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About ISCB. The International Society for Computational Biology (ISCB) was the first and continues to be the only society representing computational biology and bioinformatics worldwide. ISCB serves a global community of 3,000 scientists dedicated to advancing the scientific understanding of living systems through computation by:

- convening the world's experts and future leaders in top conferences
- partnering with publications that promote discovery and expand access to computational biology and bioinformatics
- delivering valuable information about training, education, employment, and relevant news
- providing an influential voice on government and scientific policies that are important to our members

SAVE THE DATE FOR ISMB 2014 – THE PREMIER CONFERENCE FOR THE WORLD'S COMPUTATIONAL BIOLOGISTS

The 22nd Annual Intelligent Systems for Molecular Biology (ISMB) conference will be a world class scientific meeting that brings together computational biologists and bioinformaticians of every career stage from diverse scientific disciplines. ISMB 2014 will convene at the John B. Hynes Memorial Convention Center in Boston, Massachusetts on July 11-15, 2014. ISMB is the flagship conference of the International Society for Computational Biology (ISCB). This unique meeting draws scientists from a broad range of fields that use computational biology and bioinformatics, including sequence analysis, comparative genomics, proteomics, structural biology, data mining, and systems biology.

ISMB 2014 is anchored by six keynote presentations from world-renowned scientists. Isaac (Zak) Kohane, the Director of the Children's Hospital Informatics Program and the Henderson Professor of Pediatrics and Health Sciences and Technology at Harvard Medical School, will be speaking on Sunday, July 13. Kohane's unique background in both pediatric endocrinology and computer science has enabled him to develop a research program that uses genomics to better understand the genetic basis of diseases, including autism and cancer. He has also developed computer systems that permit the use of information from electronic health records for genetic studies while maintaining patient privacy.

Sunday, July 13 will also feature a keynote presentation by Eugene (Gene) Myers, the 2014 recipient of the ISCB Accomplishment by a Senior Scientist Award. This award honors luminaries in the fields of computational biology and bioinformatics who have made significant contributions to these areas through research, education, and service. Myers is the Director and Tschira Chair of Systems Biology at the Max Planck Institute of Molecular Biology and Genetics in Dresden, Germany. Myers is well known for his work on developing the BLAST algorithm for sequence comparison, as well as his work on using shotgun sequencing to sequence the human genome at Celera Genomics. His research is now focused on computational bioimaging. He has developed new microscopic devices and software that are used for building 3D biological models, and these tools are providing unparalleled insights into the inner workings of cells and systems.

Michal Lineal, a Professor of Biochemistry, Molecular Biology, and Bioinformatics at The Hebrew University of Jerusalem, Israel, will be a keynote speaker on Monday, July 14. Linial is the Director of The Sudarsky Center for Computational Biology and is the first woman head of the Israel Institute for Advanced Studies. Her broad research activities encompass both "wet lab" projects and computational modeling, with particular interests in neuronal cell differentation and synapse formation, proteomic analysis of membrane proteins, and functional genomics.

The 2014 winner of the Overton Prize, Dana Pe'er, is featured as a keynote speaker on Monday, July 14 as well. The Overton Prize recognizes early- or mid-career scientists working in computational biology or bioinformatics who are rising leaders in these fields. Pe'er is an Associate Professor in the Department of Biological Sciences and Systems Biology at Columbia University. Her research focuses on understanding cellular and molecular networks at a holistic level by using computational approaches to analyze complex data sets.

Robert Langer, a Professor in the Department of Chemical Engineering at the Massachusetts Institute of Technology will give a keynote presentation on Tuesday, July 15. Langer is a prolific researcher who works on developing novel drug delivery systems, with a particular interest in using polymers to deliver therapeutic molecules like DNA and genetically engineered proteins. Langer's innovative work was recognized most recently when he was selected as a recipient of the 2014 Breakthrough Prize in Fundamental Physics and Life Sciences.

The last keynote presentation will be given on Tuesday, July 15 by Russ Altman, a Professor of Bioengineering, Genetics, and Medicine and Computer Science. Altman has been selected as this year's ISCB Fellows Keynote Speaker. He works on building and applying new algorithms to explore diverse topics including RNA structure, how drug efficacy is impacted by genomics, and how to model motion and dynamics of biological structures.

Beyond the keynote speakers, ISMB will be brimming with talks on cutting edge discoveries across diverse areas. The Special Sessions track will run

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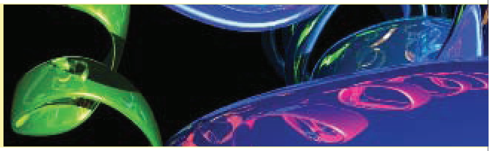


ISMB 2014 continued

throughout the meeting and will feature hot topics that have not been featured in previous ISMB meetings. The Highlights and Proceedings tracks are also popular conference tracks that include oral presentations based on recently published papers selected through rigorous peer review processes. The Proceedings papers are also published as an online-only open access section of the Bioinformatics journal. The Technology track features presentations that showcase the use of novel software or hardware relevent to computational biologists. The Late Breaking Research track will also feature talks from a wide range of topics of significant interest to the bioinformatics community.

A large poster session will provide an opportunity for trainees and scientists from every career stage to present their latest research findings in a collegial and collaborative atmosphere. Birds of a Feather sessions and workshops will be more informal sessions that encourage discussion and collaboration. These sessions will feature such themes as bioinformatics curriculum guidelines, personalized medicine, bioinformatics core facility management, trends in digital publishing, and data analysis. The exhibit hall will showcase a wide variety of organizations and companies that are developing tools and reagents relevent to computational biologists and bioinformaticians, and attendees will be able to see some of these items in action at exhibitor presentations.

The ISCB Student Council will be organizing several high profile events throughout ISMB 2014. The annual Student Council Symposium will convene just prior to ISMB 2014 and will include talks by a keynote speaker and student presenters as well as a poster session. Opportunites for career guidance and social events are also included. In addition, the ISCB Student Council will be coordinating an Art & Science Exhibition during the ISMB meeting that will feature images and videos of scientific material derived from research projects or artwork generated from scientific tools or methods.

An Official Conference of the International Society for Computational Biology

ISMB 2014

boston, usa

JULY 11–15

22nd Annual International Conference on Intelligent Systems for Molecular Biology

www.iscb.org/ismb2014

Friday, July 11th and Saturday, July 12th will be filled with substantive specialized meetings that precede the main ISMB meeting. Topics cover numerous research areas and these smaller meetings will provide ISMB attendees an excellent reason to get to Boston early. 3DSig, a satellite meeting focused on structural bioinformatics and computational biophysics, will be celebrating its 10th meeting on July 11th and 12th. This year's 3DSig satellite meeting will include highlights of the 2013 Nobel Prize in Chemistry awarded to Martin Karplus, Michael Levitt, and Arieh Warshel. The other major satellite meeting, Critical Assessment of Massive Data Analysis (CAMDA) 2014, will also be held on July 11th and 12th, and will focus on the contemporary challenges of analyzing large, complex datasets in the era of Big Data.

Several two-day special interest group (SIG) meetings will also run concurrently with these satellite meeting and include Automated Function Prediction, BioLINK, Bio-Ontologies, BioVis, Bioinformatics Open Source Conference, and High Throughput Sequencing Algorithms and Applications. In addition, one-day SIGs occuring on Friday, July 11th will include Integrative RNA Biology and NetBio. Saturday, July 12th will feature four one-day SIGs: Mass Spectrometry, New Challenges in Computational Single Cell Biology, Regulatory Genomics, and Vari SIG (formerly SNP-SIG).

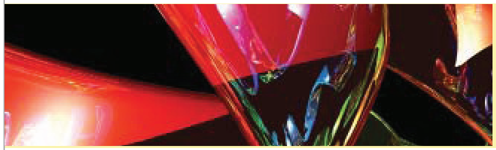
Two half-day tutorial sessions will also be held on July 12th and will feature (1.) *Computational Metagenomics* and (2.) *Wikipedia: WikiProject Computational Biology.*

Several social events will balance out the program for ISMB 2014 and will create ample opportunities for attendees to gather together and network in informal settings. An orienteering event will take place on the evening of Friday, July 11th that will provide attendees with a navigation challenge in and around Boston Common. ISMB will have four prime networking events open to all attendees: an opening reception scheduled for the evening of Saturday, July 12th, poster viewing receptions on both Sunday, July 13th, and Monday, July 14th, and an evening networking event at the Massachusetts Institute of technology (MIT) on Monday, July 14th.

The exhibit hall promises to be a hub of activity throughout the meeting. Designed to be ISMB's place to meet and network, the exhibit hall will be the site of poster sessions, coffee breaks, concessions, and exhibits from key players in the computational biology industry. Exhibits will be intermingled with posters to enable attendees to interact with poster presenters and exhibitors in one convenient location. As a unique event for 2014, a World Cup viewing area will be set up in the Exhibit Hall throughout the meeting so attendees won't miss a single shot.

As a long-standing center of biological and computational research breakthroughs, Boston promises to be an excellent host to ISMB 2014. Both local Boston- and Cambridge-area scientists, as well as visitors from every corner of the globe will be showcasing diverse topics that span from personalized medicine, to machine learning in systems biology, to open source bioinformatics software development. ISMB 2014 has something for everyone and is an excellent destination to start your next collaboration and find great science.

Burkhard Rost, ISCB President and Michal Linial, ISCB Vice President, awarding Overton Prize to Ziv Bar-Joseph



TRAINING AND DEVELOPMENT AT ISMB - SIG AND SATELLITE MEETINGS

ISMB 2014 will hold a number of one and two-day specialized meetings in computational biology. These meetings consist of Special Interest Group Meetings (SIGs) and Satellite Meetings (SMs) and will be held prior to the main conference. A SIG meeting is a one- or two-day focused workshop. It provides a broad and/or deep perspective on developments in a field of research, and is intended as a way to address a topic more extensively than can be done in the main conference. A Satellite Meeting is similar to a SIG meeting but is more of a mini-conference.

Program information and details are noted below.

ONE-DAY SIGS – FRIDAY, JULY 11, 2014

- Integrative RNA Biology SIG (IRB-SIG)
- NetBio SIG

ONE-DAY SIGS – SATURDAY, JULY 12, 2014

- Mass Spectrometry SIG (MS-SIG)
- New Challenges in Computational Single Cell Biology
  Regulatory Genomics Special Interest Group (RegGenSIG)
- Vari SIG (formerly SNP-SIG)

TWO-DAY SIGS – FRIDAY, JULY 11 AND SATURDAY, JULY 12, 2014

- Automated Function Prediction (AFP-SIG)
- BioLINK SIG
- Bio-Ontologies
- BioVis SIG
- BOSC:15th Annual Bioinformatics Open Source Conference
- HitSEQ: High Throughput Sequencing Algorithms & Applications

SATELLITE MEETINGS

3Dsig: Structural Bioinformatics & Computational Biophysics

URL: http://bcb.med.usherbrooke.ca/3dsig14
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

3Dsig, a Satellite Meeting of the ISMB/ECCB conference, focused on structural bioinformatics and computational biophysics and has become the largest meeting in this growing field. This year we are celebrating our 10th meeting and highlighting the 2013 Nobel prize in Chemistry awarded to Martin Karplus, Michael Levitt & Arieh Warshel, the pioneers of the field.

In addition to keynotes our diverse program will include talks selected from submitted abstracts, our traditional after dinner speaker, daily discussion on important topics to this community, laptop software demos and poster sessions. Simply put, 3DSIG is the most comprehensive conference in the field and should not be missed by anyone using macromolecular structure to computationally unravel the mysteries of living systems.

Over the years, 3DSig has brought the leaders of the field of Structural Bioinformatics and Computational Biophysics in an ideal environment for personal contacts and discussions. The list of past keynotes includes: Russ Altman, Patricia Babbitt, Ivet Bahar, Nir Ben-Tal, Tom Blundell, Phil Bourne, James U. Bowie, Steven Brenner, Janusz Bujnicki, Stephen Burley, Wah Chiu, Cyrus Chothia, Charlotte Deane, Keith Dunker, Arne Elofsson, Dmitrij Frishman, Adam Godzik, David Goodsell, Nick Grishin, Kevin Karplus, Amy E. Keating, Tanja Kortemme, Gunnar von Heijne, Barry Honig, David Jones, Thomas Lengauer, Michael Levitt, Olivier Lichtarge, Andrei Lupas, François Major, George I. Makhatadze, John Moult, Klaus Mueller, Ruth Nussinov, Arthur Olson, Christine Orengo, Robert Preissner, Burkhard Rost, Rob Russell, Andrej Sali, Chris Sander, Jeffrey Saven, Tamar Schlick, Torsten Schwede, Luis Serrano, Brian Schoichet, Michael Schroeder, Kim A. Sharp, Manfred Sippl, Michael Sternberg, Joel Sussman, Devarajan Thirumalai, Janet Thornton, Anna Tramontano, Ron Unger, Alfonso Valencia, Sandor Vajda, Rebecca Wade, Haim Wolfson, Ada Yonath.

CAMDA 2014 Critical Assessment of Massive Data Analysis

URL: www.camda.info/
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

Currently, the Big Data explosion is the grand challenge in life sciences. Analyzing large data sets is emerging to one of the scientific key techniques in the post genomic era. Still the data analysis bottleneck prevents new biotechnologies from providing new medical and biological insights in a larger scale. This trend towards the need for analyzing massive data sets is further accelerated by novel high throughput sequencing technologies and the increasing size of biomedical studies. CAMDA focuses on the analysis and integration of the massive data sets in life sciences. It provides new approaches and solutions to the big data problem, presents new techniques in the field of bioinformatics, data analysis, and statistics for handling and processing large data sets.

CAMDA focuses on the specific challenges and opportunities in the analysis of the massive data sets that are increasingly produced in several fields of the life sciences. The conference offers researchers from the computer sciences, statistics, molecular biology, and other fields a unique opportunity to benefit from a critical comparative evaluation of the latest approaches in the analysis of life science's "Big Data".

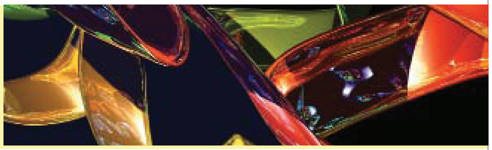
SIG Meetings

Automated Function Prediction (AFP-SIG)

URL: http://biofunctionprediction.org
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

The Automated Function Prediction Special Interest Group (AFP-SIG) The accurate annotation of protein function is key to understanding life at the molecular level. However, with its inherent difficulty and expense, experimental characterization of function cannot scale up to accommodate the vast amount of sequence data already available. The computational annotation of protein function has

Training continued



the vast amount of sequence data already available. The computational annotation of protein function has therefore emerged as a problem at the forefront of bioinformatics. Recently, the availability of genomic-level sequence information for thousands of species, coupled with massive high-throughput experimental data, has created new opportunities as well as challenges for function prediction. Many methodologies have been developed by research groups worldwide, many based in comparing unsolved sequences with databases of proteins whose functions are known. Other methods aim at mining the scientific literature associated with some of these proteins, yet others combine sophisticated machine-learning algorithms with an understanding of biological processes to decipher what these proteins do. Indeed, we may have already identified a protein that is an ideal drug target for cancer, but it is lost in the myriad of data labeled as "function unknown".

The mission of the Automated Function Prediction Special Interest Group (AFP-SIG) is to bring together computational biologists, experimental biologists, and biocurators who are dealing with the important problem of gene and gene product function prediction, to share ideas and create collaborations. The AFP-SIG holds annual meetings alongside the ISMB. This year, we are also conducting a multi-year Critical Assessment of Functional Annotation, or CAFA, experiment.

About the CAFA experiment
The problem: There are far too many proteins in the databases for which the sequence and various other information are known, but the function is not. A major challenge in the field of bioinformatics is to predict the function of a protein from its sequence, structure, or other data. At the same time, how can we judge how well these function prediction algorithms are performing and whether they are useful for experimental scientists?

Our approach: The Critical Assessment of protein Function Annotation (CAFA) is a challenge designed to provide a large-scale assessment of computational methods dedicated to predicting protein function. The first CAFA challenge took place between September 2010 and January 2011 with an initial evaluation meeting held at AFP-SIG during ISMB 2011 in Vienna. The experiment and the associated meeting were highly successful – resulting in 15 peer-reviewed publications and an overview article published in Nature Methods. The CAFA 2 experiment has been running since September 2013, and the methods will be initially evaluated during the second day of AFP-SIG 2014 in Boston. Among the new challenges for CAFA 2 are the prediction of subcellular localization and the prediction of human phenotypes. We will also provide a re-assessment of the prediction accuracy from the 2010-2011 CAFA experiment, now on a significantly larger number of protein targets.

BioLINK

URL: http://biolinksig.org/biolink-2014
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

With the increasing availability of text data related to biology and medicine in the scientific literature, database annotations, the electronic health record, clinical trials data, and health information online, exciting opportunities arise to provide access to pertinent biomedical information and to advance biomedical knowledge. An evolving research direction is the integration of information from diverse data sources, including textual data, to support deeper understanding of biological systems, the genomic basis of disease, and genotype-phenotype relationships. We hope to attract research to this SIG meeting that directly integrates text mining into computational methods addressing biological problems. We therefore plan to dedicate part of the workshop to the role of text mining for automated function prediction and SNP interpretation, joining up with the Automated Function Prediction SIG and the SNP SIG, respectively, to have shared sessions.

The second day of the SIG, July 12th, will be "Phenotype Day", a joint session with the BioOntologies SIG and which will address the systematic description of phenotypic variation. It will bring together researchers across many disciplines to discuss phenotype-related issues and resources, and to share their experience with defining, representing, processing and using phenotype data.

Bio-Ontologies

URL: www.bio-ontologies.org.uk
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

The Bio-Ontologies SIG provides a forum for discussion of the latest and most innovative research in the appplication of ontologies and more generally the organisation, presentation and dissemination of knowledge in biomedicine and the life sciences. Bio-Ontologies has existed as a SIG at ISMB for 17 years, making it one of the longest running.

BioVis SIG: 4th Symposium on Biological Data Visualization

URL: http://biovis.net
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

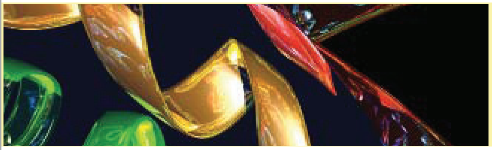
The rapidly expanding field of biology creates enormous challenges for computational visualization techniques for enabling researchers to gain insight from their large and highly complex data sets.

The Symposium on Biological Data Visualization (BioVis) is the premier international and interdisciplinary event for all aspects of visualization in biology. The symposium brings together researchers from the visualization, bioinformatics, and biology communities with the purpose of educating, inspiring, and engaging visualization researchers in problems in biological data visualization as well as bioinformatics and biology researchers in state-of-the-art visualization research. The full call for participation can be found at http://biovis.net/year/2014/info/cfp.

BOSC: 15th Annual Bioinformatics Open Source Conference

URL: www.open-bio.org/wiki/BOSC_2014
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

The Bioinformatics Open Source Conference (BOSC) is sponsored by the Open Bioinformatics Foundation, a non-profit group dedicated to promoting the practice and philosophy of Open Source software development within the biological research community.



BOSC covers the wide range of open source bioinformatics software packages that have been successfully developed and adopted by the community, and encompasses the growing movement of Open Science, with its focus on transparency, reproducibility, and data provenance. We welcome submissions relating to all aspects of open source bioinformatics software and open science, including new computational methods, reusable software components, visualization, interoperability, and other approaches that help to advance research in the biomolecular sciences. Two full days of talks, posters, panel discussions, and informal discussion groups will enable BOSC attendees to interact with other developers and share ideas and code, as well as learning about some of the latest developments in the field of open source bioinformatics.

HitSEQ: High Throughput Sequencing Algorithms & Applications
URL: http://hitseq.org
Date: Friday, July 11 & Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

The Conference on High Throughput Sequencing Methods and Applications (HiTSeq 2014) is a Satellite of the ISMB 2014 conference and brings together biologists and computational scientists interested in exploring the challenges and opportunities in the analysis of high-throughput sequencing (HTS) technologies. HiTSeq 2014 is devoted to the latest advances in computational techniques for the analysis of high-throughput sequencing data including novel algorithms, analysis methods and applications in biology where high-throughput sequencing data has been transformative. It provides a forum for in depth presentations of novel algorithms, analysis methods, and applications in multiple areas of biology that HTS is transforming. HiTSeq seeks full papers submissions to be peer-reviewed. If accepted, these contributions will be presented at the conference and published online. Short abstract submissions will be also accepted for either brief oral presentations or posters.

Integrative RNA Biology - SIG (IRB-SIG)
URL: www.irbgroup.org/irb-sig-14/
Date: Friday, July 11
Start Time: 8:30 a.m - 6:00 p.m.

The meeting for Integrative RNA Biology is focused on deriving new RNA Biology using a combination of computational and experimental techniques. The meeting is designed to bring computational experts attending ISMB together with world experts in different aspects of RNA processing.

Many computational challenges are involved in the study of RNA, ranging from quantifying gene isoforms and secondary structure modelling, to detecting miRNA regulatory networks and deciphering splicing regulation. RNA processing involves complex and highly regulated mechanisms that affect many biological processes, such as cell type differentiation, sex-determination, or apoptosis. One important component of RNA processing is alternative splicing (AS), by which pre-RNA can be spliced differently to produce different mRNA isoforms. Other components involved in RNA processing that have gained much research attention include alternative polyadenylation (APA) and the expression of many non-coding RNAs, such as micro-RNAs (miRNAs), small-interfering RNAs (siRNAs), PIWI-interacting RNAs (piRNAs), or long nuclear RNAs.

While many of these phenomena have been studied separately, accumulating evidence now points towards the interplay between transcription, RNA processing, RNA turnover and the effects non-coding RNAs exert on these machineries. This interplay leads to a new, interconnected system view of gene expression regulation. In parallel, the advent of high-throughput methodologies enabled researchers to obtain genome-wide measurements of the make-up and the regulation of the transcriptome within a well-defined biological context. However, the complexity of these data also poses interpretation challenges, particularly when considering that the snapshot of the transcriptome that high-throughput methodologies permit us to obtain are the result of many integrated regulation processes.

In this meeting we aim to bring computational experts attending ISMB together with world experts in the fields of RNA processing and non-coding RNAs to discuss recent advances in RNA biology and related computational and experimental methodology. We hope the meeting will foster new interactions and help bridge the gap between researchers in the different fields.

Mass Spectrometry SIG (MS-SIG)
URL: http://igenomed2.stanford.edu/BeyondProteomics_2014/
Date: Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

MS-SIG aims to bring together experts from the global research community to discuss current progress and challenges in the field of mass spectrometry based proteomics and computational biology. Our meeting will contain three portions: oral presentation, panel discussion, and poster presentation. We invite abstract submissions on a wide range of topics list below. The poster session will provide an opportunity to present your work in an informal setting. We will also have a limited number of talks selected from abstracts slots in the program.

NetBio SIG
URL: http://nrnb.org/netbiosig/
Date: Friday, July 11
Start Time: 8:30 a.m - 6:00 p.m.

Biological networks provide a context for integrating and analyzing massive amounts of diverse kinds of measurement data, such as expression data from RNA-Seq, protein abundance and interaction data from mass spectrometry, and genetic data from association studies. Network theory provides powerful analysis techniques that can be used to develop insights into large amounts of data. Our use of networks in biology has changed from purely representational and didactic purposes to more analytic and hypothesis formulation purposes. This shift has resulted, in part, from the confluence of advances in computation, informatics, and high throughput techniques in systems biology.

We will solicit abstracts that cover new developments in network biology, focusing on two major areas: (1) the development of network-related tools and resources, and (2) the application of network analysis and visualization in the study of biology, synthetic biology and medicine. The meeting will provide a unique meeting space for tool developers and users in the field of network biology. Through these complementary lenses, the meeting will bring into focus the current state of the field, its future

New Challenges in Computational Single Cell Biology
URL: www.easychair.org/conferences/?conf=sigcscb2014
Date: Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

Single cell technologies are transforming biological research and give rise to a new breed of challenges in computational biology.

Recent advances in single cell biology have lead to dramatic improvements in the ability to monitor biological systems in terms of temporal, spatial and molecular resolution at the single cell level. Single cell proteome profiling approaches are capable of jointly monitoring up to 100 different markers. While single cell transcriptomics approaches routinely allow to monitor this amount of transcripts, new sequencing techniques are enable researchers to evaluate whole transcriptomes and genomes for single cells. These improvements enable to acquire informative data about phenotypes of multicellular organisms that result from an intricate dynamic interplay of heterogeneous cell populations. These technologies are driving a systems level characterization of complex diseases such as cancer that feature a disruption of this interplay or itself are the result of a pathologically altered cell population. Single cell technologies are enabling comprehensive molecular and functional characterization of such heterogeneous cell populations and will therefore constitute a cornerstone of a systems-level understanding of complex biological systems, their pathological alterations and opens the perspective to rationally specify novel therapeutic targets.

The complexity of the data acquired by these technologies require computational approaches to perform inference of systems level models of the underlying biological systems. Single cell resolved data of heterogeneous cell populations lends itself to computationally define cell types in a data driven way and thereby opening the perspective to discover novel functionally relevant cell types. The marker breadth represented in this data still poses big challenges to the development of suitable clustering and dimensionality reduction techniques. The analysis of single cell time series experiments has elicited a flurry of modeling approaches for the temporal dynamics of intracellular signaling and transcription networks that range from probabilistic graphical models to deterministic and stochastic dynamical systems. Furthermore, computational approaches have enabled researchers to exploit single cell resolved data to infer intrinsic and extrinsic cell-to-cell variability phenomena in apparently homogeneous cell populations. In summary, single cell technologies enable novel insights on the single cell and cell population level, but at the same time give rise to a diverse spectrum of computational challenges whose solution are combining and will continue to combine concepts from the fields of statistics, machine learning and dynamical systems theory.

Regulatory Genomics Special Interest Group (RegGenSIG)
URL: http://light.ece.ohio.edu/~reggen/2014/
Date: Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

Regulatory genomics involves the study of the genomic ‘control system,’ which determines how, when and where to activate the ‘blueprint’ encoded in the genome. Regulatory genomics is the topic of much research activity worldwide. Since computational methods are important in the study of gene regulation, the RegGenSIG meeting focuses on bioinformatics for regulatory genomics. An important goal of the meeting is to foster a collaborative community wherein scientists convene to solve difficult research problems in all areas of computational regulatory genomics.

RegGenSIG will include presentations and posters that cover the broad spectrum of topics important to regulatory genomics research. The goal is to bring together experts in experimental methods and computational methods to consider sequence-based reconstruction of regulatory networks and prediction of gene expression. Topics to be addressed in the SIG include the following:

1. inference of gene regulatory networks;
2. utilization of information pertaining to epigenetics, chromatin structure, and histone modifications;
3. determination of the roles of regulatory RNAs;
4. prediction of transcriptional regulation from RNA-seq data and ChIP-seq data;
5. pattern discovery in sequences; and
6. sequence based modeling of gene expression.

Vari SIG (formerly SNP-SIG)
URL: http://varisig.biofold.org
Date: Saturday, July 12
Start Time: 8:30 a.m - 6:00 p.m.

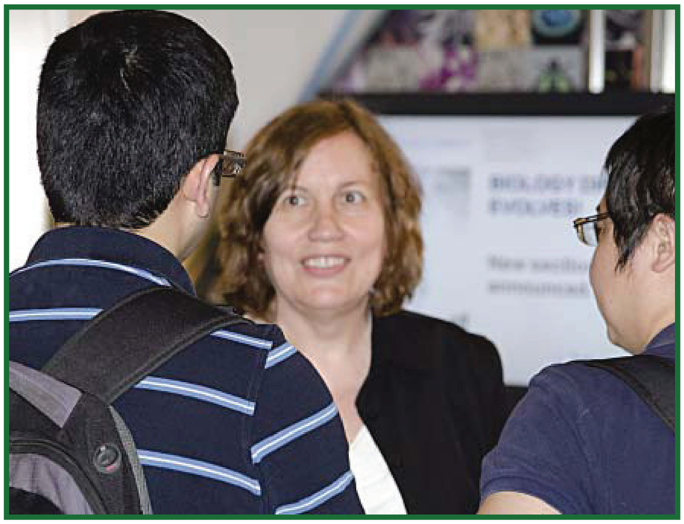
The primary goal of the VarI-SIG is to outline and discuss the recent advances in the methodology for the annotation and analysis of genomic variation data. Genetic variants are generally very interesting in the context of their phenotypic manifestations. The discrepancy between the significant availability of SNV data and the current lack of its interpretation requires the development of methods for the annotation/prediction of the genetic variant impact. In the near future the analysis of genetic variation will be a key factor for the understanding of the information encoded in the genome The VarI-SIG provides a forum for the organization of a research network facilitating the exchange of ideas and the establishment of new collaborations bringing together varying expertise. It will thus support the unprecedented collaborative effort to manage the complexity of the analysis and evaluation of genetic variation.

The SIG will be divided into two sessions - “SNVs as markers: evolution, populations, GWAS” and “Genetic variants as effectors: function, structure, and regulation”. For detailed information please see the SIG website.
We are interested in submissions describing original work in all the fields of genomic variation research including, but not limited to:

- Databases, data mining algorithms and visualization tools for genetic variants analysis.
- Methods for predicting regulatory/structural/functional impacts of SNVs
- Personal Genomics, GWAS studies and SNV prioritization
- Population genomics and phylogenetic analysis

HOW TO BECOME COSI WITH A COMPUTATIONAL BIOLOGIST

By Christine Orengo



"That was a great meeting. Let's stay in touch." How often have you said this at the end of a meeting after connecting with new colleagues you wanted continue sharing ideas with? The internet has given us access to infinitely more data than we know how to manage and the potential for great insights if we know how to transform this data into knowledge. How can we better connect scientists within specialized research areas and facilitate meetings and discussions that only require the cost of a cup of coffee and a good internet connection?

In the best spirit of being a scientific society, the International Society for Computational Biology (ISCB) is exploring strategies to make this happen. ISCB is well known for organizing the Intelligent Systems for Molecular Biology (ISMB) meeting for nearly two decades. ISMB is the premiere annual computational biology meeting that brings together thousands of world-class researchers and has been host to many pivotal moments in computational biology and bioinformatics history. Since 2004, ISCB has supported affiliate meetings in countries across the globe, particularly in Africa, Latin America, and Asia.

In the 21st century, ISCB envisions connecting computational biologists in a virtual meeting place and is considering how to promote virtual networks and make the Society a year-round hub of electronic activity by setting up web communities that can share information, hold meetings, and discuss ideas "long distance" via the internet. These Communities of Special Interest (COSIs) will be built around major research themes within computational biology, or important activities such as networks of training, mentoring, or financial support. The COSIs will be founded initially with communities originating from Special Interest Groups (SIGs) or workshops who have been organizing events at ISMB.

SIG meetings have become highly successful events and are an important feature of ISMB. SIGs are one- or two-day meetings that take place prior to ISMB and often attract more than 100 participants and include diverse programs with multiple internationally respected speakers. Some of the SIGs, like BOSC and 3DSIG, have been running for more than ten years!

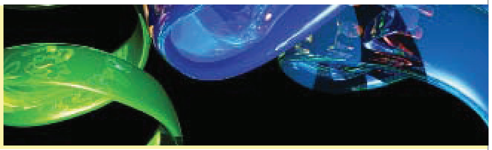
Workshops run in parallel tracks during ISMB and also attract ~100 participants. Workshops provide a vital means for people to stay in touch and learn new scientific techniques, such as next generation sequencing, or learn about new training strategies, career opportunities, and bioinformatics support materials.

A number of communities have expressed an interest in becoming a COSI (see table below). ISCB plans to nurture these communities by hosting a web portal that provides access to dedicated websites for each community. ISCB will support the computational infrastructure for the COSI websites using Wikimedia tools. ISCB will establish mechanisms to help the COSIs raise funds to support the COSI web portal and will provide free ISCB membership to individuals who populate the COSI web pages with information. ISCB intends the content of the COSI pages to be useful, up-to-date, and accurate in order to attract new followers and maintain members!

This year, a special session is being planned for ISMB to launch the COSIs. Representatives from each COSI will describe their community and their current and future activities. This launch will also give the COSIs a chance to advertise social events or birds of a feather-type activities for people who didn't attend their corresponding SIG or workshop and will provide a venue for COSI members and meeting attendees to interact in person. ISCB will also make sure that all the talks that relate to COSI themes or activities are tagged as such in the conference program to make it easier for attendees to find talks that best fit their research interests or COSIs.

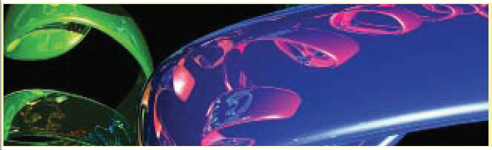
Some of the communities approached to become COSIs have expressed an interest in having their SIGs or workshops video-recorded so that researchers who are unable to attend ISMB can watch highlights via the COSI website. Another suggestion is for researchers who want to give a SIG talk should submit a video of their research abstract. Even if these individuals aren't selected to give a talk, their video abstract could still be selected for upload to the COSI website. Other ideas for COSI activities include year-round "virtual conferences" with video archives of talks, news boards and forums that are maintained for specific topics, and F1000-like article recommendations and reviews. We hope to make progress on some of these ideas over the coming year.

COSI continued



COSIS BEING LAUNCHED AT ISMB, BOSTON, JULY 2014

3D-SIG	3D-SIG Structure-based drug discovery. Structure representation, classification and prediction Structure-based function prediction. Docking - protein-protein, protein-ligand and protein-nucleic-acid. Protein dynamics; Structural Evolution; Macromolecular assemblies; Structural genomics
Automated Function Prediction (AFP)	The mission of the Automated Function Prediction COSI is to bring together computational biologists, experimental biologists and biocurators who are dealing with the important problem of gene and gene product function prediction, to share ideas and create collaborations.
Bioinfo-Core	Bioinfo-core is a worldwide body of people that manage or staff bioinformatics cores within organizations of all types. We provide a forum for bioinformatics core managers and staff to discuss issues pertaining to the operation of their core, evaluation of data analysis software tools, and management of relationships with the users of cores.
Bio-Ontologies	The latest and most innovative research in the application of ontologies and more generally the organisation, presentation and dissemination of knowledge in biomedicine and the life sciences.
CAMDA	CAMDA presents a crowd sourcing and open-ended data analysis challenge format which focuses on big heterogeneous data sets that are increasingly produced in several fields of the life sciences.
Computational Biology Education (COBE)	The ISCB Computational Biology Education (CoBE) COSI focuses on bioinformatics and computational biology education and training across the life sciences. A major goal of this COSI is to foster a mutually supportive, collaborative community in which bioscientists can share bioinformatics education and training resources and experiences, and facilitate the development of education programs, courses, curricula, etc., and teaching tools and methods.
Computational Mass Spectrometry (COMP-MS)	The ISCB CoSI CompMS is a joint initiative with the HUPO Computational Mass Spectrometry Initiative (HUPO CompMS). It promotes the efficient, high quality analysis of mass spectrometry data through dissemination and training in existing approaches and coordination of new, innovative approaches. The CompMS initiative aims to exploit synergies between different application domains, in particular proteomics and metabolomics.
Network Biology	As more research fields turn to network visualization and analysis for perspective, our Network Biology Community serves to introduce novel methods and tools, identify best practices and highlight the latest research in the growing and interconnected field of network biology.
Open Bioinformatics Forum (OBF)	The Open Bioinformatics Foundation or OBF is a non-profit, volunteer-run group dedicated to promoting the practice and philosophy of Open Source software development and Open Science within the biological research community.
Variant Interpretation (VarI-COSI)	The Variant Interpretation Community of Special Interest (VarI-COSI) is a community of scientists interested in “breaking” the genomic code. The main goal of our COSI is to promote the formation of a collaborative network of scientists interested in the understanding of the meaning of genomic variation as applied to a range of questions, including population studies, functional and evolutionary impacts, and disease.
RegGenSIG	Regulatory genomics, the study of genomic ‘control systems,’ which determine how, when and where to activate the ‘blueprints’ encoded in genomes, is the topic of much research activity worldwide. The ISCB Regulatory and Systems Genomics Community of Special Interest - RegSys COSI - focuses on computational methods that are important in the study of regulation of genes and systems. An important goal of the COSI is to foster a collaborative community wherein scientists consider difficult research problems in all areas of computational regulatory and system genomics.



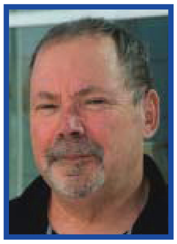
BOURNE TO LEAD NIH DATA SCIENCE INITIATIVE

By Christiana N. Fogg, Ph.D.

Biomedical research has a “Big” problem. Each day, massive amounts of digital data are flooding databases or are being stored by the terabyte in hard drives across the globe. The shear volume of data is expected to increase significantly in the future as biomedical data becomes more digitized. This Big Data problem creates a huge discovery bottleneck for researchers, and the field of data science is becoming an increasingly vital to productivity in numerous areas, including genomics, biomedical imaging, and clinical studies. Many members of the ISCB community are working on the frontlines of data science by finding new ways to access, analyze, and archive these types of data.

In March 2012, the Obama Administration launched the Big Data Research and Development Initiative across several Federal agencies and departments to facilitate innovative uses for analyzing, sharing, and extracting new knowledge from complex digital datasets. NIH Director Francis S. Collins, M.D., Ph.D., who is familiar with such issues through his genomics research, created the Data and Informatics Working Group to advise the NIH as to how to respond to this initiative. This working group made several recommendations and strongly advised that a new leadership position dedicated to data science be based within the NIH Office of the Director.

Eric Green, M.D., Ph.D., Director of the National Human Genome Research Institute, served as Acting Associate Director for Data Science (ADDS) in 2013 as a search to recruit a permanent senior scientist to this position was underway. Green spent his tenure building the foundation for this initiative, including giving talks to members of the research community about the need for a “cultural shift” in the way biomedical research handles Big Data. Green also worked with the NIH Director, the Director's Steering Committee, and Scientific Data Council to launch the Big Data to Knowledge (BD2K) initiative. The mission of the NIH BD2K is “to enable biomedical scientists to capitalize more fully on the Big Data being generated by those research communities.” According to the NIH BD2K website (bd2k.nih.gov), the four focus areas of B2DK will be 1.) Enabling Data Utilization, 2.) Analysis Methods and Software, 3.) Enhancing Training, and 4.) Centers of Excellence.



Philip Bourne, Ph.D., officially took the helm of the National Institute of Health's (NIH) Big Data initiative on March 1, 2014, as the first permanent ADDS. He is working in close partnership with the NIH Scientific Data Council to oversee BD2K, coordinate data science activities and programs across NIH institutes, and develop strategic plans for long-term use and archiving of Big Data. Prior to coming to NIH, Bourne was Vice Chancellor for Innovation and Industry Alliances and a Professor in the Department of Pharmacology and in the Skaggs School of Pharmacy and Pharmaceutical Sciences at the University of California, San Diego. Bourne's broad research interests include ways to use “in silico bioinformatics and systems biology-related research and education (with emphasis on 3D structures) to improve understanding of living systems.” Bourne and his research group have invested significant time and effort into developing valuable resources that benefit the biomedical research community, including the RSCB Protein Data Bank (PDB) and the Immune Epitope Database (IEDB).

Bourne sees his new position as an opportunity to have NIH Institutes and Centers share data in new, groundbreaking ways. In a recent interview, Bourne described his plans for bring this idea to fruition. “My strategy, by using Big Data as a catalyst, is to catalyze more interactions at NIH,” he said. He hopes that these interactions will help the relatively independent NIH institutes recognize that the complex data they generate “adds value to other institutes.” Bourne hopes to “leverage these [interactions] and break down some of the barriers” between the institutes. He plans to tackle this new position in the same scientific and methodical manner he has used throughout his career. “I’m a firm believer of taking small steps, piloting projects and evaluating, and see how they turn out, and moving on from there,” he stated.

As ADDS, Bourne will work with NIH leadership to shape several policies about the handling, sharing, and analysis of Big Data. He and others will also consider new strategies to properly prepare and train a workforce to fill the numerous data science jobs needed to keep up with the flood of Big Data. Bourne acknowledges that even now, there are “an abundance of data science positions that cannot be filled” because too few individuals have the right credentials and training.

One major issue that looms large is where all of the Big Data is to be stored. Scientific journals are already wrestling with this issue, and Bourne has had firsthand experience with this matter as the founding Editor-In-Chief of *PLOS Computational Biology*. As the amount of data grows, he sees biomedical researchers, publishers, and funding bodies like the NIH facing the painful question of “What data do we keep and what do we throw away?” To answer this question, Bourne believes scientists and stakeholders have to look at what is happening to the data. New sustainability models will have to be tested in order for this data to be used optimally and preserved well into the future. “We haven’t done a good job so far of seeing how the data is used,” Bourne said. “Companies like Netflix and Amazon are spending inordinate amounts of time thinking about the whole business model.”

In parallel to his role as ADDS, Bourne will run a small research group housed within the National Library of Medicine, and he will continue research on systems pharmacology and protein structure. Bourne is eager to start his work at NIH and help Big Data become a prodigious source of cutting-edge discoveries for the foreseeable future.

GREAT LAKES BIOINFORMATICS CONFERENCE, MAY 16-18, 2014, CINCINNATI, OHIO

The Great Lakes Bioinformatics Consortium is pleased to announce its ninth annual conference, the Great Lakes Bioinformatics Conference (GLBIO), to be held May 16-18, 2014 in Cincinnati, OH. GLBIO 2014 will be hosted by Cincinnati Children's Hospital Medical Center, in conjunction with the University of Cincinnati.

The conference, an official conference of the International Society for Computational Biology (ISCB), provides an interdisciplinary forum for the discussion of research findings and methods, and development of long-term relationships and networking opportunities, for researchers within the region, as well as from around the world.

The program will include oral presentations, poster presentations, invited keynote speakers and tutorials. From novice to expert, attendees partake in a variety of workshops, tutorials, presentations, posters, networking events and exhibits.

Keynote speakers include Gary Bader, The Donnelly Centre at the University of Toronto, Tanya Y. Berger-Wolf, Department of Computer Science, University of Illinois, Charles Brooks, University of Michigan and Mike Hawrylycz, Allen Institute for Brain Science.

On Friday, May 16, the following tutorials will be presented:

1. Lincs Chemical Biology Data Analysis Workshop, Mario Medvedovic

2. STOCHASTIC CHEMICAL KINETICS: Theory and Systems Biological Applications, Peter Erdi

3. Gene Networks and Systems Genetics Expression Mutation, Sorin Draghici and Anil Jegga

4. Introduction to Bioinformatics, Jarek Meller and Mike Raymer

5. Synapse - Sage Bionetworks Cloud Infrastructure for Data Analysis, Larsson Omberg

6. Data Visualization - Javascript Programming, Isaac Neuhaus

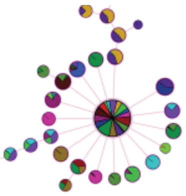
Conference educational session topics will include Algorithm Development & Machine Learning, Bioimage Analysis, Biological Networks, Chemical Biology, Disease Models & Molecular Medicine, Evolutionary, Comparative, & Meta-Genomics and many more!

Specifically, the sessions include these talks:

- High-Performance In-memory Genome Project: A Platform for Integrated Genome Data Analysis
- Biases in the Experimental Annotations of Protein Function and Their Effect on Our Understanding of Protein Function Space
- An integrative approach to understanding the combinatorial histone code at functional elements
- Wnt signaling in cancer: A mathematical systems biology modeling
- Validation of predicted mRNA splicing mutations using high-throughput transcriptome data

In addition, groundbreaking poster presentations will be made in many categories, all relevant to furthering the study of bioinformatics. For example, you will hear talks on the studies of: Algorithm, protein structure, genome assembly, function and evolution, machine learning, pattern recognition, protein structure, sequence analysis and more!

At GLBIO, you will hear speakers and be able to study and expand your education horizons in challenging highlights talks on understanding the combinatorial histone code at functional elements, biases in the experimental annotations of protein function, Bermuda: Bidirectional de novo assembly of transcripts with low expression and uneven coverage utilizing alternate de Bruijn graphs, quantitative systems pharmacological approach: anxiolytic drugs and altered hippocampal theta rhythms and applying molecular crowding models to simulations of virus capsid assembly In vitro.



ATTENTION STUDENTS! GLBIO 2014 is pleased to be the inaugural meeting for the newly formed Student Council of the Great Lakes Bioinformatics Consortium. With student-led education sessions, a mentoring program, student council meeting and a students-only social event – you will want to get involved and network with your peers! Get more info here www.iscb.org/glbio.

GLBIO 2014 will also feature professional and career development sessions sponsored by FASEB MARC. This unique program will include a sponsored career fair, wherein students will receive career guidance (including a CV critique) and will have the opportunity to meet with recruiters.

GLBIO has established a strong reputation for building relationships among a nationally prominent bioscience research community, showcasing the North American Great Lakes region as a perfect place to conduct computer-aided research in the life sciences. Of the 250 attendees of GLBIO 2013, 70% of conference attendees said they would attend the 2014 conference, and 96% stated they would recommend the GLBIO conference to a colleague.

Interested in supporting GLBIO 2014 through sponsorship or exhibiting? Please contact Stacy Slagor, Director of Corporate Relations and Development, ISCB, at stacy.slagor@iscb.org.

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FASEB PUBLIC AFFAIRS BENEFITS FOR ISCB MEMBERS

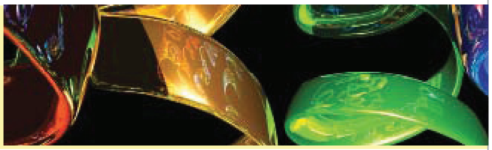
By Allison Lea

ISCB has been a member of the Federation of American Societies for Experimental Biology (FASEB) since 2003. A coalition of 26 scientific societies representing over 115,000 researchers, FASEB works with the representatives of its member societies to develop and promote policies to advance research and education in biomedical science and engineering. The FASEB Office of Public Affairs (OPA) provides analytic, communications, and technical support for FASEB's public policy initiatives.

ISCB is represented on the FASEB Board by Judith A. Blake, PhD, Associate Professor of Bioinformatics and Computational Biology at The Jackson Laboratory Bar Harbor, Maine, and on the FASEB Science Policy Committee by Harel Weinstein, PhD, Chairman of the Department of Physiology and Biophysics and Director of the Institute for Computational Biomedicine at Cornell University. Both representatives bring the views of the ISCB members to the policy development and advocacy processes.

The FASEB Policy & Government Affairs webpages have many useful advocacy tools and materials that are freely available.

- FASEB's e-Action Alerts provide important updates on major public policy issues. Sign-up to receive the alerts here.
- FASEB's Congressional Visit Toolbox provides information on how to communicate with you elected officials on Capitol Hill and in your home districts, tips for making the most out of your visit, and printable advocacy materials to bring along and distribute.
- FASEB's has developed several factsheets to help biomedical scientists convey the importance of National Institutes of Health funding to individual states and districts, the value of federally funded biomedical and biological research, and the damaging effects of sequestration cuts.
- FASEB's Legislative Action Center can help you identify your local elected officials as well as find up-to-date news on recent votes and elections and current legislation.
- OPA's bi-weekly electronic newsletter and blog, The Washington Update, features federal policy issues important to biological and biomedical research, as well as updates on recent OPA activities, recommendations, and published reports. You can sign-up to receive the newsletter by visiting the Washington Update homepage.
- FASEB's Breakthroughs in Bioscience series illustrate recent breakthroughs in biomedical research and their importance to society.

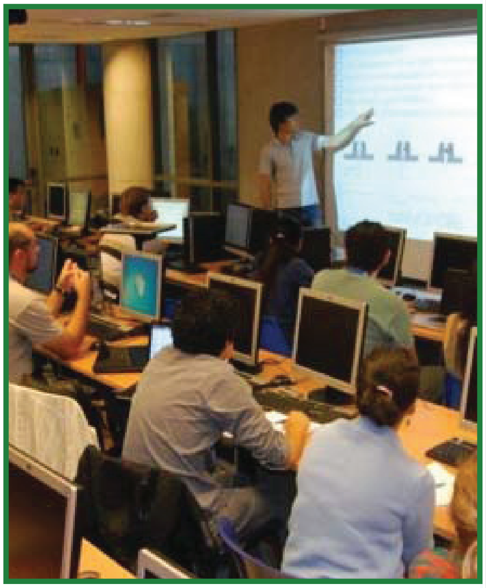


ROCKY 2013 WRAP-UP!

The annual Rocky Mountain Conference on Bioinformatics, better known just as "Rocky," celebrated its tenth anniversary meeting in December 2013. Rocky has a unique approach in bioinformatics, bringing attention to new scientists and working hard to facilitate the creation of new collaborations and relationships. Set in the spectacular scenery of the Roaring Fork Valley, not far from world-renowned Aspen, Colorado, Rocky offers a world-class locale to accompany great science. Although many of the 111 attendees were from the Rocky Mountain region, scientists came from as far away as Egypt and Singapore to join the meeting. Rocky runs two-and-a-half days, organized with keynote addresses bracketing lightning talks and ski breaks.

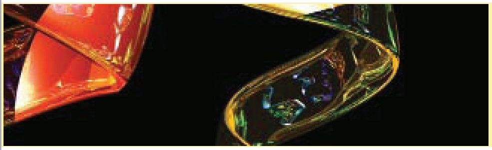
The 2013 keynotes included well-known academic stars Melissa Haendel, Peter Karp and Gary Bader, rising young informaticians Greg Carter, Chikoke Elekawachi, Ben Good and Catherine Lozupone. Lozupone described novel metagenomic methods that she used to characterize non-random co-occurrence patterns of human gut bacterial taxa. Her methods tease apart symbiotic relationships from ones driven by shared environmental preferences. Good described his work on design and promotion of scientific discovery games, including his work on The Cure, a game for identifying breast cancer survival genes. Elekwachi described eMNRLitMine and eMNRHelper, two systems that assists bioremediation engineers in identifying bacteria that might be suitable for remediating complex combinations of contaminants, and the relevant metabolic pathways. Carter described his combined analysis of pleiotropy and epistasis (CAPE) method, showing how he discovered a novel interaction network influencing kidney gene expression and disease by analyzing mouse intercross data. Peter Karp described an impressive automatically generated flux balance model for E. coli K-12 MG1655 generated from the EcoCyc knowledge base using a tool called MetaFlux, and extensive validation showing very high accuracy in a variety of challenges. Gary Bader described how integrating genome data with expression and promoter methylation data could move from traditional correlationals model to a more mechanistic understanding of cell function and perturbations. Jordan gave an exciting roundup of IBM supercomputing applications in biomedicine, including touching on Watson-derived technology. Haendel gave an impassioned plea to know where your data is coming from, and the need for more informatics tools that support reproducibility.

In addition to these keynote addresses, 39 scientists from around the world presented 10-minute talks on their research. The purpose of the lightning talks is to briefly introduce the work of each scientist, facilitating more detailed conversations during the abundant free time provided. The topics of the lightning talks spanned a huge range of bioinformatics, from an ENCODE analysis shedding light on the plasticity of replication timing dependent on chromatin structure to an ontological analysis of the discourse structure of scientific journal articles. Topics ranged from phylogenetics to drug response in cancer, and the methods described covered an enormous range, including, for example, mechanistic modeling, Bayesian inference, text mining, and phylogeography. The poster session include 48 contributions.



Several of the presenters were giving their first public scientific talk. Rocky is proud of its history of giving the first stage to many young investigators who have gone on to impressive careers. Given the large number of speakers, it is relatively easy to get a chance to present relevant work. There was even one undergraduate researcher reporting on his (impressive!) results. The conference environment sets a relaxed environment for graduate students, postdocs, and other early stage researchers to interact with senior scientists. A remarkably large number of Rocky participants report that new interactions and collaborations arose from their attendance at the meeting, and nearly all say the experience exceeded their expectations.

Next year's Rocky is already in preparation, and will be held at the Viceroy Hotel in Snowmass, CO, December 12–14, 2014. The later dates should help with the snow coverage, and the scientific agenda promises to once again be outstanding. We hope to see you there.



CALL FOR ISCB CALL FOR LEADERSHIP NOMINATIONS
The Nomination Period for officers is now open!

ISCB is encouraging members to submit nominations for the Society's Officer positions of Secretary and Vice President; Board of Directors; and the Student Council Leadership positions of Chair, Vice-Chair, Secretary, Treasurer, and Representative to the ISCB Board of Directors. Nominations can be submitted at www.iscb.org/nominate (you must login to your membership record to access the nomination form). In all cases, self-nominations will not be accepted.

ISCB thrives because of dedicated volunteers who have a passion for computational biology and the Society. If you know of excellent candidates that meet the eligibility requirements below, please be sure to submit your nomination(s). Details of the positions, procedures and timeline are available on the ISCB website at: www.iscb.org/leadership-nominations-and-elections. Deadline to submit nominations is **April 18, 2014**.

In order to be eligible to be an Officer candidate, a person must be an ISCB member in good standing, must have served as a Director for at least one (1) year at any time during the history of the Society leading up to the start date of becoming an Officer (first term Board members, therefore, meet the eligibility requirements for election to an Officer position), and be willing to perform the duties as stated in the Executive Officer Responsibilities. He/she must pledge to make every reasonable effort to attend the weekly Executive Committee teleconferences, the bi-monthly Board of Director teleconferences, and, at their own expense, the face-to-face Annual Board Meeting held in conjunction with the ISMB conference.

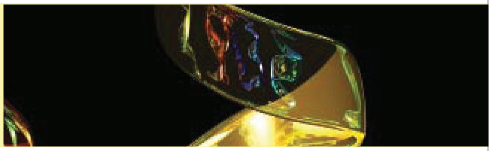
In order to be eligible to be a Director candidate, a person must be an ISCB member in good standing, and must pledge to make every reasonable effort to attend the bi-monthly Board of Director teleconference meetings, and, at their own expense, the face-to-face Annual Board Meeting held in conjunction with the ISMB conference.

Nominations for Board of Directors will be accepted through April 18, 2014. Nominations for Society Officers and Student Council Leaders will be accepted through May 30, 2014.

ISCB Board of Directors and Staff

Election of the Officers and Student Council Leaders will take place via online voting by the membership in July 2014, including availability to a dedicated voting booth at the ISMB conference. We are looking forward to an active participation by the ISCB membership in the nominations and election process, and we thank you in advance for your qualified nominations.

Anna Tramontano, Ph.D., ISCB Board Director



The ISCB-SC Developing nations internship program

Help train the next generation of Computational Biologists!

Internships are a great way to supplement formal education by providing students with hands-on experience in the workplace. While commonplace in the developed world, students from developing nations have significantly fewer opportunities for such internships. With an aim to create more opportunities, the ISCB Student Council (SC) has created an **internship program for students from developing nations**!

How does it work?

If you, a Principal Investigator (PI), have a funded internship position in your lab, please contact us. We will advertise it to students in developing nations through our **extensive network of Regional Student Groups (RSGs)** and provide you with applications to select from. Our volunteers can also **help screen and shortlist applications** as per criteria that you provide!

The program so far

In the past **4 years**, the SC internship program has filled **6 positions**, placing students from **Brazil**, **Estonia**, **Kenya** and **India** with labs and research groups in **Europe** and **Australia**. We are currently in the process of filling a 7th position at the Bateman lab in EMBL-EBI. See http://iscbsc.org/internships for more details.

Get involved

If you are interested in tapping the research potential in developing nations' student community, please get in touch with us. Help nurture talent in the next generation of Computational Biologists!

We are also seeking sponsors who can help fund some of the costs associated with the internships. Your support will allow us to help more students!

All questions ideas and offers can be directed to internships@iscbsc.org. We look forward to hearing from you!

Testimonials from students

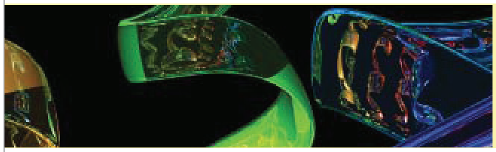
"The acquired knowledge helped me in how to present my work, asking new questions and designing new projects." – Mohd Rehan

"The academic community in the research group and university created a very stimulating, inspiring environment." – Dedan Githae

"I was able to use the skills I had learned in the next project that I started working on" – Kaur Alasoo

"It was great to meet another culture, country structure and differences between Brazil and Germany." – Miriam Nunes

"Collaborative projects and exchange of intellectual and professional expertise through internship programs not only open great opportunities but also increase chances of success in various projects as a result." – Dedan Githae



BREAKING THE ICE – WAYS TO ENHANCE YOUR NETWORKING

We have all been there – the fear of walking into a conference or group meeting for the very first time. While for some of us, networking and chatting about science may come easily, others may find it challenging. And now to make the situation more anxiety-ridden, there is the added encouragement or pressure of using social networking tools.

The truth is networking plays a vital role in the professional existence. It is an essential piece of our daily development and success. Networking not only enables us to meet new people, but it provides us with a wealth of information.

Successful networking can be easy by just following a few simple tips and tricks.

1. Become involved by volunteering. The easiest way to enhance your networking skills is through practice, and what is better practice than with a small group of individuals that have a common interest in mind. Find meet-ups or small regional group meetings in your area. ISCB has many affiliated groups and student regional groups that may have local activities.

2. Be yourself. You do not have to be a great small talker to be a good at networking. Stick to conversation that makes you comfortable. Talk about your organization, hobbies, or recent success stories. Sometimes, just listening, can be a helpful tool. The listener is then able to ask great questions.

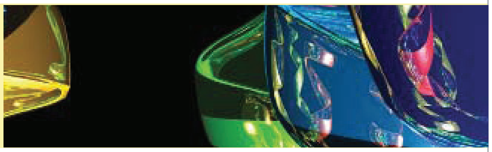
3. Ask open-ended questions. This means questions that ask who, what, where, when, and how as opposed to those that can be answered with a simple yes or no. This form of questioning opens up the discussion and shows listeners that you are interested in the topic.

4. Remember to self-edit. With the rise of social networking, it is important to remember that posting entries through social networking platforms is like chiseling into stone. Yes, you can remove and edit your information, but somewhere it is stored exactly as you originally drafted. Choose your words carefully when blog-ing, tweeting, or FaceBook-ing. Remember your audience, proof before you post, and ask yourself “would I want my mother to read this in the daily newspaper?” or “Am I damaging myself or my career?”

5. Have fun. Getting to know others and creating personal relationships should be fun. If you consider yourself to be a shy or timid person, ask a colleague to attend with you. If you do not know anyone, introduce yourself at the registration table. Let them know you are attending the event for the first time, and more likely than not, they will be able to get you connected with someone who can show you the ropes.

Networking does not have to be intimidating, it can be enriching and fun!

AFFILIATES CORNER - SPOTLIGHT APBIONET, JSBI, ASBCB



APBioNet

The Asia-Pacific Bioinformatics Network (APBioNet; www.apbionet.org) is a nonprofit, nongovernmental, international organization founded in 1998 that focuses on the promotion of bioinformatics in the Asia-Pacific region. Its mission, since its inception, has been to pioneer the growth and development of bioinformatics awareness, training, education, infrastructure, resources, and research among member countries and economies (http://dx.plos.org/10.1371/journal.pcbi.1003317). In 2012, APBioNet was incorporated in Singapore as a public limited liability company to ensure quality, sustainability, and continuity of its mission to advance bioinformatics across the region and beyond. In the same year, APBioNet became a founding member of The Global Organization for Bioinformatics Learning, Education and Training (GOBLET; http://mygoblet.org) to coordinate bioinformatics training activities worldwide, and participated in its annual general meeting (AGM) this year.

As an effort to promote Bioinformatics education in the region and beyond, APBioNet Executive Committee member, Dr. Ge Gao, and his colleague Dr. Liping Wei of Peking University, China, jointly launched the second in the world Massive Open Online Course (MOOC) entitled "Bioinformatics: Introduction and Methods" (www.coursera.org/course/pkubio-info). As a support to other conferences, APBioNet sponsored 2,000 USD to the International Symposium on Computational Biology and Drug Design that was held in India from July 10-12, 2013. Notably, many of the initiatives and activities of APBioNet have been initiated through its flagship annual conference, the International Conference on Bioinformatics (InCoB).

This year, the 12th International Conference on Bioinformatics (InCoB2013) was held for the first time in China (http://incob.apbionet.org/incob13; Sept. 20-22). APBioNet awarded 2,000 USD, plus 2,000 USD support from International Society of Computational Biology (ISCB) as travel grants to deserving attendees. Accepted manuscripts to the conference have been published in *BMC Genomics* (16 papers), *BMC Bioinformatics* (13 papers), and several (16) for the first time in BMC Systems Biology (10) and the new open access journal PeerJ (6). Additionally, accepted papers and posters were offered the opportunity to submit their presentations to F1000 Posters for public dissemination.

During the APBioNet AGM at InCoB2013, a resolution was passed to introduce APBioNet membership fees in order to sustain and streamline operations, and in return to progressively offer good tangible benefits to the members that commensurates with the membership categories. InCoB2014 will be held in Sydney, Australia (http://incob.apbionet.org/incob14; July 31 to August 2, 2014) sharing keynote speakers with the International Union for Pure and Applied Biophysics [IUPAB] 2014 Congress.

JSBI - JAPANESE SOCIETY FOR BIOINFORMATICS

Membership:
Regular member: 465
Student member: 139
Corporate member: 23 companies

Director: Kiyoshi Asai, Prof., the University of Tokyo / Director, Computational Biology Research Center, National Institute of Advanced Industrial Science and Technology

Vice Director: Kentaro Shimizu, Prof., the University of Tokyo

Number of BoD Members: 22
The Japanese Society of Bioinformatics (JSBi) was founded in 1999 with 79 proposing members for promoting research and educational activities in bioinformatics as well as for promoting relevant technologies and industries in Japan. Our activity is rich in variety as described below; we hold an annual conference as the core of our activity (attended by 582 in 2013), support 3 SIGs, 6 regional branches, scientific awards, a certification program and more.

Annual Conference:
JSBi 2013 / The 2nd Joint Conference on Informatics in Biology, Medicine and Pharmacology

The Japanese Society for Bioinformatics (JSBi) held its annual 3-day meeting, joint with the Chem-Bio Informatics Society (CBI) and Japan Association for Omics-based Medicine (Omix), at Tower Hall Funabori in Tokyo. 582 delegates (including CBI and Omix members) attended.

Awards:
Oxford Journals - Japanese Society for Bioinformatics Prize

Founded in 2001, granted by Oxford University Press. One winner is selected yearly. The selection criteria is detailed at www.jsbi.org/en/about/ojp_criteria/

The 2013 Winner was Dr. Takeshi Obayashi, Associate Professor, Graduate School of Information Sciences, Tohoku University for his research entitled "Development of Gene Function Prediction Platform Using Gene Coexpression."

The 12 winners from previous years are listed here www.jsbi.org/en/about/ojp_criteria/ojp/

Poster Awards JSBi2013
The JSBi2013 program committee selected one best and 7 excellent poster awards from 94 submissions.
The winners are listed here:
www.jsbi.org/en/announcement/topics/jsbi2013pa-en/

Certificates:
JSBi manages "The Certification Examination for Bioinformatics Engineers" which has certified bioinformatics skilled technicians based on an annual examination (in the Japanese language) since 2007. The level of the examination is roughly on par with a full undergraduate course on bioinformatics. In 2013, 134 examinees participated in this exam.

SIGs
In addition to our annual meeting and other activities, JSBi also has several active SIG communities, including one on Bio-Systems Theory chaired by Prof. W. Fujibuchi of Kyoto Univ., one on Pharma-Informatics chaired by Dr. Teruki Honma of RIKEN and one on agribioinformatics chaired by Prof. K. Shimizu of the Univ. of Tokyo. Various regions of Japan are served by six regional branches from the northern of Hokkaido all the way to the especially active group located in semi-tropical Okinawa.

ASBCB –AFRICAN SOCIETY FOR BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

Website: www.asbcb.org/index.php

Membership:
Regular member: 465
Student member: 139
Corporate member: 23 companies

Governing Board:
President: Nicky Mulder
Vice President: Segun Fatumo
Secretary: Ezekiel Adebiyi
Treasurer: Alia Benkahla
Additional Member: Daniel Masiga
Additional Member: Seydou Doumbia
Webmaster (Membership): Jaco de Ridder
Newsletter Editor: Beatrice Kilel

About ASBCB:
ASBCB, established in February 2004, is a non-profit professional association dedicated to the advancement of bioinformatics and computational biology in Africa.
The Society is serving as an international forum and resource devoted to developing competence and expertise in bioinformatics and computational biology in Africa.
It complements its activities with those of other international and national societies, associations and institutions, public and private, that have similar aims. It also promotes the standing of African bioinformatics and computational biology in the global arena through liaison and cooperation with other international bodies.

Achievements in 2013:
The key event for the society in 2013 was the ISCB Africa ASBCB Conference on Bioinformatics and its associated workshops, held in Casablanca, Morocco in March. The conference was originally supposed to take place in Tunis, but due to unrest in Tunisia, we had to move the conference to Morocco, which involved many last minute changes!

Figure 1. Photo of workshop trainers and participants outside the venue at the Institute Pasteur Morocco.

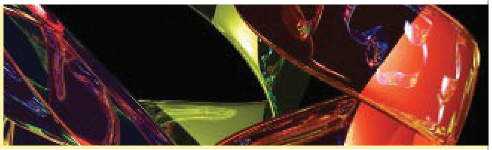
Several workshops were held at the Institute Pasteur Morocco prior to the conference, see figure 1 for some of the participants. The conference itself took place at the Novotel Casablanca City Center Hotel and ran over 3 days. Sessions were full of high quality peer reviewed and keynote talks in the areas of host-pathogen systems biology, database and tool development, molecular epidemiology and evolution, vaccines and drugs, and functional, structural and comparative genomics. In total there were 34 peer reviewed talks and six keynote speakers, including Muntaser Ibrahim, Jean-Michel Claverie, Erik Bongcam-Rudloff, Alfonso Valencia, Jessica Kissinger and Seydou Doumbia. The Conference was attended by 80 scientists from around the world, with the majority coming from Africa. Through generous sponsorship from the Wellcome Trust, as well as H3ABioNet and the National Institute of Allergy and Infectious Diseases (NIAID), we were able to offer a total of 31 travel fellowships for African students to attend the conference and workshops (Figure 2).

Figure 2. Photo of travel fellowship recipients together with some of the conference organizers.

In 2013 the society decided to update its logo and after a vote from our members, we settled on the one shown here:

ASBCB

GET TO KNOW YOUR ISCB LEADERS



ISCB thrives and grows as a scientific society through the stewardship of its members. ISCB leaders in particular have devoted great time and energy toward making ISCB an asset to the computational biology community and a trusted representative of its membership.

In this column, ISCB leaders will be profiled to better acquaint members with the scientists who work in earnest for the betterment of the society. This first installment profiles members of ISCB Executive Committee.

BURKHARD ROST, PH.D.
President, ISCB

Alexander von Humboldt Professor and Chair, Bioinformatics & Computational Biology, Computational Sciences, Technical University Munich, Munich, Germany

Burkhard Rost is professor at the TUM in Munich (Technische Universitaet) in the Department of Informatics with an affiliation at Institute for Food and Plant Sciences (WZW), a fellowship at the Institute of Advanced Studies (TUM-IAS), and the Department of Biochemistry & Molecular Biophysics at Columbia University in New York.

Our lab develops computational methods that aid in the annotation of genomes, in particular, that predict aspects of protein function and structure. Our special expertise is the combination of evolutionary information with machine learning. Having introduced the first breakthrough implementing this concept two decades ago, the lab has been refining the technology ever since. The most recent focus is on trying to understand the implications of sequence variations, e.g. in the context of personalized health.

Dr. Rost has been president of ISCB since 2007 and has guided the Society through a major growth and development period. His work as President has been vital to linking the U.S. and European computational biology communities, and his vision to have ISCB support regional computational biology and bioinformatics meetings around the world has helped give ISCB a global presence.

ALFONSO VALENCIA, PH.D.
President-elect, ISCB

Structural and Computational Biology Program, Spanish National Cancer Research Centre (CNIO), Madrid, Spain

Dr. Valencia research interests explore how protein complexes influence cellular processes that contribute to cancer, including DNA splicing and repair, genome stability, and cell cycle control. He uses computational approaches to study and compare different cancer genomes to better understand how DNA mutations contribute to cancer. Dr. Valencia has served ISCB in many capacities throughout his career, including serving on the founding Executive Committee. He will begin his term as President in January of 2015.

TERRY GAASTERLAND, PH.D.
Vice President, ISCB

Professor, Genomics and Bioinformatics, University of California, San Diego, Scripps Genome Center, Scripps Institution of Oceanography, La Jolla, CA, USA

Dr. Gaasterland's work is focused on developing computational methods for analyzing and integrating a variety of data, including genomes, transcriptomes, and mass spectrometry-derived peptides. Dr. Gaasterland has worked extensively on building algorithms that use this integrated data to better understand how basic biological mechanisms work. Dr. Gaasterland is a founding member of the ISCB Executive Committee. She was a Co-Chair of ISMB 2012, has served on several other ISCB committees, and has represented ISCB as a FASEB advisor.

THOMAS LENGAUER, PH.D.
Vice President, ISCB

Director, Max Planck Institute for Informatics, Saarbrücken, Germany

Dr. Lengauer has diverse research interests in the field of computational biology, with a focus on disease-oriented bioinformatics, especially viral evolution and resistance analysis, genomic and epigenomic analysis as well as protein bioinformatics. He coordinates the data analysis effort the German Epigenome Program DEEP (Deutsches Epigenom Programm) and is involved in global research efforts to generate standardized epigenomes from a variety of human and mouse cell types (IHEC). Dr. Lengauer is a founding ISCB Executive Committee member and has supported ISCB's extensive activities through his serviceon numerous committees and as a Chair and Co-Chair of ISMB in 1999 and 2007, respectively.

Leaders continued

MICHAL LINIAL, PH.D.
Vice President, ISCB

Professor of Biochemistry,
Department of Biological
Chemistry, The Sudarsky Center
for Computational Biology,
The Hebrew University of
Jerusalem Life Sciences Institute,
Jerusalem, Israel

Dr. Linial's research encompasses two main areas, the molecular and cell biology of the neuron, and bioinformatics. She uses genomic and proteomic analysis to understand the differentiation and developmental program of neurons, and she has developed computational tools to examine protein-protein interactions, protein function classification, and structural genomics. Dr. Linial has served ISCB as a Student Council Liaison and been a member of the Conference, Education, and Fellows Committees. She has also Co-Chaired ISMB 2008, 2010, and 2011.

CHRISTINE ORENGO, PH.D.
Vice President, ISCB

Professor, Bioinformatics,
Department of Structural and
Molecular Biology,
University College London,
London, United Kingdom

Dr. Orengo's work is focused on developing computational tools that classify proteins into evolutionarily relevant groups. She studies other aspects proteins and uses bioinformatics tools to predict structure and reveal functional networks. She and her group have developed and maintain several bioinformatics resources, including CATH, a resource for analyzing and comparing protein domains. Dr. Orengo has served ISCB as Chair of the Workshops Committee, a Co-Chair of the Conference Committee, and a member of the Finance, Awards and SIG Committees.

REINHARD SCHNEIDER, PH.D.
Treasurer, ISCB

Head of Bioinformatics Core
Facility, Luxembourg
Centre for Systems Biomedicine
(LCSB),University of
Luxembourg, Luxembourg

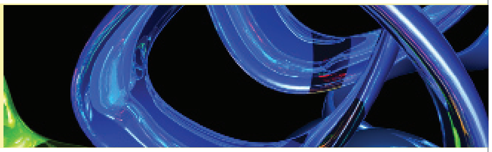
Dr. Schneider heads the Bioinformatics Core Facility at the Luxembourg Centre for Systems Biomedicine (LCSB), where he works at the interface between bench science and computation. He has been involved with the development of numerous algorithms and bioinformatics tools and is responsible for coordinating the analysis and annotation of large volumes of clinical data generated by the LCSB and outside partners. Dr. Schneider has been ISCB Treasurer for two consecutive terms and has been Chair of the Governance, Audit, and Fundraising Committees. He has also served on several other ISCB committees.

SCOTT MARKEL, PH.D.
Secretary, ISCB

Principal Bioinformatics Architect,
Accelrys, Inc.,
San Diego, CA, USA

Dr. Markel works as a Principal Bioinformatics Architect in the research and development group at Accelrys. He focuses on software products for workflow and data pipelining in the areas of sequence analysis and next gen sequencing. Dr. Markel serves on the editorial boards of *PLOS Computational Biology* and *Briefings in Bioinformatics*. Dr. Markel is a member of the FASEB Publications and Communications Committee, is Chair of the ISCB Publications and Communications Committee and has served on several other ISCB committees.

UPCOMING CONFERENCES & EVENTS



ISCB CONFERENCES

GLBIO 2014
May 16 - 18, 2014
Cincinnati, OH
www.iscb.org/glbio2014/
Hosted by: Cincinnati Children's Hospital Medical Center
The 4th GLBIO provides an interdisciplinary forum for the discussion of research findings and methods. An important goal for the conference is to foster long term collaborative relationships and networking opportunities within the domain of computational approaches to biology.

The NGS Conference
June 2 - 4, 2014
Barcelona, Spain
www.iscb.org/ngs2014
The goal of this conference is to bring together bioinformatics researchers and biologists facing new high-throughput sequencing challenges. The conference will feature presentations showing how current platforms can be used to address key biological questions and what is the current state of the art for data analysis. Sizeable space will also be dedicated to emerging and future trends in high-throughput sequencing and their associated computational challenges.

Intelligent Systems for Molecular Biology 2014
July 11 - 15, 2014
Boston, Massachusetts, USA
www.iscb.org/ismb2014
The Intelligent Systems for Molecular Biology (ISMB) conference brings together computational biology researchers of every career stage from around the world. Hosted by the International Society for Computational Biology (ISCB), ISMB has grown over 22 years to become the world's largest bioinformatics/computational biology conference.

ISCB Latin America Conference on Bioinformatics
Oct 28 - 30, 2014
Belo Horizonte, Brazil
www.iscb.org/iscb-latinamerica2014
The conference will feature an exceptional slate of keynote speakers and provide a forum for the dissemination of the latest developments in Computational Biology and Bioinformatics research conducted around the world and regionally.

GIW/ISCB-Asia International Conference on Genome Informatics
Dec. 15 - 17, 2014
Tokyo, Japan
www.jsbi.org/giw2014/
The 25th anniversary of GIW – International Conference on Genome Informatics will feature a remarkable line up of keynote speakers over 3 days.

ISCB AFFILIATED CONFERENCES

Bio-IT World Conference & Expo 2014
April 29 - May 1, 2014
Boston, MA
www.bio-itworldexpo.com
The Expo provides the perfect venue to share information and discuss enabling technologies that are driving biomedical research and the drug development process. Spanning three days, the meeting includes 13 parallel conference tracks and 16 pre-conference workshops.

CHI's Structure-Based Design
May 21 – 22, 2014
Boston, MA
www.healthtech.com/structure-based-drug-design
Cambridge Healthtech Institute's Fourteenth Annual Structure-Based Drug Design event will showcase informative, high-quality case studies, innovative techniques, and strategies to move from computation to experiment, and finally, to drug. Top scientists from pharma and biotech will address how they are hitting epigenetic targets, provide updates on the newest wave of GPCRs and other membrane proteins, and discuss the latest in fragment-based drug design. Attendees will return to their organizations with fresh perspectives and new ideas to maximize productivity and increase successes in drug discovery.

4th Symposium on Biological Data Visualization (BioVis)
Jul 11 – 12, 2014
Boston, MA
http://biovis.net
The premier international and interdisciplinary events for presenting peer-reviewed scientific work in the field of Biological Data Visualization (BioVis 2014).

For the first time, this year the symposium will be held as a special interest group meeting at ISMB in Boston, MA, USA

HiTSeq 2014 High Throughput Sequencing Algorithms & Applications
Jul 11 – 12, 2014
Boston, MA
www.hitseq.org/
The Conference on High Throughput Sequencing Methods and Applications (HiTSeq 2014) is a Satellite of the ISMB 2014 conference and brings together biologists and computational scientists interested in exploring the challenges and opportunities in the analysis of high-throughput sequencing (HTS) technologies. HiTSeq 2014 is devoted to the latest advances in computational techniques for the analysis of high-throughput sequencing data including novel algorithms, analysis methods and applications in biology where high-throughput sequencing data has been transformative.

InCoB2014 – 13th International Conference on Bioinformatics
Jul 31 - Aug 02, 2014
Sydney, Australia
http://incob2014.org
The main local host is Macquarie University, one of the leading research centres in Australia in the field of Bioinformatics. InCoB2014 will build on the established platform for experts and budding bioinformaticians to discuss and exchange ideas and thoughts on the development of bioinformatics in the Asia-Pacific region.

ECCB'14, the 13th European Conferences on Computational Biology
Sep 07 – 10, 2014
Strasbourg, France
www.eccb14.org
ECCB'14 is the key European computational biology event in 2014 gathering scientists working at the intersection of a broad range of disciplines including computer science, mathematics, biology, and medicine. New challenges are emerging today in these fields with the recent advances in low-cost ultra-fast sequencing, bio-imaging and big-data approaches.

While ISCB provides for news, conference and event listings that may be of interest to members and bioinformaticians at large, ISCB is not responsible for the content provided by outside sources. Such listings are not meant as an endorsement by ISCB.

UPCOMING ISCB CONFERENCES

GLBIO 2014

GREAT LAKES BIOINFORMATICS CONFERENCE

An official conference of the International Society for Computational Biology

May 16 - 18, 2014
Cincinnati, OH
Cincinnati Children's Hospital Medical Center

www.iscb.org/glbio2014

NGS'14

FRED SANGER 1918 - 2013

NEXT GENERATION SEQUENCING CONFERENCE

KEYNOTE SPEAKERS

KRISTIN ARDLIE
The Broad Institute of Harvard and MIT, USA

THOMAS GINGERAS
Cold Spring Harbor Laboratory, USA

JOHN MARIONI
EMBL-EBI
United Kingdom

CORNELIA VAN DUIJN
The Erasmus University Medical Center
Netherlands

JUNE 2 - 4, 2014
BARCELONA
SPAIN

An Official Conference of the International Society for Computational Biology

CRG Centre for Genomic Regulation

www.iscb.org/ngs2014

ISCB Latin America Conference on Bioinformatics

MARK YOUR CALENDARS for
October 28 - 30, 2014
Belo Horizonte, Brazil

www.iscb.org/iscb-latinamerica2014

An Official Conference of the International Society for Computational Biology

RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges 2014

November 10 - 14, 2014 San Diego, CA

www.iscb.org/recomb-regsysgen2014

An Official Conference of the International Society for Computational Biology

ROCKY 2014

December 11 - 13, 2014
Aspen/Snowmass, USA

12th Annual Rocky Mountain Bioinformatics Conference

www.iscb.org/rocky2014

An Official Conference of the International Society for Computational Biology

www.iscb.org

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Anna Dehof
Saarland University, Germany
"Reflections on Protein Structures"