

ISCB NEWSLETTER

FALL 2016 ISSUE 03

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The Dark Proteome

EXCITING HIGHLIGHTS FROM ISMB 2016

The 24th annual Intelligent Systems for Molecular Biology (ISMB) meeting kicked off on Sunday July 10th, 2016 at the Swan and Dolphin Hotel in Orlando, Florida. As in years past, the flagship ISCB meeting was preceded by two days of well-attended smaller meetings organized around specific topics, including special interest group (SIG) and satellite meetings and applied knowledge exchange sessions (AKEs). ISMB 2016 conference co-chair Pierre Baldi officially opened the conference and welcomed delegates, and he acknowledged the tireless work of his co-chair Teresa Przytycka, the steering committee, the scientific organizing committee and theme chairs in shaping this year's conference program.

Ruth Nussinov of Leidos Biomedical Research, Inc., National Cancer Institute/NIH, United States and the Sackler School of Medicine, Tel Aviv University, Israel was the ISCB Fellows keynote speaker and delivered the first major talk of the conference titled "Ras signaling: a challenge to the biological sciences." Activating Ras mutations have been found in numerous cancers, including pancreatic, colorectal, and lung cancer and melanoma, but no drugs or therapies exist that target Ras. Nussinov discussed her work examining structural and mechanistic characteristics of different Ras isoforms, which can guide the development of drugs that target Ras without inducing drug resistance.

The second keynote talk was delivered by Debora Marks of the Department of Systems Biology, Harvard Medical School, United States, winner of the 2016 Overton Prize for early

Marks's talk, "Molecular structure and organism fitness from genomic sequences," highlighted her recent work on de novo 3D structure prediction using a global probability model of a sequence, for which several structures have been validated by 3D structural studies published by other groups. Marks also discussed her most recent work using couplings and context information to predict epistatic interactions and understand impact of mutations.

Sandrine Dudoit of the Division of Biostatistics and Department of Statistics, University of California, Berkeley, United States delivered the third keynote address on Monday, July 11 titled, "Identification of Novel Cell Types in the Brain Using Single-Cell Transcriptome Sequencing." She described her work showing that olfactory stem cells help replace sensory neurons and non-neural support cells, and presented her "SCONE" software package for single cell transcriptome normalization that was instrumental to this work. She also discussed the importance of computational reproducibility and how it differs from biological reproducibility, an issue that is at the heart of much of the work presented at ISMB.

Sarah Teichmann of EMBL-EBI and Head of Cellular Genetics at Wellcome Trust Sanger Institute, Hinxton, United Kingdom gave the fourth keynote talk on Monday afternoon on "Understanding Cellular Heterogeneity." Dudoit and Teichmann's talks both highlighted the emerging field of single-cell transcriptomics (RNAseq), which was seen throughout ISMB 2016. She discussed her work using high throughput single cell RNA sequencing to quantify cell-to-cell variation at the transcriptome level. Her research combines bioinformatics and wet lab work,

IN THIS ISSUE

[Highlights from ISMB 2016](#)

[Meet Your New Board](#)

[Call for ISCB Fellows Nominations](#)

[Call for ISCB Award Nominations](#)

[Mark Your Calendars!](#)

[A Learning Experience in](#)

[Computational Biology](#)

[2016 Wikipedia Competition](#)



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Plenary Keynote Speakers



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Associate Professor, Chemistry and
Biochemistry; Director, National Bio-
medical Computation Resource,
University of California, San Diego



Edison T. Liu, M.D.
President and CEO,
The Jackson Laboratory



Rainer Fuchs, Ph.D.
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ISMB 2016 ~~APPS~~ ~~CVU~~Continued...

which has come together recently in many of her findings, including her observation that T helper 1 cells and T follicular helper cells originate from a single cell.

Serafim Batzoglou of the Department of Computer Science, Stanford University, United States is the inaugural winner of the ISCB Innovator Award, and delivered the fifth keynote talk on the morning of July 12th. His talk was titled "Computational Challenges in Personalized Genomics." He discussed the radical transformation of sequencing technology and algorithms that have contributed to the current state of rapid and low cost sequencing. Like Dudoit and Teichmann, he highlighted his work using technologies that enable single cell RNA expression analysis, and he ended his talk pointing out the current challenges facing the field, particularly where to store data, and how to share, analyze, and learn from it.


The final keynote speaker was Søren Brunak of the Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark, winner of the 2016 Accomplishments by a Senior Scientist Award. Brunak gave a talk titled, "Creating disease trajectories of time-ordered comorbidities from big biomedical data covering millions of patients," during which he described his research using genomic and electronic health record data from a large portion of the Danish population to predict chronic disease trajectories. Brunak's project highlighted the potential power of population-wide genome studies, especially when coupled with health-related data.

Other highlights of ISCB 2016 included the bustling poster sessions and the annual ISCB Town Hall meeting, during which ISCB President Alfonso Valencia and other members of the executive board presented "The State of the ISCB," and members of the audience were invited to ask questions and provide feedback toward shaping the future of the Society.

The enduring work of former ISCB President Burkhard Rost was also recognized during the meeting when he was awarded the 2016 Outstanding Contributions to ISCB. Other awards were also presented on the closing day, including presentation of the Wikipedia competition winners and awards for outstanding presentations and posters.

See you next year at
ISMB/ECCB 2017 in Prague, Czech Republic!
July 15-19, 2017





RegSyGen with Dream Conference 2016

The RECOMB/ISCB Conference on Regulatory and Systems Genomics (RSG), with DREAM Challenges and Cytoscape Workshop, is scheduled to be held on November 7-9 this year in Phoenix, AZ. Now in its ninth year, the RSG conference is one of the premier annual meetings in the fields of regulatory genomics, systems biology, and network visualization.

This year, features an outstanding lineup of keynote lectures as well as oral presentations of research abstracts selected by a program committee of eminent researchers. Keynote speakers include men and women working at the forefront of the fields of transcriptional regulation, protein-RNA interactions, regulatory networks, tumorigenesis, genome visualization, and biostatistics. In addition to eight keynote lectures, the conference is scheduled to have nearly 30 research talks and multiple poster sessions.

As in other years, the RSG conference is co-organized with the DREAM challenges workshop where ongoing community participation in several current challenges will be showcased through talks and posters. The DREAM challenges are an open science effort where highly topical problems in bioinformatics and systems biology are tackled in a crowdsourced manner, with several teams registering to first compete with each other and then collaborate in solving the problem ("challenge") on a specific data set. This year's challenges include problems related to drug synergy, viral susceptibility, disease modules, tumor subclonality and transcription factor-DNA binding.

A workshop dedicated to the popular biological network visualization tool Cytoscape will be another highlight of this year's conference. With so much exciting research packed into just three days, the RSG conference is shaping up to be a one-stop shop for regulatory genomics and systems biology researchers.

For more information, visit www.iscb.org/recomb-regsysgen2016

ISCB-LA 2016: EXCITING SCIENCE IN ARGENTINA



Mark your calendars for the dynamic ISCB-LA A2B2C!

The fourth International Society for Computational Biology Latin America Bioinformatics Conference (ISCB-LA), jointly organized with A2B2C, will take place in Buenos Aires, Argentina, on November 21 - 23, 2016.

ISCB-LA A2B2C will attract top regional and international scientists in the life sciences and offers a strong scientific program focused on scientific discovery in diverse subject areas through bioinformatics/computational biology. Topics of interest will include sequence analysis, evolution and phylogeny, comparative genomics, protein structure, molecular and supramolecular dynamics, molecular evolution, gene regulation and transcriptomics, RNA biology, proteomics, systems biology, ontologies, biological networks, databases and data integration, text and data mining and information extraction, and human health. See you in Argentina for 5 distinguished keynotes, 40+ talks, numerous posters and so much more!

For more information, visit www.iscb.org/iscb-latinamerica2016



**UPCOMING
CONFERENCES: MARK
YOUR CALENDAR!**

RegSyGen with DREAM Challenges & Cytoscape Workshop

November 6-9, 2016
Phoenix, AZ

ISCB-Latin America 2016

November 21-23, 2016
Buenos Aires, Argentina

Rocky 2016

Dec 8-10, 2016
Aspen/Snowmass, CO

NGS 2017


April 3-5, 2017
Barcelona, Spain

GLBIO 2017

May 15 - 17, 2017
Univ. of Illinois at Chicago

ISMB ECCB 2017

July 15-19, 2017
Prague, Czech Republic





ISCB's Annual Wikipedia and Wikidata Competition -- Furthering Computational Biology Knowledge and Training the Next Generation of Wikipedians

Wikipedia has become one of the most widely used sources of scientific information in the world, especially for students and the general public. Since 2012, ISCB has hosted an annual competition to judge Wikipedia entries created by students or trainees, which has supported the education mission of the Society and improved the coverage of computational biology topics in Wikipedia. Winners of the competition are awarded prize money as well as an annual membership to ISCB.

ISCB recently hosted a Wikipedia and Wikidata editathon at ISMB 2016 to promote the competition and highlight the Wikipedia Year of Science 2016. This editathon provided informal training for creating and editing Wikipedia articles and Wikidata entries. For the competition, Wikipedia entries must fulfill the criteria required of all Wikipedia articles and must also be within the scope of computational biology. Entries can include completely new articles, but most competitors work on existing articles within the Computational Biology WikiProject. ISCB has created various guidelines and resources for this competition, including the WikiProject Computational Biology page and the "Ten Simple Rules for Editing Wikipedia" article from PLOS Computational Biology. As of 2015, ISCB has also supported a separate Wikidata competition in parallel with the Wikipedia article competition to improve the Wikidata entries related to computational biology.

TCourse instructors have started using the competition as an exercise for students, which has helped drive up the number of high quality entries that are contributed each year. Alex Bateman of EMBL-EBI is one of the organizers of the ISCB competition and has helped guide this initiative since its inception. He has observed that students that work in pairs or groups are often more successful in creating well balanced and clearly written entries. This reflects the collaborative environment of Wikipedia, whereby editors across the globe work toward creating articles that are accurate, neutral in tone, able to be understood by the general public yet informative to subject-matter experts.

This year's competition is open from July 13, 2016 to December 31, 2016: https://en.wikipedia.org/wiki/Wikipedia:WikiProject_Computational_Biology/ISCB_competition_announcement_2016

Encourage students or trainees to try their hand at a Wikipedia entry, not only for their own training and experience, but as a way to improve their science communication skills and give back to the computational biology community.




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DO YOU HAVE A RECORDED RESEARCH
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SUBMIT TO THE COMMUNITY ON **ISCBtv!**

Send your video to ncostello@iscb.org



Meet the Newly Elected Members of the 2017 Executive Committee and Board!

Incoming ISCB Officers




President-Elect – Thomas Lengauer, Department of Computational Biology and Applied Algorithmics, Max Planck Institute for Informatics, Saarbrücken, Germany. Thomas Lengauer, Ph.D. (Computer Science, Stanford University, 1979), Dr. rer. nat. (Mathematics, Free University of Berlin, 1976), is a Director at the Max Planck Institute for Informatics and Adjunct Professor at Saarland University and the University of Bonn. He is a founding member of ISCB and is currently serving as a member of the Board of Directors, in which he served in all years except 2002 to 2005, and of the Executive Committee where he currently serves as Vice President. Lengauer has chaired the ISCB Awards Committee from 2005 to 2007, where he assisted in the development of a revised selection process. He was also Scientific Chair of ISMB 1999 (Heidelberg) and 2007 (Vienna), as well as an Area Chair in several ISMB conferences. Lengauer is a Fellow of our Society. He will be President-Elect from January 2017 to January 2018 and will become President of the Society in January 2018, serving a three-year term. His research interests and activities include structural bioinformatics, molecular docking and computational chemistry, computational epigenetics and bioinformatics for disease, especially, viral resistance analysis.




Vice President – Janet Kelso, Bioinformatics Research Group Leader, Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany. Janet Kelso, Ph.D. (Bioinformatics, University of the Western Cape, 2003), is a Bioinformatics Research Group Leader and Minerva Professor of Bioinformatics at the Max-Planck Institute for Evolutionary Anthropology. She is currently serving as a member of the ISCB Board of Directors (2005 - present), is the ISCB Conference Council Co-chair, has served on the ISMB Steering Committee since 2006, as well as an ISMB Conference Co-chair in 2014 and 2015. Kelso has played instrumental roles in the development of the ISCB conference series and served on the Executive Committee in both the position of Secretary (2006-2011) and Vice President (2011-2013). Kelso is a Fellow of our Society. She is also the Executive Co-editor for Bioinformatics, and serves on several other editorial boards. Kelso will serve her three-year term as Vice President starting in January 2017. Her research interests span questions in evolutionary and comparative genomics. She has participated in the development of methods for the analysis of ancient DNA and in the analysis of the genomes of archaic and early modern humans. Most recently her group has studied the functional implications of the admixture between humans and Neanderthals.


Incoming Board Members




Michelle Brazas, Ph.D. Program Manager, Informatics & Biocomputing, Ontario Institute of Cancer Research. Brazas has been involved in bioinformatics training and education throughout her career, including her work on ISCB's Education Committee, as an ISMB tutorial chair and with GOBLET (Global Organization for Bioinformatics Learning, Education and Training). At the Ontario Institute of Cancer Research, Brazas manages operations and cultivates collaborations of the interdisciplinary research teams at the Institute.



Dan DeBlasio, Ph.D. ISCB Student Council Representative. Department of Computational Biology, Carnegie Mellon University. DeBlasio has been a member of the ISCB Student Council and has served as web committee co-chair and on the Student Council Symposium organizing committee. DeBlasio received his Ph.D. in 2016 from the University of Arizona and is currently a Lane Fellow in the Computational Biology Department of the School of Computer Science at Carnegie Mellon University.



Nicholas Le Novère, Ph.D. Group Leader, Babraham Institute. Le Novère has been an active member of ISCB and has served as an ISMB SysMod Special Interest Group organizer and Common NetBio/SysMod COSI organizer. Le Novère has research interests in both computational biology and neurobiology, and he has also developed systems biology resources, including the SMBL and SBGN standards and the BioModels database.



Hagit Shatkay, Ph.D. Associate Professor, Computer & Information Sciences, University of Delaware. Shatkay has actively served ISCB in different capacities, including work on the ISMB Proceedings Papers Committee and the Conferences Advisory Council. Shatkay's research interests include biomedical literature mining, and she applies machine learning approaches to a variety of biomedical data.

Re-Elected Board Members



Burkhard Rost, Ph.D. Alexander von Humboldt Professor Chair, Bioinformatics & Computational Biology Department, Technical University Munich. Rost has served ISCB tirelessly as ISCB president, past president, and vice president. Rost has research interests in protein structure and function prediction, with a focus on predicting protein-protein interactions and understanding the effects of individual amino acids.



Reinhard Schneider, Ph.D. Head of Bioinformatics Core Facility, Luxembourg Center for Systems Biomedicine, University of Luxembourg. Schneider has served ISCB in multiple ways, including his tenure as treasurer and vice president. Schneider's work as head a bioinformatics core group includes handling large amounts of data generated by researchers at his institution and developing new algorithms to advance data analysis.

BUSY FALL FOR FASEB PUBLIC AFFAIRS

During a busy summer for the Federation of American Societies for Experimental Biology (FASEB), FASEB's Office of Public Affairs focused its efforts on advocating for issues important to our members and envisioning the Federation of the future.

FASEB successfully lobbied the Western Interstate Commission for Higher Education to remove mention of creationism from its Interstate Passport Initiative governing student transfers. FASEB also is continuing efforts to prevent an increase in the Small Business Innovation Research set-aside, which would reduce the funding available for competitive grants to all other parts of the research community.

Of prime concern to FASEB this fall is the completion of the appropriations process to fund federal science agencies. During a long August congressional recess, FASEB staff and volunteer leadership organized local meetings in congressional districts across the country to discuss these funding bills. A FASEB e-action alert supporting a three-month continuing resolution (CR) generated more than 7,200 messages to Congress in September. Congress approved the CR, which will keep federal offices open and funded until December 9.

Once Congress returns to Washington after the election, FASEB's Office of Public Affairs will focus on encouraging Congress to move quickly to complete action on an omnibus funding bill. Such a bill would combine the 12 individual measures passed by the appropriations committees earlier this year, including a \$2 billion increase for NIH proposed by the Senate Labor, Health and Human Services Subcommittee. Increased funding is also pending for competitive research supported by the United States Department of Agriculture. Failure to pass an appropriations package would leave these funding increases on the table.

In August, FASEB's annual Science Policy Symposium explored how the contributions of scientists are measured and evaluated. The symposium, titled "Making an Impact: Evaluating Research and Investigators' Contributions in the Biological Sciences," kicked off with a keynote address by Hannah Valentine, MD, Chief Officer for Scientific Workforce Diversity at the National Institutes of Health (NIH). The symposium featured robust conversations about the metrics used to evaluate researchers and their work.

Also, this summer, the Federation began a series of strategic discussions about the Future of FASEB. Dynamic dialogue during the June Board meeting led FASEB President Hudson Freeze, PhD, to create four task forces to address the future of FASEB's mission, governance, campus, and services. Recommendations from the task forces will be discussed by the FASEB Board this fall.

The International Society for Computational Biology (ISCB) is a member of FASEB, and its delegate to the FASEB Board is Harel Weinstein, DSc. ISCB member David Rocke, PhD, is FASEB Treasurer and heads the Federation's Finance Committee

To learn more about FASEB's efforts to support science funding, sign up to receive the Washington Update newsletter and FASEB's e-action alerts.





ISCB Members are Gamifying genome annotation: a learning experience in computational biology

Ivan Erill¹, Steven Caruso¹ & Jim Hu²

¹ Department of Biological Sciences, University of Maryland Baltimore County

² Department of Biochemistry and Biophysics, Texas A&M University

With the advent of high-throughput technologies, the life sciences have progressively shifted their balance from the bench to the desktop, posing novel challenges to research and education in this field. In spite of many notable efforts, equipping the task force of tomorrow to efficiently navigate the complexity of big-data life sciences remains an outstanding challenge in undergraduate science education. Among other things, the next generation of biologists and biomedical practitioners must be able to aptly navigate biomedical repositories, make use of bioinformatics pipelines, interpret their results and put them into context. The informed use of bioinformatics pipelines and biomedical repositories obviously requires some degree of training in the fundamental bioinformatics methods and principles underlying such platforms, as well as familiarity with their use. However, and perhaps most importantly, being able to assess and appropriately contextualize the information generated by these platforms also requires the ability to access, critically read and interpret primary literature sources. Here we explore the use of an intercollegiate annotation competition in the context of a bacteriophage genome annotation course as a means to provide basic training in bioinformatics methods and biomedical repositories, while stimulating students to read scientific articles and critically interpret the findings reported therein.

As part of the HHMI SEA-PHAGES program, the UMBC Department of Biological Sciences offers two laboratory Phage Hunters courses for biology majors. The first is dedicated to the isolation and characterization of bacteriophages using microscopy and molecular microbiology methods. The second is devoted to the annotation of the genomes that are sequenced for some of the isolated phages. The functional annotation of the gene products encoded by bacteriophage genomes is a fundamental component of the genome annotation course. Due to their high diversity and rapid divergence, performing functional annotation on phage genomes is notoriously difficult. The proliferation of high-throughput sequencing has made available many phage genome sequences, but experimental work characterizing gene functions on these novel phages is scant. As a consequence, the functional assignment is almost exclusively done through orthology. In the Phage Hunters genome annotation course, students are given theoretical and hands-on training on biomedical repositories, (e.g. PhagesDB, NCBI RefSeq and UniProt), the Phamerator phage comparative analysis suite and two mainstream tools for orthology detection

(BLAST and HHpred), making special emphasis on the assumptions underlying these algorithms, the critical interpretation of their output and the pitfalls of in silico chains of inference.

To enhance the quality of student annotations, and to guarantee that the annotation effort would become visible and useful for the scientific community, in 2015 UMBC Phage Hunters teamed up with Jim Hu, of Texas A&M University, which runs the inter-collegiate annotation competition CACAO (Community Assessment of Community Annotation with Ontologies) as part of the wiki-based Gene Ontology Normal Usage Tracking System (GONUTS). The first CACAO-Phage Hunters competition was piloted as an intramural competition at UMBC in 2015 and it was extended into a multi-college competition involving five SEA-PHAGES colleges in 2016. The Gene Ontology (GO) provides a hierarchical, comprehensive systematization of the biological role of a gene product, enabling curators to formally describe the involvement of a given gene product in a particular biological process, molecular function or cellular location. Given their broad use by the scientific community, the submission of GO annotations has to meet formal requirements to guarantee the accuracy of annotations. In particular, all GO annotations must cite a verifiable source containing the evidence on which the annotation is based. For regular GO annotations, the source is typically a peer-reviewed scientific article. When annotating phage genomes via orthology, the methods and criteria used to establish homology must be well-defined and citable. To this end, we created a specific GO reference (GO_REF:0000100) that accurately describes the SEA-PHAGES standards for orthology assignment.

The CACAO-Phage Hunters competition is organized in alternating, bi-weekly innings dedicated to annotations and challenges. Students work in teams, which compete against other teams from the same and other colleges using the CACAO wiki interface. Before the competition starts, students are given theoretical and hands-on training on ontologies and their usage, with particular emphasis on GO and its related tools (e.g. QuickGO). To perform annotations on a given gene, students must first identify orthologs of their gene of interest and assess whether these have available GO annotations. Since these are most frequently lacking, students must identify and read original research articles describing research on the identified orthologs to perform regular GO annotations, and use these as the basis for the orthology-based annotation of the phage gene.

A Learning Experience Continued...

Their claims can be challenged by competing teams, and students must address those challenges by revisiting their methods and their literature sources, and revise their annotations accordingly. On average, students read between one and three scientific articles for every successful annotation. Students and their teams are given credit for both accurate annotations and challenges, prompting them to carefully read and assess the experiments reported in the articles they and others use as sources for the annotations, as well as the validity of the bioinformatics methods used to infer orthology. As a result of the peer-competition scheme, students perceive the computational work and the reading of scientific literature as a competitive challenge, rather than an obligation, and discuss the in silico methodology and their interpretation of the findings in scientific articles with their peers, thereby bolstering the learning experience associated with the reading of primary literature and solidifying their understanding of the computational methods they employ.

The use of an intercollegiate competition framework to perform functional annotation of bacteriophage genomes provides an ideal framework to introduce essential bioinformatics concepts to biology undergraduate students, enabling them to critically assess their strengths and weaknesses and to take ownership of the inferences made through their use. It also motivates students to read primary literature sources, and to critically assess reported experiments in the context of bacteriophage biology. The approach has so far been validated in bacteriophage genome annotation, but the general framework is easily extensible to any other organism. If you have a genome to annotate, consider giving it a GO.

View this exciting research on
<https://f1000research.com/posters/5-2419>



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www.iscb.org/ISMB2016-career



CompBio Jobs



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ISCB congratulates Suzi Smith on her retirement!

Saying goodbye is always hard, ISCB would like to thank Suzi Smith for her 13 years of service to the Society. She will be greatly missed.

Messages to admin@iscb.org are still being received. Feel free to use this email for all ISCB related requests. If you wish to contact a staff member directly, you may do so by contacting:

Nadine Costello at ncostello@iscb.org for membership, marketing, travel fellowship eligibility, OUP sponsored memberships, mailing lists, and advertisement sales

Bel Hanson at bhanson@iscb.org for conference registration, affiliated conference application and approval, ISCBconnect, affiliated groups, ISCB committees, GLBIO, RegSyGen with DREAM

Diane Kovats at dkovats@iscb.org for payment processing, accounts payable, student council

The International Society for Computational Biology (ISCB) announces new **Emerging Global Threats Challenge Award**



Using computational approaches to combating the latest **emerging** global threats!

Deadline for submission is **April 10, 2017**

<https://www.iscb.org/iscb-global-threats-challenge>



JOIN YOUR **COSI** Community of Special Interest AND CONNECT



Communities of Special Interest (COSIs) are member communities of shared interest that are self-organized and have multiple activities or interactions throughout the year, rather than solely meeting during the SIG program of the ISMB 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.

Which COSIs
are right for
you?

Find
out at

www.iscb.org/iscb-cosis

Find out more and join in... <http://www.iscb.org/iscb-connect>

MEMBER GET A MEMBER CAMPAIGN

Do you have a vast network of potential professional members?



You've seen first-hand the value in ISCB membership, and now its time to share that value, your stories of ISCB with your students, colleagues, and friends.

Through our member-get-a-member campaign, we are asking members to be advocates of ISCB, to help us recruit new members and encourage previous members to come back. Our goal is to grow our membership, be the leading professional society for computational biology and bioinformatics, and the voice of our science.

Why is membership growth important? ISCB strives to develop a variety of programs for our members. Unfortunately, implementing these programs comes at a cost to the organization.

Through our Student Council, ISCBconnect, ISCBtv, and worldwide conferences, we strive to get our members connected and engaged. Through increased membership participation, we can do even more! Imagine more travel fellow-ships, online training, complimentary e-books, or even recorded talks from all of the official ISCB conferences. As membership grows, ISCB can use the additional funding to invest back in the organization and offer new programs.

<http://www.iscb.org/member-get-a-member>



ISCB ANNUAL AWARDS

Nominate a Deserving Scientist Today for One of Four ISCB Annual Awards!

ISCB Overton Prize Award

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CALL FOR **FELLOWS** NOMINATIONS!

The International Society for Computational Biology 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. During the inaugural year of the program, ISCB conferred the Fellow status on the seven winners-to-date of the ISCB Accomplishment by a Senior Scientist Award, and recognized these distinguished scientists during the ISMB/ECCB 2009 conference in Stockholm, Sweden. Since then ISCB has sought nominations from our community of members, which are reviewed and voted upon by a selection committee. New Fellows are introduced at each year's ISMB conference.

NOMINATE A FELLOW



UPCOMING AFFILIATED CONFERENCES

7th Annual Computational & Molecular Biology PhD Symposium

Ireland – Dublin

Dec 01, 2016 through Dec 02, 2016

Event URL: <http://compmolbiosymp.ucd.ie//>

ISCB Member Discount: 20 percent

Pacific Symposium on Biocomputing 2017

United States - HI - Big Island of Hawaii

Jan 03, 2017 through Jan 07, 2017

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

ISCB Member Discount: 50 USD

BIOSTEC'17: 10th International Joint Conference on Biomedical Engineering Systems and Technologies

Portugal – Porto

Feb 21, 2017 through Feb 23, 2017

Event URL: <http://www.biostec.org/>

ISCB Member Discount: 60 EUR

24th International Molecular Medicine Tri- Conference 2017

United States - CA - San Francisco

Feb 19, 2017 through Feb 24, 2017

Event URL: <http://www.triconference.com/> ISCB

ISCB Member Discount: 20 percent

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