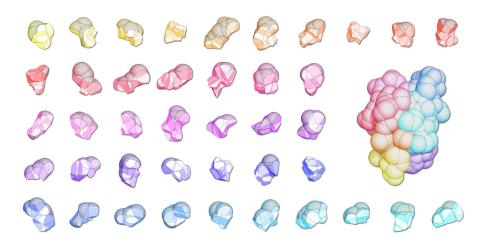
ISCB NEWSLETTER



Congratulations to the 2019 ISCB Art in Science Award Winner!

Dr. Kliment Olechnovic
Disassembled tessellation

ISMB/ECCB 2019 Recap

The ISMB/ECCB 2019 conference in Basel, Switzerland welcomed over 2,000 delegates! The conference was opened by the ISCB President, Thomas Lengauer, welcoming attendees and introducing the conference opening keynote, Nikolaus Rajewsky of the Max-Delbrück-Centrum for Molecular Medicine in the Helmholtz Association. Completing the opening evening, attendees were invited to the welcome reception with exhibitors giving them the opportunity to seek out information on new technologies, platforms and ideas, in addition to peruse the ISCB jobs board and introduce themselves to recruiters onsite for professional development opportunities.

ISMB/ECCB 2019 provided an intense multidisciplinary forum for disseminating the latest developments in bioinformatics/computational biology, and foster dialogue. Over the course of the conference, attendees had innumerable amounts of opportunities to come face to face with cutting edge science presented through outstanding keynotes (Nikolaus Rajewsky, William 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).

continued...

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 present 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. For those who only choose to submit a poster at ISMB 2020, be on the lookout for the Comp Bio Ignite talks sign up!

In addition to having access to incredible science through talks and presentations, professional development and a focus on opportunities in the field was a prominent part of the conference with the ever popular ISCB Career Fair.

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News from the Student Council



With nearly 400 attendees participating and interacting with 25+ recruiting entities from industry, university and the like, the Career Fair was a notable event. The Career Fair allowed for a designated time for engaging discussion among talented candidates seeking positions in the field of computational biology and bioinformatics. If you are a recruiter looking for talent, be sure to reserve your spot for next year! Spots go FAST!

If you missed ISMB/ECCB 2019, not to worry --- you can still check out many of the presentations online on the ISCB's You tube channel. https://www.youtube.com/c/ISCBScienceonDemand

Thank you to all who attended to make ISMB/ECCB 2019 a smashing success! We hope you enjoyed the conference. A special thanks to our conference chairs, Conference Co-chair Nicola Mulder and Conference Co-chair Torsten Schwede.

ISCB would also like to thank all of the many volunteers who dedicated time to review papers, abstract submissions, posters, technology talks, and travel fellowship applications. Without this dedicated community, we would not be able to produce such an outstanding event.

With over 1,000 posters, new events and 2,000+ attendees, ISMB/ ECCB 2019 was a robust meeting with intense science and something for everyone at every level of the career --- don't miss next year when

ISMB 2020 crashes Montreal, it will surely be the conference of the year

Visit our flickr page to view the conference photos! – https://www.flickr.com/photos/ismb/albums





JOIN US AT THE PREMIER COMPUTATIONAL BIOLOGY MEETING OF THE YEAR!

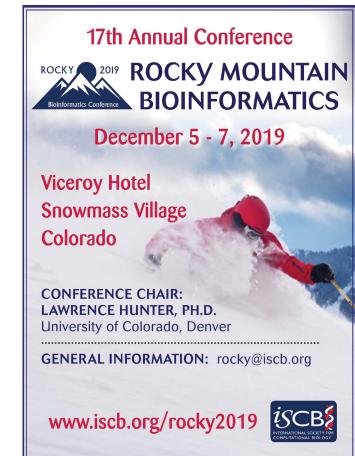
DISCOVER, INNOVATE AND CONNECT











Share the value & stories of ISCB with your students, colleagues, and friends!

MEMBER GET A MEMBER CAMPAIGN

START RECRUITING TODAY!

Recruit 5 members = 10% off ISMB registration
Recruit 10 members = 25% off ISMB registration
Recruit 15 members = 40% off ISMB registration
Recruit 25 members = complimentary registration to an
ISCB conference of your choice!



Meet the Incoming 2020-2023 ISCB Officers and Board of Directors

2020 will mark the Society's 23rd years of operation. As a member Society, each year the organization holds elections for the main leadership positions within ISCB. In July 2019, ISCB held its annual elections for Vice President, President-elect, and members of the Board of Directors.

Per the bylaws of the organization, the members of ISCB are the body who elect our officers and the current membership of the Board of Directors elect the open positions on the Board. Candidates for both categories are nominated by the membership in the open nomination period that begins in mid-February.

ISCB is pleased to welcome the newest elected members.

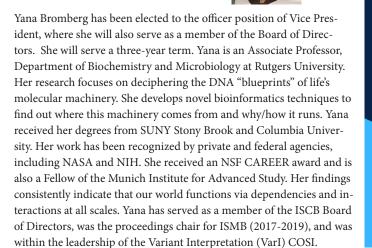
OFFICERS

President-elect Christine Orengo University College London



Christine Orengo has been elected to the officer position of President-elect. She will serve a one-year term as President-elect, a threeyear 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.

Vice President Yana Bromberg, **Rutgers University**



ISCB BOARD OF DIRECTORS

Michelle Brazas Ontario Institute for Cancer Research



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.



ISCB CAREER CENTER

ENGAGE INFORM RECRUIT

REPRESENTING ORGANIZATIONS WORLDWIDE START YOUR JOB SEARCH HERE!

IISC MEMBERS HAVE COMPLIMENTARY ACCESS TO THE ISCB **JOBS BOARD**

POST A CV:

ISCB MEMBERS GET FREE UPLOADS NONMEMBERS MAY PARTICIPATE FOR \$100 PER CV

ISCB MEMBERS RECEIVE COMPLIMENTARY POSTINGS AND CV REPOSITORY ACCESS NONMEMBERS CAN REGISTER & POST FOR \$300 PER JOB POSTING

LOOKING FOR A STRONG JOB CANDIDATE? ISCB'S CAREER CENTER IS THE PLACE TO START!

WWW.ISCB.ORG/CAREERCENTER



Cath Brooksbank EMBL-EBI

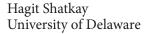
Communities of Special Interest Representative to the Board of Directors

Tijana Milenkovic University of Notre Dame



Tijana Milenkovic has been elected by the COSI Committee as the a COSI Representative to the Board of Directors. Tijana is an Associate Professor in the Department of Computer Science and Engineering and College of Engineering at the University of Notre Dame. She is the director of the Complex Networks Lab, and her research interests are in Complex networks and network mining,

Computational and systems biology, and Synthetic biology. Tijana has contributed to the organization of the Network Biology COSI meeting for the past 3 years. Significantly, in 2019, she took on the role of chairing Abstract Selection and Program Scheduling for NetBio. She has also been an active organizer of the Great Lakes Bioinformatics Conference. Tijana has also served as a member of the University of Notre Damn Committee on Women Faculty and Students, as the Department's Diversity and Inclusion coordinator, and a member of the organizing committee on establishing a new University initiative – that of Health and Well-being.



board for the Crick African Network.



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.

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 Interna-

tional Society of Computational Biology and a member of the advisory



MAKE THE MOST OF ISCB

Whether you're a lifetime member of ISCB or have just become a member, the resources below will help you make your membership with ISCB work for YOU!

The International Society for Computational Biology (ISCB) is a scholarly society for advancing understanding of living systems through computation and for communicating scientific advances worldwide.



Xuegong Zhang Tsinghua University

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.

I. Apply!

First, visit online and fill out the member form - it takes less than five minutes and your membership bomces activated the MINUTE you hit the submit button!

- LOGIN and complete or update your member profile
- ACCESS members-only resources, such as the career center, ISCB Live,
- FIND a long list of upcoming conferences and events near you at discounted rates!

2. Get Connected!

Next, get connected to other poeple in the field, find your COSI and take yourself to the next level

- CONNECT with other members through the online database of other ISCB members (3,500+ connections
- KEEP UP ISCB news and events through the bi-weekly ISCB Buzz and quarterly online Newsletters
- FIND the COSI (Community of Special Interest) that best fits your specialty and interest through involvment in topically-focused collaborative communities

3. Get Involved!

Now, use your expertise and time to give back to your profession

- VOLUNTEER your time and get involded with conferences, reviewing submissions and using your interests and expertise to help guide society committee!
- VOTE for the leadership of the society --- help shape the future!
- SUPPORT those in the filed broaden their involment and growth by donating to the society or helping to fund travel fellowships to help the next generation of scientsts!



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.

ISCB Overton Prize Award

The Overton Prize was established by the ISCB in memory of G. Christian Overton, a major contributor to the field of bioinformatics and a member of the ISCB Board of Directors who died unexpectedly in 2000. The annual prize is awarded for outstanding accomplishment to a scientist in the early to mid-career stage (up to a decade post-degree), who has already made a significant contribution to the field of computational biology.

ISCB Accomplishments by a Senior Scientist

The Senior Scientist Accomplishment Award recognizes a member of the computational biology community who is more than two decades post-degree and has made major contributions to the field of computational biology.

ISCB Outstanding Contributions to ISCB Award

The Outstanding Contributions to ISCB Award is in recognition of outstanding service contributions by any member toward the betterment of ISCB through exemplary leadership, education, service, or a combination of the three. *Nominees must be members of ISCB!*

ISCR Innovator Award

The ISCB Innovator Award is given to a leading scientist, 10-20 years post-degree, who consistently makes outstanding contributions to the field of computational biology and continues to forge new directions.









Annual Awards Deadline - December 2. 2019

Submit a Nomination!

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

Mark Your Calendar!

Upcoming official ISCB Conferences

Adv Comp Bio 2019 Nov 28 - 29, 2019 La Pedrera. Barcelona, Spain

ROCKY 2019

December 5 - 7, 2019

Aspen/Snowmass,

Colorado, USA

PSB 2020 January 3 - 7, 2020 The Big Island of Hawaii

ISMB 2020 SAVE THE DATE! July 12 - 16, 2020 Montréal, Canada

preLights – a community platform for preprint highlights

A recent explosion of preprints in biology

The posting of preprints (non-peer-reviewed manuscripts) has rapidly taken off in the biological sciences in the past 5 years. Since the launch of bioRxiv in 2013, both preprint submissions and readership numbers have grown exponentially: currently, bioRxiv registers over 2,000 uploaded preprints and over a million downloads per month. Among the various fields in biology, computational biologists are one of the largest users of bioRxiv, also shown by the fact that the second largest category on the server is 'Bioinformatics'.

The recent adoption of the preprint workflow by biologists, and their use in physics and mathematics for nearly three decades, can be explained by the numerous benefits that preprints offer. They are freely available, speed up the dissemination of research and accelerate the progress of science by allowing researchers to build on new findings, often months before publication in a journal. Authors can also benefit from community feedback, which strengthens their manuscripts and generates additional attention for their research. While some scientists still have concerns about preprinted work getting 'scooped', preprints can and have been used as a way to establish priority, since they are date-stamped and citable. Posting preprints is particularly useful for early-career researchers (ECRs), as it facilitates career progression; many hiring committees and funders now consider and encourage citing preprints in applications. But, above all, preprints promote a culture of 'openness' in science, and the majority of publishers now have journal policies compatible with preprint posting.

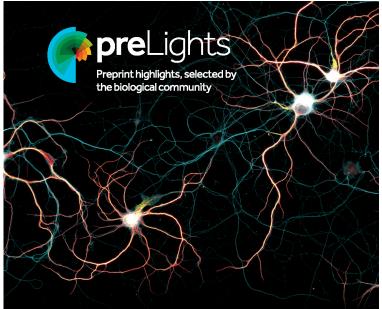
ECRs in the spotlight: selecting, highlighting and commenting on preprints for the community

While preprints can open up discussion of non-peer-reviewed research by the entire scientific community, there has been limited public commenting on preprints so far. A further challenge of preprint posting is volume: over time, it will become increasingly difficult to navigate and keep up with the preprint literature. To address these challenges, The Company of Biologists launched preLights (https://prelights.biologists.com/) - a community platform for selecting, highlighting and commenting on preprints across the biological sciences - in February 2018. At the heart of preLights is the team of ECRs (called 'preLighters') who select which preprints to feature and then summarize the key findings of the preprint, highlighting why they think the study is interesting/ important. Uniquely, the preLighters often directly question preprint authors about their work, and the resulting discussions are published at the end of the article.

Not only does preLights raise awareness of preprints and the associated research but it also aims to promote and support the ECRs who write the posts. Becoming a preLighter provides a great opportunity to gain experience in science communication, to keep up-to-date with the latest research in the field and to build a scientific network through exciting interactions with fellow scientists. Each preLighter also has the opportunity to create their own 'Community' profile, and several have been featured in the 'Meet the preLighters' interview series on the site.

Become a prelighter!

We are keen to grow our team of ECRs (PhD students, postdocs and early PIs) and increase the contribution from the computational biology/bioinformatics community. Interested? For more information and details of how to apply, go to https://prelights.biologists.com/about-us/.



preLights is the preprint highlighting service run by the biological community and supported by The Company of Biologists. Our dedicated team of early-career researchers select, highlight and comment on preprints they feel are of particular interest to the community.

We are looking for new preLighters from the fields of computational biology and bioinformatics.

Join the team if you:

- are an early-career researcher who enjoys writing and communicating science
- would like to join a network of scientists who are enthusiastic about preprints
- are willing to regularly select, highlight and comment on preprints in your field

Interested? Apply by sending an email to prelights@biologists.com

prelights.biologists.com

@preLights #preLights f/preLights





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 2020 ISCB Fellows.

Nomination are accepted from any ISCB member and must be made using the online nomination form, which requires a one-two sentence description of why this person is being proposed, a detailed half-page statement of motivation (500 words maximum) on why this is a good nominee, and a CV (as either an uploaded document or a bullet-point list created by the nominator).

We newly consider two types of fellow nominations:

- (i) Academic nominees: These are nominees who have done the bulk of their work in academia, including government and research institutions. Such nominations must demonstrate primarily excellence in research, which includes the development of methods or resources that advance research. The nomination can be strengthened by pointing to service to the computational biology community, education and/or administration.
- (ii) Industry nominees: These are nominees who have done the bulk of their work in industry. Such nominations must demonstrate primarily the impact of their industrial work on the field. The nomination can be strengthened by pointing to research, education, or service to the computational biology community, e.g. by providing research infrastructure.

Nominees will be assessed on the magnitude and quality of contributions to the field of computational biology based on the information provided during the nomination process. Once elected, fellows will not be classified as type (i) or (ii) above. This distinction is only relevant during the election process.

ISCB is accepting nominations through December 4, 2019. Visit https://www.iscb.org/iscb-fellows-program to learn more about the program and to submit your nomination! *https://www.iscb.org/cb-login*

COSI Session Highlights from ISMB/ECCB 2019

BioVis: Biological Data Visualizations

The 9th edition of BioVis attracted over 300 participants, which broke last year's record. We had great keynotes by Lindsay Edwards and Petra Isenberg. We started with an overflowing room for Lindsay's talk about the importance of visualization for understanding deep learning models. In the afternoon, Petra gave an inspiring talk about the value of visualization and how to actually assess that. The program featured a further 13 abstract talks and 17 poster lightning talks concerning exciting visual analysis systems that tackle biological data, from phylogenetic trees to T-SNP data. The award for the best talk went to Mathias Witte Paz. The best poster award went to Mark Keller, Welles Robinson, and Mark Leiserson.





3D-SIG: Structural Bioinformatics and Computational Biophysics

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.

NetBio: Network Biology

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.



RegSys: Regulatory and Systems Genomics



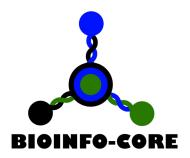
RegSys, over the course of two days hosted six exceptional keynote talks and multiple sessions. Contributed talks of first day started with reports of new experimental and computational methods developed for characterizing the 3D organization of the genome. Later talks focused on the use of computational methods including deep learning techniques for characterizing changes in miRNA expression, TF binding and cooperativity as well as chromatin accessibility, and linking them to different cellular outcomes. Enhancers and their diverse roles were common themes across many talks highlighting the importance of studying non-coding regions in Regulatory and Systems Genomics. The second day of RegSys attracted a large number of participants who enjoyed three amazing keynotes and ten contributed talks organized in three sessions. The main themes of the day were cutting edge developments in the field of single-cell experiments, and in transcription factor binding to specific DNA sequences. We heard about exciting discoveries enabled by comparing single-cell (sc) data from different organisms or by integrating different modalities such as scRNA-seq and scATAC-seq. Benchmarking work of single-cell network inference methods highlighted the limitations of current methods. Several presentations demonstrated the power of interpretable machine learning methods, including deep learning techniques that are able to work at the basepair resolution, in enabling a better understanding of gene regulatory programs through refined characterization of transcription factor binding.

BOSC: Bioinformatics Open Source Conference

BOSC 2019, the 20th annual Open Source Bioinformatics Conference, kicked off two days with a full room and a flurry of tweets (#BOSC2019). Chair Nomi Harris started things off, noting that BOSC has been held in 12 different countries, 6 US states and 2 Canadian provinces. Heather Wiencko introduced the Open Bioinformatics Foundation, BOSC's parent organization, and Kai Blin discussed the OBF's participation in Google's Summer of Code. The two morning sessions focused on data--representing it, storing it, crunching it. BOSC-related lunchtime Birds of a Feather (BoFs) included a "Welcome to BOSC" get-together and a well-attended CWL discussion (CWL originated as a BOSC BoF five years ago!). In the afternoon, the audience was treated to a keynote talk by University of Cape Town professor and ISCB Board Member Nicola Mulder, who spoke on "Building infrastructure for responsible open science in Africa." Sharing data in Africa involves technical, ethical and social challenges ("It's really hard to convince people to share their data and their tools when they have such a history of being exploited," she observed), but despite these obstacles, the H3ABioNet Consortium (of which Prof. Mulder is a PI) is making progress in building, a pan-African bioinformatics network.

The final afternoon session focused on Open Data; FAIR was a common buzzword. BOSC finished out the day with an hour devoted to additional BoFs. The evening ended with a poster session included 55 BOSC posters. The second day included many Late Breaking Lightning Talks, Workflows, Containers, and Open Science. BOSC attendees shared their enthusiasm in nearly 2000 tweets (hashtag #BOSC2019) over the two days of the meeting. The meeting closed with an announcement about our two-day Collaboration Festival (#CoFest) on Friday and Saturday at the nearby Swiss Innovation Hub for Personalized Medicine. BOSC 2020 will be held in collaboration with Galaxy's Community Conference (as we did in 2018) in Toronto, but we hope to return to ISMB in 2021. The OBF/BOSC thank our sponsors for helping to support the CoFest and our ongoing Travel Fellowship program: AWS, Google Cloud, eLife, PLOS Comp. Biol., GigaScience, The Hyve, KNIME and the Software Sustainability Institute.





Bioinfo-core

The bioinfo-core COSI held a heavily attended session 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. The discussions were presented to the room and we look forward to our upcoming social events for further sharing and brainstorming. Please see our wiki for more details, slides and notes. (http://bioinfo-core.org/)

IRB: Integrative RNA Biology

The RNA (IRB) COSI got off to a great start with our first of 3 keynote talks by Ana Claudia Marques, who provided strong evidence that miRNA-dependent decay of transcripts requires translation, explaining a lack of effect of miRNAs on lncRNAs. Many of rest of the day's talks, chosen from abstracts and proceedings, continued on the same theme integrating genomic and transcriptomic data and drawing important biological conclusions, while others discussed innovative novel tools covering diverse aspects of RNA biology. After a memorable and informative quiz at the traditional dinner on a river-side terrace last night, the RNA (IRB) COSI got to a great start this morning with talks on transcriptome annotation, assembly and analysis across different organisms and in disease. The RNA COSIfeatured two great keynote presentations today. Uwe Ohler discussed the importance of taking RNA abundance into consideration and multitask learning for bias correction for the identification of RBP binding sites in transcripts, finishing off with an approach for ribosome profiling with insights including into micropeptide identification and translation of lncRNAs. Mihaela Zavolan presented the importance and contribution of each position of miRNAs on mRNA decay and translation, then leading to the wider and insightful characterization of the regulation of translation, finding it to be pervasive, coupled to many other processes and dynamic. Other contributed talks of the day discussed novel tools and approaches as well as studies characterizing splicing/alternative splicing, A to I editing and alternative poly-adenylation, leading to important biological insights. Overall, the 2-day RNA COSI featured diverse and thought-provoking talks, great scientific exchanges and many opportunities to network.



Must See ISCBtv!

Did you miss ISMB/ECCB 2019?

Not to worry! Recorded talks from the premier comp bio conference of the year have now been posted to ISCB's YouTube channel!

Check them out now & visit https://www.youtube.com/c/ISCBScienceonDemand!

Interested in being a part of the COSI grroups? Visit ISCBconnect and sign up for COSIs that interrest you!

https://www.iscb.org/cms_addon/cosi/

Message from the ISCB Student Council Symposium Africa 2019

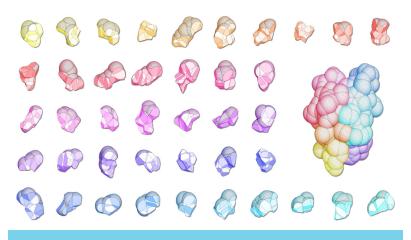
Wisdom A Akurugu (SCS Africa 2019 Co-Chair), Mahtaab Hayat (SCS Africa Chair), Sayane Shome (RSG Chair), and Farzana Rahman ((ISCB Board of Directors Representative)

On 11 November 2019, the ISCB Student Council's (ISCB-SC) African region celebrated its 3rd edition of the Student Council Symposium (SCS Africa 2019) in Kumasi, Ghana. The SCS Africa took place during the annual bioinformatics 2019 meeting organised by the International Society for Computational Biology and the African Society for Bioinformatics and Computational Biology (ASBCB). Since SCS Africa's inception in 2014, the African regional students and early career scientists played an active role to organise the biennial SCS Africa meetings. SCS Africa 2019 was chaired by Mahtaab Hayat (University of the Witwatersrand, South Africa) and Wisdom A Akurugu (University of Cape Town, South Africa). Several student leaders and volunteers from African and European region were instrumental in making the 3rd edition of African SCS a success. The symposium started with a welcome message from Dr. Samson P. Salifu from the Kwame Nkrumah University of Science and Technology, Ghana.

The delegates were delighted to have listened to outstanding keynotes from Prof. Christine Orengo (Founder of CATH Database and Professor at UCL, UK) and Dr Amel Ghoulia (Bioinformatician at H3ABioNet and Mozilla Science Fellow). Prof. Christine Orengo inspired delegates as she talked about her journey to Bioinformatics from Physics and her group's work on evolutionary tales of LUCA (Last Universal Common Ancestor). Dr. Amel Ghoulia gave an encouraging keynote on open science and importance of scientific collaboration. Eight students and early career researchers presented their research in the oral presentation sessions. Wisdom A. Akurugu (University of Cape), David Twesigomwe (University of Witwatersrand) and Isabel Mensah's (Kwame Nkrumah University of Science and Technology) presentations were voted best three presentations at SCS Africa 2019. Prof Alia Benkhala, the President of ASBCB, announced and presented the best presentation awards to the award winners. The SCS Africa team thanks to the generous support of ISCB, ISCB Student Council and ASBCB team for collaborating to make the 2019 symposium an outstanding event.



Executive Committee



Upcoming Events of Interest

CAGI Worrkshop: Assessing the Future of Genome

Interprretation

UNITED STATES — CA — San Francisco DEC 6, 2019 THROUGH DEC 8, 2019 https://genomeinterpretation.org

GIW/ABACBS 2019

JOINT INTERNATIONAL CONFERENCE ON GENOME INFORMATICS AND ABACBS ANNUAL CONFERENCE AUSTRALIA — NSW — SYDNEY DEC 09, 2019 THROUGH DEC 11, 2019 https://www.abacbs.org/ conference2019/about

2019 ISCB Student Regional Group — Southeast USA Computational Biology Symposium UNITED STATES — FL — ST. PETERSBURG DEC 13, 2019 THROUGH DEC 14, 2019 http://rsg-se-usa.iscbsc.org/

BIOSTEC 2020

13TH INTERNATIONAL JOINT CONFERENCE ON BIOMED-ICAL ENGINEERING SYSTEMS AND TECHNOLOGIES FEB 24, 2020 THROUGH FEB 26, 2020 ISCB Member Discount: 10% http://www.biostec.org

24th International Conference on Research in Computational Molecular Biology (RECOMB 2020) Italy - PD - Padova May 10, 2020 through May 13, 2020 https://www.recomb2020.org/ Thomas Lengauer, Ph.D.

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