iSCB
INTERNATIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY
OFFICIAL CONFERENCE

GLBIO

Great Lakes Bioinformatics Conference

GLBIO 2019

University of Wisconsin-Madison
Madison, Wisconsin

May 19-22, 2019
Program Booklet

Thomas LENGAUER, President
Bonnie BERGER, Vice President
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Scott MARKEL , Secretary
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INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

Dear GLBIO Conference Participant,

Welcome and thank you for making the decision to attend. The International Society for Computational Biology (ISCB) once again has the privilege of being a host along side the Great Lakes Bioinformatics Consortium (GLBC) to bring you this conference. ISCB is grateful for the partnership with GLBC to produce this outstanding conference, which will provide you the opportunity to share the rapidly growing body of knowledge through presentation of research results, information exchange, networking, and open discussion.

ISCB is dedicated to providing high quality meetings to our members and the scientific community. Serving over 3,200 members worldwide, we strive to connect, train, and empower the community. Each sponsor, exhibitor, individual on the organizing and program committees have helped advance our mission. Putting on a conference of this caliber takes a tremendous amount of effort. We are grateful to all of our dedicated volunteers who have worked selflessly to execute the conference especially: Program Chairs, **Anthony Gitter**, University of Wisconsin-Madison, **Chad Myers**, University of Minnesota, **Sushmita Roy**, University of Wisconsin-Madison as well as our Conference Chairs **Russell Schwartz**, Carnegie Mellon University and **Lonnie Welch**, Ohio University, as well as **Belinda (Bel) Hanson,** ISCB, for her professional execution of the logistics of the conference. Please take a moment to review the list of committee members and volunteers on the website and share your warm appreciation if you see them.

If you are not already a member of ISCB, we encourage you to join. We are confident that your membership experience and the benefits will exceed the investment. To our members, thank you for your continued support of the Society. We are a small society driven by your passion, your visions, and by your activities. We encourage you to get involved to help drive our society forward.

Together with our partners, we encourage you to make the best of every networking, learning, sharing and teaching moment of the conference. An opportunity like this to share high-level science in such a vibrant computational biology and bioinformatics region does not present itself every day. Enjoy it to the fullest!

Sincerely,

Thomas Lengauer
ISCB President

Diane E. Kovats
ISCB Executive Director

Dear GLBio 2019 Participants,

We enthusiastically welcome you to the premier regional bioinformatics meeting of the Great Lakes states and provinces - the 13th Great Lakes Bioinformatics Conference!!!

Organized in a partnership between the Great Lakes Bioinformatics Consortium and the International Society for Computational Biology, GLBio features an outstanding opportunity to meet research leaders and to hear presentations of cutting-edge research. This year's Program Chairs (Sushmita Roy, Anthony Gitter, and Chad Myers) have put together a rich offering of research presentations on topics such as Precision Medicine, Gene Regulation, Machine Learning, Microbiomes, RNA Structure, Networks, and Education.

We hope that you enjoy the scientific program and the networking opportunities during your time in Madison.

Warm regards,
Russell Schwartz and Lonnie Welch
Steering Committee Co-Chairs of GLBio 2019

GLBIO

GREAT LAKES BIOINFORMATICS CONFERENCE May 19-22, 2019

The University of Wisconsin-Madison

iSCB INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY Official Conference

To our friends and colleagues from the and beyond - Welcome to Madison!

We are excited to host the Great Lakes Bioinformatics (GLBIO) conference at the University of Wisconsin-Madison! The GLBIO conference, which started as an effort to bring together the bioinformatics community in the Great Lakes area, is now in its 13th year. This year’s program includes a collection of outstanding keynotes, special sessions, workshops, and poster presentations. The special sessions focus on emerging areas of computational biology and include topics ranging from education, precision medicine, challenges in the RNA world, and understanding the microbiome. This year we are also proud to showcase a student-organized workshop focusing on the very timely topic of “dimensionality reduction”, which we think is going to be of interest to many of you. The general track has been organized into different thematic topics spanning comparative functional genomics, network biology, gene regulation, macromolecular function, and clinical informatics. The talks cover the whole spectrum of computational biology research ranging from fancy algorithms to applications of tools to tackle fundamental questions in biology. Interleaved with the scientific program, we have planned two social events: The Lunch & Learn event to learn about different career paths in computational biology and The Game Night Networking Event at the Sett, where you might try out your bowling skills. We hope that you will enjoy the scientific program, which we think should be intellectually stimulating and a fun learning event. Don’t forget to check out the diversity of Madison dining options and the beautiful lake side view at the Memorial Union with local specialties like Babcock ice cream!

Use #GLBIO19 to follow along on social media.

We look forward to welcoming you!

Sincerely,

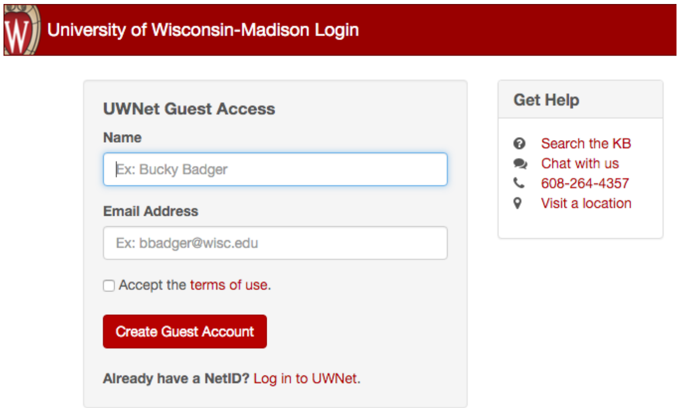
Anthony Gitter, University of Wisconsin-Madison
Chad Myers, University of Minnesota
Sushmita Roy, University of Wisconsin-Madison

On behalf of the GLBIO 2019 Organizing Committee

WiFi Info:

Once in range select the wireless network 'UWNet' and you will be automatically redirected to the UWNet registration page. For all attendees **NOT** affiliated with the University of Wisconsin use the **GUEST** option:

To register, simply enter your full name and email address. Once you have read and agreed to the Terms of Use, click **Create Guest Account** to submit your information.



University of Wisconsin-Madison Login

UWNet Guest Access

Name: Ex: Bucky Badger

Email Address: Ex: bbadger@wisc.edu

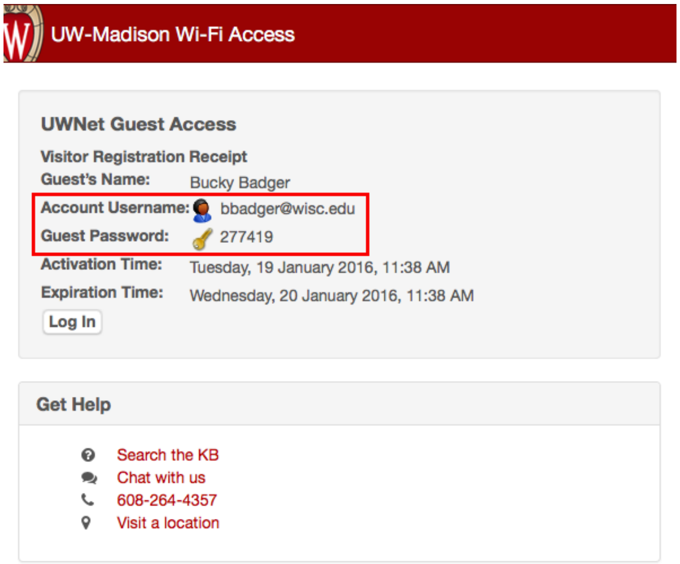
☐ Accept the terms of use.

Create Guest Account

Already have a NetID? Log in to UWNet.

Get Help

- Search the KB
- Chat with us
- 608-264-4357
- Visit a location



UW-Madison Wi-Fi Access

UWNet Guest Access

Visitor Registration Receipt

Guest's Name:	Bucky Badger
Account Username:	bbadger@wisc.edu
Guest Password:	277419
Activation Time:	Tuesday, 19 January 2016, 11:38 AM
Expiration Time:	Wednesday, 20 January 2016, 11:38 AM

Log In

Get Help

- Search the KB
- Chat with us
- 608-264-4357
- Visit a location

After submitting your email address, you will be taken to a resulting page that will assign you a username and passcode. You will need to make note of these credentials, as they allow you to access UWNet with other devices you may have, such as a smartphone. You are allowed to have up to five concurrent sessions (i.e. five different devices connected at the same time). When you are brought to the UWNet registration screen on another device, you should enter use those credentials in the NetID login fields used by affiliates.

Note: Once you have completed guest registration, you will not be able to do so again, as the system will report that your email address is already in use. If you lose or forget your temporary UWNet credentials, please contact the DoIT Help Desk.

Get the Conference App:

https://mobile-mobile.swoogo.com/app/oi3s1a

or search 'Swoogo Attendee Mobile' on Google play or the Apple App store and download the App. Once you have downloaded the App, please search 'GLBIO 2019'

Thank you for attending the GLBIO 2019 Conference. Please read all of the information provided below and visit the conference registration desk should you have any additional questions about conference activities.

ATM

Please stop by registration for information regarding the closest ATMs

Awards

The following awards will be presented at the closing ceremony:
Best Presentation and Best Poster

Badge Policy and Ribbons

Your name badge functions as your admission to all official conference activities. As a safety tip, please remember to take off your conference badge any time you go outside the conference area.

Cell Phones

As a courtesy to your fellow attendees, and especially the presenters and speakers, please turn off or silence your cell phone or any other portable electronic devices.

Certificates of Attendance

Certificate of attendance will be sent via email at the end of the conference.

Conference Evaluation Forms

The conference evaluation will be emailed to all registrants. Please take a few moments to complete the evaluation, as it provides valuable feedback that assists in planning future conferences.

Emergencies

In the event of a medical emergency, please call 911 from your cell phone. Be prepared to give the building and floor where the emergency has occurred on and the room number you are in or nearest to, as well as the type of emergency.

Endorsements

GLBIO does not endorse the products or services displayed or sold by sponsors, exhibitors or advertisers, or the views expressed by any speaker or other conference participant.

Job Opportunities

A poster board will be available near the ISCB Exhibit Table for companies to post jobs and candidates to post resumes. If you require any assistance on-site with the job opportunities board, please ask at the registration desk.

Meeting Room Overcrowding

GLBIO will make every effort to schedule topics in rooms of adequate proportions. However, as many topics are extremely popular, it is wise to arrive early and have pre-selected alternative sessions as you plan your conference schedule. Law requires GLBIO and the University of Wisconsin, to follow room capacity regulations set forth by the fire marshal. We ask that you respect request from conference staff in regards to room overcrowding. We appreciate your cooperation. Thank you.

Membership

If you are interested in joining ISCB, please proceed to the registration desk or www.iscb.org for more information.

Poster Sessions

Poster presentations will be held during two sessions, Odd Number Session and Even Number Session. Posters are listed by number online at https://www.iscb.org/glbio2019-program/glbio2019-posters and assigned number will be located on the poster boards.

If you are in the Odd Number Session, you may set up your poster any time between 8:30am and noon on Tuesday and must remove your poster by 5pm on Tuesday. All remaining posters will be discarded.

If you are in the Even Number Session, you may set up your poster any time between 8:30am and noon on Wednesday and must remove your poster by 5pm on Wednesday. All remaining posters will be discarded.

Registration

DISCOVERY BUILDING - LOBBY
SUNDAY, MAY 19 8:30AM-5:30PM
UNION SOUTH – VARSITY HALL LOUNGE
MONDAY, MAY 20 8:30AM-5:30PM
TUESDAY, MAY 21 8:30AM-5:30PM
WEDNESDAY, MAY 22 8:30AM-3:30PM

Social Events

COFFEE BREAKS

Beverages and light snacks will be available during the session breaks in the morning and afternoon.

LUNCH

Will be provided, buffet style, during the Lunch N Learn Recruitment event on Monday. Lunch will be 'on-own' if you do not plan to attend this event. On Tuesday and Wednesday, box lunches, will be provided during both poster sessions.

WELCOME RECEPTION

Light hors d'oeuvres and one YELLOW drink ticket will be provided at the Sunday evening event.

GAME NIGHT NETWORKING EVENT

Tailgate style and one ORANGE drink ticket will be provided at the Tuesday evening event, for those who purchased tickets.

Smoking Policy

Please note that smoking is NOT permitted in any University buildings. Smoking is only permitted in designated areas.

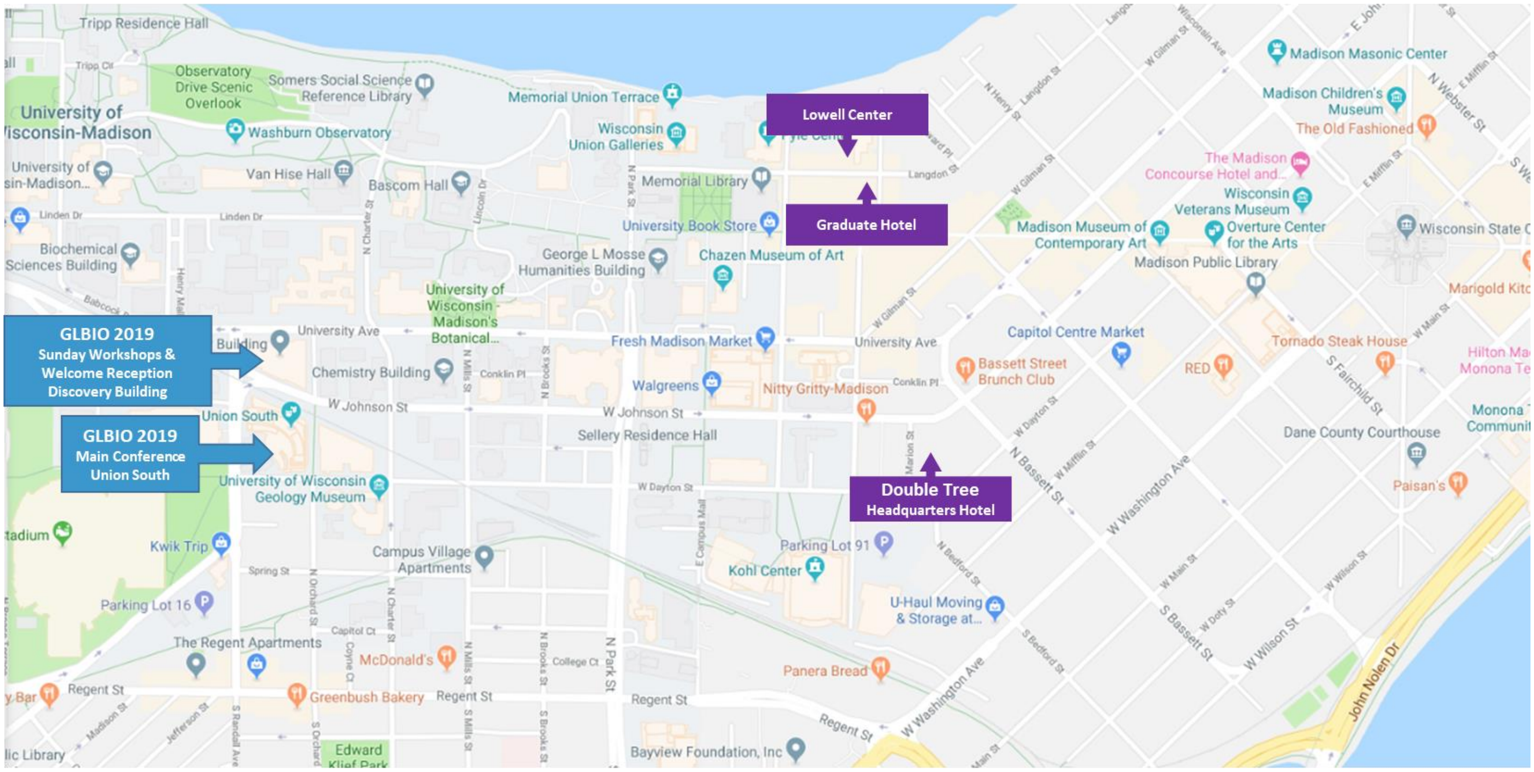
Transportation

Please note that transportation is NOT provided by ISCB for this conference. Conference locations are approximately a 12-15 minute walk from the three conference hotels. Additionally, your hotel may have a shuttle. Please check with your hotel directly.

Website for GLBIO

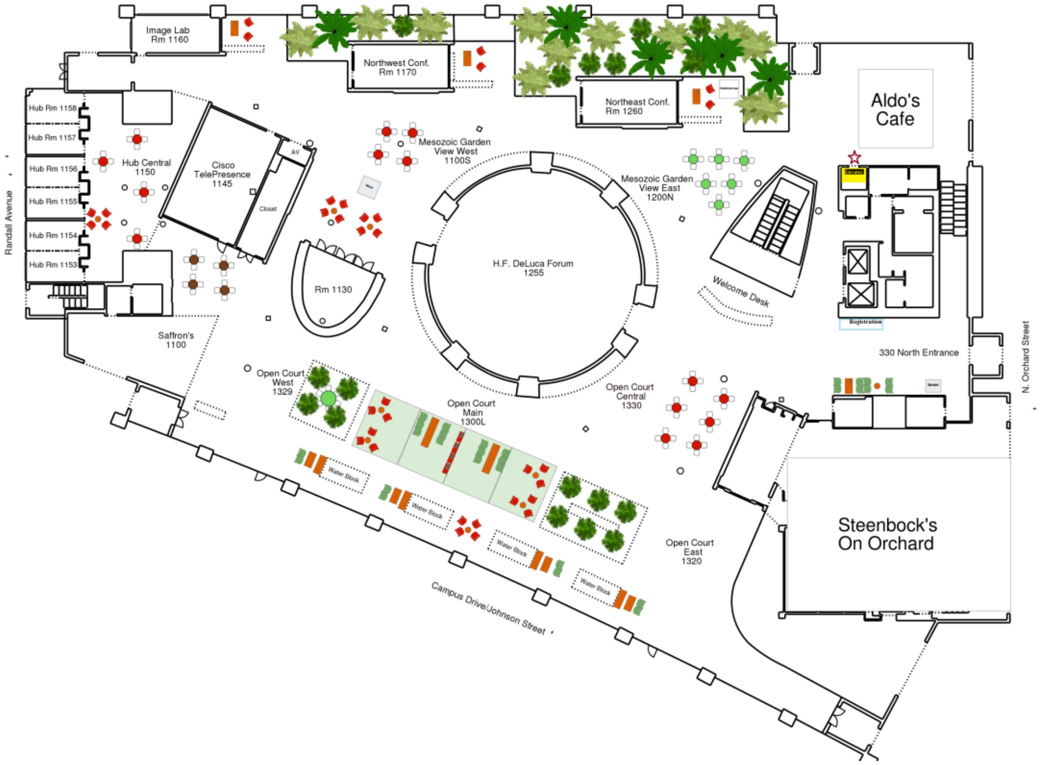
For additional and more detailed information please visit the conference website at https://www.iscb.org/glbio2019

Madison Map – Conference Venues and Hotels



🟦 Conference Activities
🟪 Conference Hotels

Discovery Building – Ground Floor



Union South Building – 2nd Floor

Agenda at a Glance - Sunday & Monday

Sunday – All events will occur at the Discovery Building		
Start Time	End Time	
8:30 AM	5:30 PM	Registration in Discovery Building Lobby
9:00 AM	12:00 PM	Workshop on UCSC Genome Browser (Orchard View Room)
12:00 PM	1:00 PM	Lunch on Own
1:00 PM	5:00 PM	Workshop on Docker (Orchard View Room)
5:30 PM	7:00 PM	Welcome Reception in Discovery Building Lobby Music by Sonora Strings

Monday – All events will occur at the Union South Building				
Start Time	End Time	The Marquee	Fifth Quarter	Varsity Hall I
8:30 AM	3:30 PM	Registration in Union South - Varsity Hall Lounge		
9:00 AM	9:30 AM	Welcome		
9:30 AM	10:30 AM	Keynote #1 Sunduz Keles		
10:30 AM	11:00 AM	Coffee break in Varsity II & III		
11:00 AM	12:00 PM	General Track - Macromolecular Structure & Function	Precision Medicine I	Education I
12:00 PM	1:30 AM	Lunch on own or Lunch N Learn Recruiting Roundtable		
1:30 PM	2:30 PM	General Track – Gene Regulation I	Precision Medicine II	Education II
2:30 PM	3:00 PM	Coffee break in Varsity II & III		
3:00 PM	5:00 PM	General Track - Comparative Genomics & Phylogenetics	Precision Medicine III	Education III
5:00 PM	6:00 PM	Keynote #2 Dan Knights		
7:00 PM	10:00 PM		Student Led Workshop	

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Agenda at a Glance - Tuesday & Wednesday

Tuesday – All events will occur at the Union South Building

Start Time	End Time	The Marquee	Fifth Quarter	Varsity Hall I
8:30 AM	5:30 PM	Registration in Union South - Varsity Hall Lounge		
9:00 AM	10:00 AM	Keynote #3 Quaid Morris		
10:00 AM	10:30 AM	Coffee break in Varsity II & III		
10:30 AM	12:00 PM	General Track – Gene Regulation II	Microbiome I	RNA Sequence to Structure I
12:00 PM	1:30 PM	Poster Session #1 (odd numbered) in Varsity II & III (boxed lunches)		
1:30 PM	2:30 PM	General Track - Networks I	Microbiome II	RNA Sequence to Structure II
2:30 PM	3:00 PM	Coffee break in Varsity II & III		
3:00 PM	5:00 PM	General Track - Algorithms & Machine Learning	Microbiome III	RNA Sequence to Structure III
5:00 PM	6:00 PM	Keynote #4 Hae Kyung Im		
7:00 PM	10:00 PM	Game Night Networking Event at The Sett		

Wednesday – All events will occur at the Union South Building

Start Time	End Time	The Marquee	Varsity Hall I
8:30 AM	3:30 PM	Registration in Union South - Varsity Hall Lounge	
9:00 AM	10:00 AM	Keynote #5 - R. Stephanie Huang	
10:00 AM	10:30 AM	Coffee break in Varsity II & III	
10:30 AM	12:00 PM	General Track - Networks II	General Track - Clinical and Health Informatics I
12:00 PM	1:30 PM	Poster Session #2 (even numbered) in Varsity II & III (boxed lunch)	
1:30 PM	2:30 PM	General Track - Genome Informatics	General Track - Clinical and Health Informatics II
2:30 PM	3:00 PM	Coffee break in Varsity II & III	
3:00 PM	4:00 PM	Keynote #6 - Mark Craven	
4:00 PM	4:30 PM	Award Ceremony and Closing	

The Marquee on Monday, May 20, 2019

Start Time	Title	Author(s)
9:00 AM	Keynote #1	Sunduz Keles Introduction by Sushmita Roy
General Track - Macromolecular Structure & Function **Chair: Catherine Welsh**		
11:00 AM	Improved protein structure refinement using machine learning based restrained relaxation	Debswapna Bhattacharya
11:15 AM	Improving the prediction of loops and drug binding in GPCR structure models.	Bhumika Arora, Venkatesh Kareenhalli, Denise Wootten and Patrick Sexton.
11:30 AM	Modeling the Functional Activity of Protein Sequence Variants Using Graph Convolutional Neural Networks	Sam Gelman, Zhiyuan Duan, Philip Romero and Anthony Gitter
11:45 AM	Chemoinformatic signature analysis of aspen seedling root exudates under biotic and abiotic stress conditions	Peter Larsen
General Track - Gene Regulation I **Chair: Matthew Weirauch**		
1:30 PM	Integrative analysis of epigenetics data identifies gene-specific regulatory elements	Florian Schmidt, Alexander Marx, Marie Hebel, Martin Wegner, Nina Baumgarten, Manuel Kaulich, Jonathan Goeke, Jilles Vreeken and Marcel Schulz.
1:45 PM	WACS: Improving Peak Calling by Optimally Weighting Controls	Aseel Awdeh, Marcel Turcotte and Theodore Perkins.
2:00 PM	refine.bio: A resource of harmonized public gene expression data sets.	Jaclyn N. Taroni, Kurt G. Wheeler, Richard W. W. Jones, Deepashree Venkatesh Prasad, Ariel Rodriguez Romero, Candace L. Savonen and Casey S. Greene.
2:15 PM	Leveraging public epigenomic datasets to examine the role of regulatory variation in the three-dimensional organization of the genome	Brittany Baur, Jacob Schreiber, Shilu Zhang, Yi Zhang, Mohith Manjunath, Jun Song, William Stafford Noble and Sushmita Roy.
General Track - Comparative Genomics & Phylogenetics **Chair: Dannie Durand**		
3:00 PM	TreeCluster: Clustering Biological Sequences using Phylogenetic Trees	Metin Balaban, Niema Moshiri, Uyen Mai and Siavash Mirarab
3:30 PM	JalviewJS: Reintroducing Jalview as JavaScript on the Web	Robert Hanson, Geoffrey Barton, James Procter, Mungo Carstairs and Benedict Soares.
3:45 PM	Cross-species transcription factor binding prediction via domain adapted neural networks	Kelly Cochran, Divyanshi Srivastava, Akshay Balsubramani, Anshul Kundaje and Shaun Mahony.
4:00 PM	Evolution of the Metazoan Protein Domain Toolkit	Maureen Stolzer, Yuting Xiao and Dannie Durand.
4:15 PM	Mechanism of biocide resistance of bacterial isolates from hydraulic fracturing-impacted streams from Pennsylvania	Lindsey Schenten, Jeremy Chen See, Maria Fernanda Campa, Terry Hazen, Regina Lamendella and Stephen Techtmann.
4:30 PM	snacc: Sequence Non-Alignment Compression and Comparison for Inferring Microbial Phylogenies	Alex Sweeten, Rafal Mostowy and Leonid Chindelevitch.
5:00 PM	Keynote #2 - Less is More: Extracting features from shallow sequencing data	Dan Knights Introduction by Chad Myers

Fifth Quarter on Monday, May 20, 2019

Start Time	**Title**	**Author(s)**
Precision Medicine I Chair: Aritro Nath		
11:00 AM	Imputed gene expression associations identify replicable trans-acting genes enriched in immune traits	Heather Wheeler
11:20 AM	Testing and controlling for horizontal pleiotropy with the probabilistic Mendelian randomization in transcriptome-wide association studies	Xiang Zhou
11:40 AM	Integrative analysis of transcriptomic annotation data and biobank-scale GWAS summary statistics identifies risk factors for Alzheimer's disease	Qiongshi Lu
Precision Medicine II Chair: Heather Wheeler		
1:30 PM	Long non-coding RNAs are crucial pharmacogenomic biomarkers of anticancer agents beyond protein-coding genes	Aritro Nath, R. Stephanie Huang
1:50 PM	Using cancer eQTL profiles and GWAS to prioritize drug targets in cancer	Paul Geeleher
2:10 PM	Peering into germline and somatic breast cancer genomes in women of African descent	Yonglan Zheng
Precision Medicine III Chair: Qiongshi Lu		
3:00 PM	Patient derived xenografts for precision cancer medicine	Arvind Singh Mer, Wail Ba-Alawi, Petr Smirnov, Yi Wang, Ben Brew, Anna Goldenberg, Benjamin Haibe-Kains
3:15 PM	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts	Angela Andaleon, Lauren S. Mogi, Heather E. Wheeler
3:30 PM	NeTFactor, a framework for identifying transcriptional regulators of gene expression-based biomarkers	Gaurav Pandey, Mehmet Eren Ahsen, Supinda Bunyavanich, Alexandar Grishen, Galina Grishina, Yoojin Chun
3:45 PM	Systematic characterization of a set of variants from heterogeneous information	Xiaoman Xie, Casey Hanson, Saurabh Sinha
4:00 PM	Characterization of clonal evolution in microsatellite unstable metastatic cancers through multi-regional tumor sequencing	Russell Bonneville, Lianbo Yu, Julie Reeser, Thuy Dao, Michele Wing, Hui-Zi Chen, Melanie Krook, Jharna Miya, Eric Samorodnitsky, Amy Smith, Nicholas Nowacki, Sameek Roychowdhury
4:15 PM	iFunMed: Integrative Functional Mediation Analysis of GWAS and eQTL Studies	Constanza Rojo, Qi Zhang, Sunduz Keles
4:30 PM	A Pathway Perspective on Drug Response for Targeted Therapies in Acute Myeloid Leukemia	Aurora Blucher, Steve Kurtz, Cristina Tognon, Brian Druker, Guanming Wu, Shannon McWeeney
4:45 PM	GraPhyC: Using Consensus to Infer Tumor Evolutionary Histories	Layla Oesper, Kiya Govek, Camden Sikes

Varsity Hall I on Monday, May 20, 2019

Start Time	**Title**	**Author(s)**
Education I Chair: Anna Ritz		
11:00 AM	Interdisciplinary biology education: a holistic approach to an intractable problem	Kristin Jenkins
11:20 AM	Expanding Undergraduate Participation in Computational Biology: Resources and Lessons Learned from a Hands-on Workshop	Layla Oesper
11:40 AM	Network for Integrating Bioinformatics into Life Sciences Education (NIBLSE): Recent Activities	William Morgan
Education II Chair: Catie Welsh		
1:30 PM	Increasing data analysis skills in the pediatric cancer community with the Childhood Cancer Data Lab training workshops	Candace Savonen, Deepashree Prasad, Casey Greene and Jaclyn Taroni
1:50 PM	Bioinformatics in the Library: Bridging the Skills Gap for Biomedical Researchers	Pamela Shaw, Matthew Carson, Sara Gonzales, Kristi Holmes, Robin Champieux and Ted Laderas
2:10 PM	The ml4bio Workshop: Machine Learning Literacy for Biologists	Chris Magnano, Fangzhou Mu, Debora Treu and Anthony Gitter
Education III Chair: Pamela Shaw		
3:00 PM	Conference-based Undergraduate Experiences: Lowering the Barrier for Learning about Computational Biology	Anna Ritz
3:20 PM	Teaching introductory bioinformatics with Jupyter notebook-based active learning	Colin Dewey
3:40 PM	NIBLSE Incubators: A community-based model for the development of bioinformatics learning resources	Michael Sierk, Sam Donovan, William Morgan, Hayley Orndorf, Mark Pauley, Sabrina Robertson, Elizabeth Ryder and William Tapprich
4:00 PM	Next steps for the bioinformatics education community	Kristin Jenkins, William Morgan, Layla Oesper, Anna Ritz, Michael Sierk, Russell Schwartz

The Marquee on Tuesday, May 21, 2019

Start Time	Title	Author(s)
9:00 AM	Keynote #3	Quaid Morris Introduction by Shaun Mahony
General Track - Gene Regulation II Chair: Dennis Kostka		
10:30 AM	Direct prediction of regulatory elements from partial data without imputation	Yu Zhang and Shaun Mahony
11:00 AM	Discovering structural units of chromosomal organization with matrix factorization and graph regularization	Da-Inn Lee and Sushmita Roy.
11:15 AM	FreeHi-C enables systematic benchmarking of analysis methods for Hi-C Data and improves FDR control for differential Hi-C analysis	Ye Zheng and Sunduz Keles.
11:30 AM	Using Markov Random Field to Model Gene Expression in the 3D Genome	Naihui Zhou, Iddo Friedberg and Mark Kaiser.
11:45 AM	Analysis of ChIP-exo read profiles reveals spatial organizations of protein complexes	Naomi Yamada, Nina Farrell, B. Franklin Pugh and Shaun Mahony
General Track - Networks I Chair: Anna Ritz		
1:30 PM	Incorporating noisy priors for estimating transcription factor activities for genome-scale regulatory network inference	Alireza Fotuhi Siahpirani, Rupa Sridharan and Sushmita Roy.
1:45 PM	Building Robust Gene Co-expression Networks from RNA-seq Data	Kayla Johnson and Arjun Krishnan.
2:00 PM	Network analysis of synonymous codon usage	Khalique Newaz, Gabriel Wright, Jun Li, Patricia Clark, Scott Emrich and Tijana Milenkovic.
2:15 PM	Network Inference with Granger Causality Ensembles on Single-Cell Transcriptomic Data	Atul Deshpande, Li-Fang Chu, Ron Stewart and Anthony Gitter.
General Track - Algorithms & Machine Learning Chair: Lana Garmire		
3:00 PM	A new resolution function to evaluate tree shape statistics	Maryam Hayati, Bita Shadgar and Leonid Chindelevitch
3:30 PM	Topic modeling enables identification of regulatory complexes in a comprehensive epigenome	Guray Kuzu, Matthew Rossi, Naomi Yamada, Prashant Kuntala, Chitvan Mittal, Nitika Badjatia, Gretta Kellog, Frank Pugh and Shaun Mahony.
3:45 PM	The k is a lie	Gregory Way and Casey Greene.
4:00 PM	Machine learning is fast and accurate for network-based gene classification	Arjun Krishnan, Renming Liu, Christopher Mancuso and Anna Yannakopoulos.
4:15 PM	Nearest-neighbor Projected-Distance Regression (NPDR) detects network interactions and controls for confounding and multiple testing	Brett Mckinney, Trang Le and Bryan Dawkins.
4:30 PM	Gene Expression Prediction: A Machine Learning Approach	Paul Okoro, Ryan Schubert, Amy Luke, Lara Dugas and Heather Wheeler.
5:00 PM	Keynote #4 - Leveraging Large Scale Genome and Transcriptome to Decode the Biology of Complex Traits	Hae Kyung Im Introduction by Tony Gitter

Fifth Quarter on Tuesday, May 21, 2019

Start Time	Title	Author(s)
Microbiome I **Chair: Sailendharan Sudakaran**		
10:35 AM	Viral discovery in Freshwater Environments	Catherine Putonti, Jonathon Brenner, Thomas Hatzopoulos and Andrea Garretto
11:00 AM	Microbial communities within Lake Michigan nearshore waters in Chicago area	Carine Mores, Michael Zilliox and Catherine Putonti
11:15 AM	The microbial communities of bilge water, boat surfaces and external port water: a global comparison	Laura Schaerer, Ryan Ghannam, Tim Butler and Stephen Techtmann
11:30 AM	Environmental Monitoring of Crude Oil using Natural Microbial Communities and Machine Learning	Stephen Techtmann, Timothy Butler and Paige Webb
Microbiome II **Chair: Sailendharan Sudakaran**		
1:30 PM	Zero-Inflated Generalized Dirichlet Multinomial (ZIGDM) Regression Model for Microbiome Compositional Data	Zheng Zhen Tang
2:00 PM	Virus-Driven Metabolism of Sulfur Compounds: From Genes to Ecosystems	Karthik Anantharaman
Microbiome III **Chair: Catherine Putonti**		
3:00 PM	An Improved Species-level Taxonomic Classification Method for Marker Gene Sequences	Qunfeng Dong, Xiang Gao, Huaiying Lin and Kashi Revanna
3:25 PM	Controlling contaminant sequences in low microbial biomass microbiome studies	Lisa Karstens
3:50 PM	The microbiome in severe ocular surface diseases	Michael Zilliox, William Gange, John Thompson, Gina Kuffel, Carine Mores, Cara Joyce and Charles Bouchard
4:15 PM	The influence of environmental, dietary, and pharmaceutical agents on the human gut microbiome	Michael Burns
4:40 PM	Dynamic interaction network inference from longitudinal microbiome data	Jose Lugo-Martinez, Daniel Ruiz Perez, Giri Narasimhan and Ziv Bar-Joseph

Varsity Hall I on Tuesday, May 21, 2019

Start Time	**Title**	**Author(s)**
RNA I **Chair: Sarath Chandra Janga**		
10:40 AM	Synthetic biology approaches to study and exploit RNA regulation	Bryan Dickinson
11:20 AM	Deep learning framework for accurate transcriptome-wide identification of Gm RNA modification events at single molecule resolution from direct RNA sequencing data	Sasank Vemuri, Swapna Vidhur, Raja Shekar Varma Kadumuri, Sarath Janga
11:40 AM	RNA editing in neural transcriptomes and antiviral immunity	Helen Piontkivska, Noel-Marie Plonski, Heather Milliken Mercer, Caroline Nitirahardjo
RNA II **Chair: Heidi Dvinge**		
1:30 PM	Algorithmic decision-making in single-cell genomic data analyses	Jun Li
2:10 PM	Evaluation of Computational Methods to Deconvolute Cell Types in Single-Cell Transcriptomics data	Qianhui Huang, Yu Liu, Lana Garmire
RNA III **Chair: Heidi Dvinge**		
3:00 PM	RNA Structure Prediction	David Mathews
3:40 PM	RNA structure elucidation at single molecule resolution using an integrated framework of long read sequencing and machine learning	Swapna Vidhur Daulatabad, Molly Evans, Quoseena Mir, Julius Lucks, Sarath Chandra Janga
4:00 PM	Integrating thermodynamic and sequence contexts improves protein-RNA binding prediction	Yunan Luo, Yufeng Su, Xiaoming Zhao, Yang Liu, Jian Peng
4:20 PM	Integrative analysis of RNA-seq and eCLIP-seq with SURF for elucidating alternative splicing roles of RNA binding proteins	Fan Chen, Sunduz Keles
4:40 PM	A deep learning-based method for the normalization of data from genome-wide CRISPR-Cas9 screens	Henry Ward, Ahm Mahfuzur Rahman, Chad Myers

The Marquee on Wednesday, May 22, 2019

Start Time	Title	Author(s)
9:00 AM	Keynote #5 - Bridging Pre-Clinical Drug Screening with Patient Molecular Profiles for Biomarker Discovery and Drug Repurposing	R. Stephanie Huang Introduction by Russell Schwartz
General Track - Networks II **Chairs: Arjun Krishnan & Jason Shoemaker**		
10:30 AM	Connectivity measures for signaling pathway topologies	Nicholas Franzese, Adam Groce, T. M. Murali and Anna Ritz
11:00 AM	A computational framework for benchmarking human CRISPR screens	Ahm Mahfuzur Rahman, Maximilian Billmann, Michael Costanzo, Matej Usaj, Brenda Andrews, Charles Boone, Jason Moffat and Chad Myers.
11:15 AM	Parameter Selection in Biological Pathway Prediction with Graphlet Based Similarity Score	Chris Magnano and Anthony Gitter
11:30 AM	Rice Genes Prioritization for Cold Tolerance Using Random Walk with Restart on Multiplex Heterogeneous Network	Cagatay Dursun, Naoki Shimoyama, Mary Shimoyama, Michael Schlappi and Serdar Bozdag.
11:45 AM	Network-driven discovery of influenza virus replication host factors	Jason Shoemaker
General Track - Genome Informatics **Chair: Jaclyn Taroni**		
1:30 PM	A tool for automatically identifying and correcting plant breeding location data	Getiria Onsongo, Samantha Fritsche, Thy Nguyen, Jeffery Thompson and Kevin A.T. Silverstein.
1:45 PM	scds: Computational Annotation of Doublets in Single Cell RNA Sequencing Data	Abha Bais and Dennis Kostka.
2:00 PM	Gene Prediction and Genome Functional Annotation of the Almond 'Nonpareil' genome	Wilberforce Zachary Ouma, Tea Meulia, Thomas Gradziel and Jonathan Fresnedo Ramirez.
2:15 PM	Tracking the popularity and outcomes of all bioRxiv preprints	Richard Abdill and Ran Blekhman
3:00 PM	Keynote #6 - Inferring Host-Virus Interactions from Diverse Data Sources	Mark Craven Introduction by Tijana Milenkovic

Varsity Hall I on Wednesday, May 22, 2019

Start Time	Title	Author(s)
General Track - Clinical and Health Informatics I Chair: Serdar Bozdag		
10:30 AM	Autoimmune risk allele-dependent human gene regulation by Epstein-Barr Virus EBNA2	Matthew Weirauch, Xiaoting Chen, Ted Hong, Mario Pujato, Daniel Miller, Sreeja Parameswaran, Omer Donmez, Mariana Saint Just Ribeiro, Carmy Forney, Yongbo Huang, Kenneth Kaufman, Bo Zhao, Iouri Chepelev, John Harley and Leah Kottyan.
10:45 AM	The Clinical Implications of Subclonal Copy Number Alterations in Chronic Lymphocytic Leukemia	Mark Zucker and Kevin Coombes.
11:00 AM	Objective risk stratification of prostate cancer using machine learning and radiomics applied to multiparametric magnetic resonance images	Bino Varghese, Frank Chen, Darryl Hwang, Suzanne Palmer, Andre Luis De Castro Abreu, Osamu Ukimura, Monish Aron, Manju Aron, Inderbir Gill, Vinay Duddalwar and Gaurav Pandey.
11:15 AM	Systematic analysis of genetic interactions in Parkinson’s disease reveals interactions with known risk genes	Wen Wang, Benjamin Vandersluis and Chad Myers.
General Track - Clinical and Health Informatics II Chair: Debbie Chasman		
1:30 PM	An integrative computational modeling approach to identify repurposable metabolic drug targets in CD4+ T cells	Bhanwar Lal Puniya, Bailee Lichter, Robert Moore, Sydney Townsend, Alex Ciurej, Ab Rauf Shah, Matteo Barberis and Tomas Helikar.
1:45 PM	Linear Drug-Target Interaction Model Predicts Effective Drugs and Also Identifies Disease-Related Proteins and Pathways from Phenotypic Screens	Feng Guo
2:00 PM	Using histopathology whole-slide images quantitative features to predict liver cancer survival	Noshad Hosseini, Fadhl M. Alakwaa, Olivier B. Poiron and Lana X. Garmire.
2:15 PM	Machine Learning Classifier for Endometriosis Using Transcriptomics and Methylomics Data	Sadia Akter, Dong Xu, Susan Nagel, John Bromfield, Katherine Pelch, Gilbert Wilshire and Trupti Joshi.

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