www.cabana.online>) will be offering another native language training in Portuguese in November (<https://www.even3.com.br/xmeetingxp2020/>).

ISCB, SolBio, and BioNetMX express their gratitude to the CABANA Project trainers (María Bernardi, CABANA Project, Patricia Carvajal López, CABANA Project, Piraveen Gopalasingam, EMBL-EBI, and Mindy Muñoz, CABANA Project ) for bringing this opportunity as part of the conference. It was a unique offering that all three organization hope to continue in future years!



## GREAT LAKES BIOINFORMATICS CONFERENCE

*The University of Minnesota – Twin Cities*

**May 10-13, 2021**



**SAVE THE DATES!**

**<https://www.iscb.org/glbio2021>**



## viralHackathon@ISMB2020 (11-16 July)

**Organizers:** Ravi Abrol (California State University Northridge); Philippe Youkharibache (NCI/NIH); Allissa Dillman (ODSS/STRIDES/NIH); Jiyao Wang (NCBI/NIH); Raul Cachau (ABCS/FNL); Tom Madej (NCI/NCBI/NIH)



The viralHackathon was organized to develop analysis and annotation tools for virus - cell surface proteins interactions. The two main goals of this virtual hackathon were: a) to develop open source software modules for universal biomolecular interactions analyses with focus on SARS-CoV-2 and other virus proteins; and b) To create a sustainable community of developers and designers for continued development of such tools

Four years ago, NCBI started developing iCn3D, a web based software to visualize and analyze molecular structures in 1D/2D/3D (Wang et al. 2020). The collaboration was extended to NCI to tackle immunotherapeutic protein design. The software is open source to invite a community of developers to add modules. We had our first Moonlight hackathon at ISMB 2016 in Orlando that led to an initial 2D visualization functionality as part of a number of projects. Recently, we started a second phase of development towards more in-depth analysis of molecular interactions. With the COVID-19 pandemic, we realized that some of the capabilities for sharing structures and structural analyses with peers, and in preprints through URLs could be a valuable mechanism to enable collaborative research between scientists. New functionality is being added to iCn3D to broaden its ability to analyze membrane proteins, cell surface proteins, and to bridge the worlds of sequencing, structure, and function. The structural information also needs to be made accessible to scientists with little knowledge in structure.

With these goals in mind, the viralHackathon@ISMB2020 was organized with six project teams: Integration of externally computed DATA (led by Raul Cachau); Jupyter widget to embed an

interactive iCn3D viewer in a notebook (led by Jiyao Wang); Differential analysis of viral protein sequence-variants interactions with host proteins (led by Philippe Youkharibache); Impact of viral protein sequence variants on protein domains and interfaces with a tool to evaluate impact of a mutation (led by Xavier Watkins and Philippe Youkharibache); Adding protein-ligand interactions descriptors useful for structure-based drug discovery (led by Ravi Abrol), and Creation of a Membrane Protein Extended Topology Standard for Surface Proteins (led by Ravi Abrol). The hackathon had 30 active participants from seven different time zones. Hackathon logistics and coordination was expertly managed by Allissa Dillman. All six teams made significant progress on tool development during the hackathon, which culminated with a Birds of a Feather session on the last day of ISMB 2020 with presentations on five tools/standards that came out of the hackathon: Dmol3D for visualizing interactions, iCn-ExoDATA for integrating external data in iCn3D, iCn-Jupyter-3D as a jupyter notebook implementation of iCn3D, IMPEToS for integral membrane protein extended topology standard, and sPLinter for analyzing protein-ligand interactions.

The hackathon was a resounding success as we not only made significant progress on many tools for biomolecular interactions involving viral proteins, but we also planted a seed of sustainable community development. Many of the participants showed strong interest for continued involvement and we plan to organize biannual hackathons to sustain both tools and community development.



## ISMB 2020 Award Winners - Special Edition

### Ian Lawson Van Toch Memorial Award for Outstanding Student Paper

*Efficient Exact Inference for Dynamical Systems with Noisy Measurements using Sequential Approximate Bayesian Computation*  
Yannik Schälte, Helmholtz Zentrum München, Germany

### RCSB PDB Poster Prize

*How proteins evolved to recognize an ancient nucleotide?*  
Aya Narunsky, Tel Aviv University, Israel

### Special Session Systems Immunology: Janssen Awards

**First:**  
*Single-cell transcriptomic analysis of SARS-CoV-2 reactive CD4+ T cells*  
Benjamin Meckiff, La Jolla Institute for Immunology, United States

**Second:**  
*Dissecting the heterogeneity of protein and transcriptional responses in human blood derived immune cells after T- and monocyte-specific activation*  
Nathan Lawlor, The Jackson Laboratory, United States

### 3DSIG COSI – Best Talk Awards

**First:**  
*SARS-CoV-2 spike protein predicted to bind strongly to host receptor protein orthologues from mammals, but not fish, birds or reptiles*  
Sd Lam, Universiti Kebangsaan, Malaysia

**Second:**  
Katrin Schöning-Stierand, Universität Hamburg - Center for Bioinformatics (ZBH), Germany

### Bio-Ontologies COSI – Best Talk Award

*Applying GWAS on UK Biobank by using enhanced phenotype information based on Ontology-Wide Association Study*  
Runar Reve, King Abdullah University Of Science and Technology, Saudi Arabia

### Bio-Ontologies COSI – Best Poster Award

*Semantic Variation Graphs: Ontologies for Pangenome Graphs*  
Toshiyuki T. Yokoyama, The University of Tokyo, Japan  
Simon Heumos, Quantitative Biology Center (QBiC) Tübingen, University of Tübingen, Germany

### BioVis COSI – Best Poster Award

*Grammar-Based Interactive Genome Visualization*  
Kari Lavikka, University of Helsinki, Finland

### CAMDA COSI – Best Talk Awards

**First:**  
*Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation*  
Cory Gardner, Saint Louis University, United States

**Second:**  
*Towards a metagenomics interpretable model for understanding the transition from adenoma to colorectal cancer*  
Carlos Loucera, Clinical Bioinformatics Area (FPS), Spain

**Third:**  
*Mechanistic models of CMap drug perturbation functional profiles*  
Maria Peña-Chilet, CIBERER, Spain

### CAMDA COSI – Best Poster Award

*Metagenomic Geolocation using Read Signatures*  
Dimitri Perrin, Queensland University of Technology, Australia

## ISCB CAREER CENTER

### ENGAGE INFORM RECRUIT

REPRESENTING ORGANIZATIONS WORLDWIDE  
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ISCB MEMBERS HAVE COMPLIMENTARY ACCESS TO THE ISCB JOBS BOARD

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ISCB MEMBERS GET FREE UPLOADS  
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**POST A JOB:**  
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## ISMB 2020 Award Winners - Special Edition Cont...

### EvolCompGen COSI - Best Talk Award

*On quantifying evolutionary importance of protein sites: A tale of two measures*  
Avital Sharir-Ivry, McGill University, Israel

### EvolCompGen COSI - Best Poster Award

*Reconstructing Tumor Evolutionary Histories and Clone Trees in Polynomial-time with SubMARine*  
Linda K. Sundermann, University of Toronto, Canada

### EvolCompGen COSI – Poster Special Mentions

*Joint clustering of single cell sequencing and fluorescent in situ hybridization data to infer tumor copy number phylogenies*  
Xuecong Fu, Carnegie Mellon University, United States

*A Pangenome and Comparative Pathogenomics Workflow for Bacterial Pathogens*  
Karn Jongnarangsin, Michigan State University, United States

*Highly-regulated and diverse NTP-based biological conflict systems with implications for emergence of multicellularity*  
Gurmeet Kaur, NCBI, NIH, United States

*A Computational Molecular Evolutionary Approach to Characterize Bacterial Proteins*  
Samuel Chen, Michigan State University, United States

### General Computational Biology – Best Poster Award

*Tigerfish: A Software Tool to Design Genome-Scale Oligonucleotide Hybridization Probes to Visualize Satellite DNA*  
Robin Aguilar, University of Washington Department of Genome Sciences, United States

### iRNA COSI – Best Poster Award

*A novel unsupervised learning approach combining protein interactions and transcriptomics to characterize the mRNA maturation machinery*  
Iryna Abramchuk, University of Ottawa, Canada

### NetBio COSI – Best Talk Award

Identifiability and experimental design in perturbation studies

### NetBio COSI – Best Poster Award

*Dynamic Microbial Association Networks in the Ocean*  
Ina Maria Deutschmann, Institute of Marine Sciences (ICM-CSIC), Spain

### SysMod COSI - Best Poster Awards

*First Identifying characteristic features of metabolic states using Genome-Scale Metabolic Models*  
Chaitra Sarathy, Maastricht University, Netherlands

### Second:

*Model reduction and optimal control for multicellular biological oscillator systems*  
Narasimhan Balakrishnan, Northwestern University, United States

### Third:

*Computational model reveals a stochastic mechanism behind germinal center clonal bursts*  
Aurelien Pelissier, IBM Research, Switzerland

### TransMed COSI Best Oral Presentation Award

#### First (tie)

*Longitudinal multi-omics profiling reveals two biological seasonal patterns in California*  
Ahmed Metwally, Stanford University, United States

#### First (tie)

*POCOVID-Net: Automatic Detection of COVID-19 From a New Lung Ultrasound Imaging Dataset (POCUS)*  
Jannis Born, ETH Zurich, Switzerland

#### Third

*A deep transfer learning model for extending in vitro CRISPR-Cas9 viability screens to tumors*  
Yu-Chiao Chiu, University of Texas Health Science Center at San Antonio, United States

### TransMed COSI Best Poster Awards:

#### First

Poster title: *Emulating clinical trials for precision medicine with causal inference: application to PDX data*  
Jonas Béal, Institut Curie, Paris, France

#### Second

*Single-sample pathway analysis using Pathway Impact Evaluation (PIE) of machine-learning based cancer classifiers*  
Jasleen Kaur Grewal, Canada's Michael Smith Genome Sciences Centre, Vancouver, British Columbia, Canada

#### Third

*From Population to Subject-Specific Reference Intervals*  
Murih Pusparum, Hasselt University & Flemish Institute for Technological Research (VITO)



## ISCB ANNUAL AWARDS - Call for Nominations

Annually, ISCB recognizes four scientist through its Awards program, as well as hosts a variety of computational science related competitions.



Nominations close Dec. 2, 2020

<https://www.iscb.org/iscb-awards>

## ISCB Invites Nominations for One of Its Highest Honors - ISCB Fellow

ISCB introduced the ISCB Fellows Program in 2009 to honor members that have distinguished themselves through outstanding contributions to the fields of computational biology and bioinformatics and welcomes the submission of nominations from our community of members for the Class of 2021 ISCB Fellows.

We newly consider two types of Fellow nominations:

**(i) Academic nominees**

**(ii) Industry nominees**

Only members can nominate. If you are not a current member, please renew your membership today!

**Nominations close December 08, 2020**



ISCB ANNOUNCES

## 2020 Excellent Student & Postdoctoral Paper Highlight Award

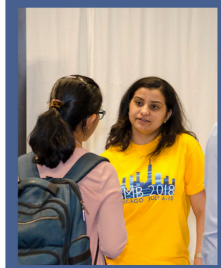
The Excellent Student and Postdoctoral Paper Highlight Award was created to celebrate the achievements of Student and Postdoc members throughout their training even during the years they are not able to attend ISCBs flagship conference, ISMB.



ARE YOU AN  
ISCB MEMBER IN  
GOOD  
STANDING?

SUBMIT YOUR  
PAPER TODAY

[HTTPS://WWW.ISCB.ORG/ISCB-EXCELLENT-STUDENT-AND-POSTDOCTORAL-PAPER-HIGHLIGHT](https://www.iscb.org/iscb-excellent-student-and-postdoctoral-paper-highlight)



ISCB'S 2020

# STUDENT SOFTWARE PRIZE

SUBMIT YOUR SOFTWARE  
TODAY

- ☐ SOFTWARE USABLE ON MAJOR OP SYSTEMS
- ☐ LICENSE RECOGNIZED BY OPEN SOURCE INITIATIVE
- ☐ SELF NOMINATIONS ACCEPTED

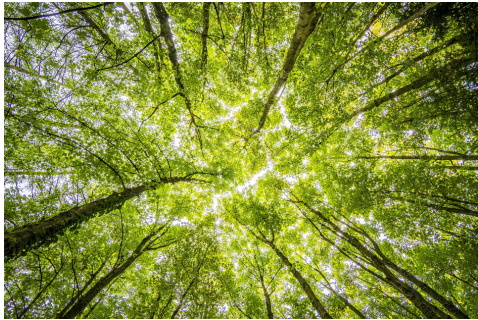
[WWW.ISCB.ORG/THE-ISCB-STUDENT-SOFTWARE-PRIZE](https://www.iscb.org/the-iscb-student-software-prize)

CONGRATULATIONS TO THE 2019 WINNER, TEPIC



## ISCBs Initiative Corner

### Green ISCB: ISCB Groves



The International Society for Computational Biology (ISCB), in partnership with All Things Small and Green and Trees for Life, has 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.

We welcome you to join us as we work towards healing our environment.

Learn more about [The ISCB Grove](#), how to [calculate your carbon emissions](#), and [purchase trees](#).

### ISCB Equity, Diversity and Inclusion



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.

Components of the 2020-2021 Equity, Diversity, and Inclusion (EDI) Strategic Plan

- Increasing social accountability for change in the society
- Obtaining data and developing measures to assess progress
- Voluntary training: The "ISCB Awareness toolkit"
- Recruitment initiative
- Mentoring

[Read ISCB's Equity, Diversity and Inclusion Strategic Plan](#)  
[Read ISCB's awareness toolkit](#)

Equity, Diversity, and Inclusion statements and policies:  
[A Safe Space \(ISCB Code of Conduct\)](#) and  
[ISCB's Statement on Countering Social Injustice](#)





## Upcoming Events of Interest

### **BBCC2020 - 15th Bioinformatics and Computational Biology Conference**

Italy - (NA) - Portici, Naples

Nov 16, 2020 through Nov 18, 2020

<https://www.bbcc-meetings.it/>

### **International Conference on Bioinformatics 2020 (InCoB2020)**

Virtual Event

Nov 25, 2020 through Nov 29, 2020

<https://incob.apbionet.org/incob20/>

### **16th International Symposium on Bioinformatics Research and Applications**

Russia - Moscow

Dec 01, 2020 through Dec 04, 2020

<https://isbra.confreg.org/>

### **Pacific Symposium on Biocomputing (PSB) 2021**

Virtual Event

Jan 05, 2021 through Jan 07, 2021

<http://psb.stanford.edu/>

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